

T  
TB 686 630 197 US

JUNE 7, 1995 EXPRESS MAIL # TB686630076U

METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE  
FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION

This is a Continuation-In-Part of Serial No. 08/360,107 filed December 20, 1994, which is a  
5 Continuation-In-Part of Serial No. 08/255,208 filed June 7, 1994, which is a Continuation-In-Part of Serial No. 08/073,028 filed June 7, 1993, each of which is incorporated herein by reference in its entirety. This invention was made with Government  
10 support under Grant No. AI-30411-02 awarded by the National Institutes of Health. The Government has certain rights in the invention.

1. INTRODUCTION

15 The present invention relates, first, to DP178 (SEQ ID NO:1), a peptide corresponding to amino acids 638 to 673 of the HIV-1<sub>LAI</sub> transmembrane protein (TM) gp41, and portions or analogs of DP178 (SEQ ID NO:1), which exhibit anti-membrane fusion capability,  
20 antiviral activity, such as the ability to inhibit HIV transmission to uninfected CD-4<sup>+</sup> cells, or an ability to modulate intracellular processes involving coiled-coil peptide structures. Further, the invention relates to the use of DP178 (SEQ ID NO:1) and DP178  
25 portions and/or analogs as antifusogenic or antiviral compounds or as inhibitors of intracellular events involving coiled-coil peptide structures. The present invention also relates to peptides analogous to DP107 (SEQ ID NO:25), a peptide corresponding to amino acids  
30 558 to 595 of the HIV-1<sub>LAI</sub> transmembrane protein (TM) gp41, having amino acid sequences present in other viruses, such as enveloped viruses, and/or other organisms, and further relates to the uses of such peptides. These peptides exhibit anti-membrane fusion  
35 capability, antiviral activity, or the ability to

modulate intracellular processes involving coiled-coil peptide structures. The present invention additionally relates to methods for identifying compounds that disrupt the interaction between DP178 and DP107, and/or between DP107-like and DP178-like peptides. Further, the invention relates to the use of the peptides of the invention as diagnostic agents. For example, a DP178 peptide may be used as an HIV subtype-specific diagnostic. The invention is demonstrated, first, by way of an Example wherein DP178 (SEQ ID:1), and a peptide whose sequence is homologous to DP178 are each shown to be potent, non-cytotoxic inhibitors of HIV-1 transfer to uninfected CD-4<sup>+</sup> cells. The invention is further demonstrated by Examples wherein peptides having structural and/or amino acid motif similarity to DP107 and DP178 are identified in a variety of viral and nonviral organisms, and in examples wherein a number of such identified peptides derived from several different viral systems are demonstrated to exhibit antiviral activity.

## 2. BACKGROUND OF THE INVENTION

### 2.1 MEMBRANE FUSION EVENTS

Membrane fusion is a ubiquitous cell biological process (for a review, see White, J.M., 1992, Science 258:917-924). Fusion events which mediate cellular housekeeping functions, such as endocytosis, constitutive secretion, and recycling of membrane components, occur continuously in all eukaryotic cells.

Additional fusion events occur in specialized cells. Intracellularly, for example, fusion events are involved in such processes as occur in regulated exocytosis of hormones, enzymes and neurotransmitters.



Intercellularly, such fusion events feature prominently in, for example, sperm-egg fusion and myoblast fusion.

Fusion events are also associated with disease states. For example, fusion events are involved in the formation of giant cells during inflammatory reactions, the entry of all enveloped viruses into cells, and, in the case of human immunodeficiency virus (HIV), for example, are responsible for the virally induced cell-cell fusion which leads to cell death.

## 2.2. THE HUMAN IMMUNODEFICIENCY VIRUS

The human immunodeficiency virus (HIV) has been implicated as the primary cause of the slowly degenerative immune system disease termed acquired immune deficiency syndrome (AIDS) (Barre-Sinoussi, F. et al., 1983, Science 220:868-870; Gallo, R. et al., 1984, Science 224:500-503). There are at least two distinct types of HIV: HIV-1 (Barre-Sinoussi, F. et al., 1983, Science 220:868-870; Gallo R. et al., 1984, Science 224:500-503) and HIV-2 (Clavel, F. et al., 1986, Science 233:343-346; Guyader, M. et al., 1987, Nature 326:662-669). Further, a large amount of genetic heterogeneity exists within populations of each of these types. Infection of human CD-4<sup>+</sup> T-lymphocytes with an HIV virus leads to depletion of the cell type and eventually to opportunistic infections, neurological dysfunctions, neoplastic growth, and ultimately death.

HIV is a member of the lentivirus family of retroviruses (Teich, N. et al., 1984, RNA Tumor Viruses, Weiss, R. et al., eds., CSH-Press, pp. 949-956). Retroviruses are small enveloped viruses that contain a diploid, single-stranded RNA genome, and

replicate via a DNA intermediate produced by a virally-encoded reverse transcriptase, an RNA-dependent DNA polymerase (Varmus, H., 1988, *Science* 240:1427-1439). Other retroviruses include, for example, oncogenic viruses such as human T-cell  
5 leukemia viruses (HTLV-I,-II,-III), and feline leukemia virus.

The HIV viral particle consists of a viral core, composed of capsid proteins, that contains the viral  
10 RNA genome and those enzymes required for early replicative events. Myristylated Gag protein forms an outer viral shell around the viral core, which is, in turn, surrounded by a lipid membrane enveloped derived from the infected cell membrane. The HIV enveloped  
15 surface glycoproteins are synthesized as a single 160 Kd precursor protein which is cleaved by a cellular protease during viral budding into two glycoproteins, gp41 and gp120. gp41 is a transmembrane protein and gp120 is an extracellular protein which remains non-covalently associated with gp41, possibly in a  
20 trimeric or multimeric form (Hammariskjold, M. and Rekosh, D., 1989, *Biochem. Biophys. Acta* 989:269-280).

HIV is targeted to CD-4<sup>+</sup> cells because the CD-4 cell surface protein acts as the cellular receptor for the HIV-1 virus (Dalglish, A. et al., 1984, *Nature* 312:763-767; Klatzmann et al., 1984, *Nature* 312:767-768; Maddon et al., 1986, *Cell* 47:333-348). Viral  
25 entry into cells is dependent upon gp120 binding the cellular CD-4<sup>+</sup> receptor molecules (McDougal, J.S. et al., 1986, *Science* 231:382-385; Maddon, P.J. et al.,  
30 1986, *Cell* 47:333-348) and thus explains HIV's tropism for CD-4<sup>+</sup> cells, while gp41 anchors the enveloped glycoprotein complex in the viral membrane.

35

### 2.3. HIV TREATMENT

HIV infection is pandemic and HIV associated diseases represent a major world health problem. Although considerable effort is being put into the  
5 successful design of effective therapeutics, currently no curative anti-retroviral drugs against AIDS exist. In attempts to develop such drugs, several stages of the HIV life cycle have been considered as targets for therapeutic intervention (Mitsuya, H. et al., 1991,  
10 FASEB J. 5:2369-2381). For example, virally encoded reverse transcriptase has been one focus of drug development. A number of reverse-transcriptase-targeted drugs, including 2',3'-dideoxynucleoside analogs such as AZT, ddI, ddC, and d4T have been  
15 developed which have been shown to be active against HIV (Mitsuya, H. et al., 1991, Science 249:1533-1544). While beneficial, these nucleoside analogs are not curative, probably due to the rapid appearance of drug resistant HIV mutants (Lander, B. et al., 1989,  
20 Science 243:1731-1734). In addition, the drugs often exhibit toxic side effects such as bone marrow suppression, vomiting, and liver function abnormalities.

Attempts are also being made to develop drugs  
25 which can inhibit viral entry into the cell, the earliest stage of HIV infection. Here, the focus has thus far been on CD4, the cell surface receptor for HIV. Recombinant soluble CD4, for example, has been shown to inhibit infection of CD-4<sup>+</sup> T-cells by some  
30 HIV-1 strains (Smith, D.H. et al., 1987, Science 238:1704-1707). Certain primary HIV-1 isolates, however, are relatively less sensitive to inhibition by recombinant CD-4 (Daar, E. et al., 1990, Proc. Natl. Acad. Sci. USA 87:6574-6579). In addition,  
35

recombinant soluble CD-4 clinical trials have produced inconclusive results (Schooley, R. et al., 1990, Ann. Int. Med. 112:247-253; Kahn, J.O. et al., 1990, Ann. Int. Med. 112:254-261; Yarchoan, R. et al., 1989, Proc. Vth Int. Conf. on AIDS, p. 564, MCP 137).

5       The late stages of HIV replication, which involve crucial virus-specific secondary processing of certain viral proteins, have also been suggested as possible anti-HIV drug targets. Late stage processing is dependent on the activity of a viral protease, and  
10       drugs are being developed which inhibit this protease (Erickson, J., 1990, Science 249:527-533). The clinical outcome of these candidate drugs is still in question.

15       Attention is also being given to the development of vaccines for the treatment of HIV infection. The HIV-1 enveloped proteins (gp160, gp120, gp41) have been shown to be the major antigens for anti-HIV antibodies present in AIDS patients (Barin, et al., 1985, Science 228:1094-1096). Thus far, therefore,  
20       these proteins seem to be the most promising candidates to act as antigens for anti-HIV vaccine development. To this end, several groups have begun to use various portions of gp160, gp120, and/or gp41 as immunogenic targets for the host immune system.  
25       See for example, Ivanoff, L. et al., U.S. Pat. No. 5,141,867; Saith, G. et al., WO 92/22,654; Shafferman, A., WO 91/09,872; Formoso, C. et al., WO 90/07,119. Clinical results concerning these candidate vaccines, however, still remain far in the future.

30       Thus, although a great deal of effort is being directed to the design and testing of anti-retroviral drugs, a truly effective, non-toxic treatment is still needed.

35

### 3. SUMMARY OF THE INVENTION

The present invention relates, first, to DP178 (SEQ ID:1), a 36-amino acid synthetic peptide corresponding to amino acids 638 to 673 of the transmembrane protein (TM) gp41 from the HIV-1 isolate LAI (HIV-1<sub>LAI</sub>), which exhibits potent anti-HIV-1 activity. As evidenced by the Example presented below, in Section 6, the DP178 (SEQ ID:1) antiviral activity is so high that, on a weight basis, no other known anti-HIV agent is effective at concentrations as low as those at which DP178 (SEQ ID:1) exhibits its inhibitory effects.

The invention further relates to those portions and analogs of DP178 which also show such antiviral activity, and/or show anti-membrane fusion capability, or an ability to modulate intracellular processes involving coiled-coil peptide structures. The term "DP178 analog" refers to a peptide which contains an amino acid sequence corresponding to the DP178 peptide sequence present within the gp41 protein of HIV-1<sub>LAI</sub>, but found in viruses and/or organisms other than HIV-1<sub>LAI</sub>. Such DP178 analog peptides may, therefore, correspond to DP178-like amino acid sequences present in other viruses, such as, for example, enveloped viruses, such as retroviruses other than HIV-1<sub>LAI</sub>, as well as non-enveloped viruses. Further, such analogous DP178 peptides may also correspond to DP178-like amino acid sequences present in nonviral organisms.

The invention further relates to peptides DP107 (SEQ ID NO:25) analogs. DP107 is a peptide corresponding to amino acids 558-595 of the HIV-1<sub>LAI</sub> transmembrane protein (TM) gp41. The term "DP107 analog" as used herein refers to a peptide which contains an amino acid sequence corresponding to the

DP107 peptide sequence present within the gp41 protein of HIV-1<sub>LAI</sub>, but found in viruses and organisms other than HIV-1<sub>LAI</sub>. Such DP107 analog peptides may, therefore, correspond to DP107-like amino acid sequences present in other viruses, such as, for example, enveloped viruses, such as retroviruses other than HIV-1<sub>LAI</sub>, as well as non-enveloped viruses. Further, such DP107 analog peptides may also correspond to DP107-like amino acid sequences present in nonviral organisms.

Further, the peptides of the invention include DP107 analog and DP178 analog peptides having amino acid sequences recognized or identified by the 107x178x4, ALLMOTI5 and/or PLZIP search motifs described herein.

The peptides of the invention may, for example, exhibit antifusogenic activity, antiviral activity, and/or may have the ability to modulate intracellular processes which involve coiled-coil peptide structures. With respect to the antiviral activity of the peptides of the invention, such an antiviral activity includes, but is not limited to the inhibition of HIV transmission to uninfected CD-4<sup>+</sup> cells. Additionally, the antifusogenic capability, antiviral activity or intracellular modulatory activity of the peptides of the invention merely requires the presence of the peptides of the invention, and, specifically, does not require the stimulation of a host immune response directed against such peptides.

The peptides of the invention may be used, for example, as inhibitors of membrane fusion-associated events, such as, for example, the inhibition of human and non-human retroviral, especially HIV, transmission to uninfected cells. It is further contemplated that

the peptides of the invention may be used as modulators of intracellular events involving coiled-coil peptide structures.

The peptides of the invention may, alternatively, be used to identify compounds which may themselves exhibit antifusogenic, antiviral, or intracellular modulatory activity. Additional uses include, for example, the use of the peptides of the invention as organism or viral type and/or subtype-specific diagnostic tools.

The terms "antifusogenic" and "anti-membrane fusion", as used herein, refer to an agent's ability to inhibit or reduce the level of membrane fusion events between two or more moieties relative to the level of membrane fusion which occurs between said moieties in the absence of the peptide. The moieties may be, for example, cell membranes or viral structures, such as viral envelopes or pili. The term "antiviral", as used herein, refers to the compound's ability to inhibit viral infection of cells, via, for example, cell-cell fusion or free virus infection. Such infection may involve membrane fusion, as occurs in the case of enveloped viruses, or some other fusion event involving a viral structure and a cellular structure (e.g., such as the fusion of a viral pilus and bacterial membrane during bacterial conjugation).

It is also contemplated that the peptides of the invention may exhibit the ability to modulate intracellular events involving coiled-coil peptide structures. "Modulate", as used herein, refers to a stimulatory or inhibitory effect on the intracellular process of interest relative to the level or activity of such a process in the absence of a peptide of the invention.

Embodiments of the invention are demonstrated below wherein an extremely low concentration of DP178 (SEQ ID:1), and very low concentrations of a DP178 homolog (SEQ ID:3) are shown to be potent inhibitors of HIV-1 mediated CD-4<sup>+</sup> cell-cell fusion (i.e.,  
5 syncytial formation) and infection of CD-4<sup>+</sup> cells by cell-free virus. Further, it is shown that DP178 (SEQ ID:1) is not toxic to cells, even at concentrations 3 logs higher than the inhibitory DP-178 (SEQ ID:1) concentration.

10 The present invention is based, in part, on the surprising discovery that the DP107 and DP178 domains of the HIV gp41 protein non-covalently complex with each other, and that their interaction is required for the normal infectivity of the virus. This discovery  
15 is described in the Example presented, below, in Section 8. The invention, therefore, further relates to methods for identifying antifusogenic, including antiviral, compounds that disrupt the interaction between DP107 and DP178, and/or between DP107-like and  
20 DP178-like peptides.

Additional embodiments of the invention (specifically, the Examples presents in Sections 9-16 and 19-25, below) are demonstrated, below, wherein  
25 peptides, from a variety of viral and nonviral sources, having structural and/or amino acid motif similarity to DP107 and DP178 are identified, and search motifs for their identification are described. Further, Examples (in Sections 17, 18, 25-29) are  
30 presented wherein a number of the peptides of the invention are demonstrated exhibit substantial antiviral activity or activity predictive of antiviral activity.

35



### 3.1. DEFINITIONS

Peptides are defined herein as organic compounds comprising two or more amino acids covalently joined by peptide bonds. Peptides may be referred to with  
5 respect to the number of constituent amino acids, i.e., a dipeptide contains two amino acid residues, a tripeptide contains three, etc. Peptides containing ten or fewer amino acids may be referred to as oligopeptides, while those with more than ten amino  
10 acid residues are polypeptides. Such peptides may also include any of the modifications and additional amino and carboxy groups as are described herein.

Peptide sequences defined herein are represented by one-letter symbols for amino acid residues as  
15 follows:

A (alanine)  
R (arginine)  
N (asparagine)  
D (aspartic acid)  
C (cysteine)  
20 Q (glutamine)  
E (glutamic acid)  
G (glycine)  
H (histidine)  
I (isoleucine)  
L (leucine)  
K (lysine)  
M (methionine)  
25 F (phenylalanine)  
P (proline)  
S (serine)  
T (threonine)  
W (tryptophan)  
Y (tyrosine)  
V (valine)

30

35

#### 4. BRIEF DESCRIPTION OF THE FIGURES

FIG. 1. Amino acid sequence of DP178 (SEQ ID:1) derived from HIV<sub>LAI</sub>; DP178 homologs derived from HIV-1<sub>SP2</sub> (DP-185; SEQ ID:3), HIV-1<sub>RF</sub> (SEQ ID:4), and HIV-1<sub>MN</sub> (SEQ ID:5); DP178 homologs derived from amino acid sequences of two prototypic HIV-2 isolates, namely, HIV-2<sub>rod</sub> (SEQ ID:6) and HIV-2<sub>NH2</sub> (SEQ ID:7); control peptides: DP-180 (SEQ ID:2), a peptide incorporating the amino acid residues of DP178 in a scrambled sequence; DP-118 (SEQ ID:10) unrelated to DP178, which inhibits HIV-1 cell free virus infection; DP-125 (SEQ ID:8), unrelated to DP178, also inhibits HIV-1 cell free virus infection; DP-116 (SEQ ID:9), unrelated to DP178, is negative for inhibition of HIV-1 infection when tested using a cell-free virus infection assay. Throughout the figures, the one letter amino acid code is used.

FIG. 2. Inhibition of HIV-1 cell-free virus infection by synthetic peptides. IC<sub>50</sub> refers to the concentration of peptide that inhibits RT production from infected cells by 50% compared to the untreated control. Control: the level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

FIG. 3. Inhibition of HIV-1 and HIV-2 cell-free virus infection by the synthetic peptide DP178 (SEQ ID:1). IC<sub>50</sub>: concentration of peptide that inhibits RT production by 50% compared to the untreated control. Control: Level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

FIG. 4A-4B. Fusion Inhibition Assays. FIG 4A: DP178 (SEQ ID:1) inhibition of HIV-1 prototypic isolate-mediated syncytial formation; data represents the number of virus-induced syncytial per cell. FIG.

4B: DP-180 (SEQ ID:2) represents a scrambled control peptide; DP-185 (SEQ ID:3) represents a DP178 homolog derived from HIV-1<sub>SP2</sub> isolate; Control, refers to the number of syncytial produced in the absence of peptide.

5       FIG. 5. Fusion inhibition assay: HIV-1 vs. HIV-2. Data represents the number of virus-induced syncytial per well. ND: not done.

10       FIG. 6. Cytotoxicity study of DP178 (SEQ ID:1) and DP-116 (SEQ ID:9) on CEM cells. Cell proliferation data is shown.

15       FIG. 7. Schematic representation of HIV-gp41 and maltose binding protein (MBP)-gp41 fusion proteins. DP107 and DP178 are synthetic peptides based on the two putative helices of gp41. The letter P in the DP107 boxes denotes an Ile to Pro mutation at amino acid number 578. Amino acid residues are numbered according to Meyers et al., "Human Retroviruses and AIDS", 1991, Theoret. Biol. and Biophys. Group, Los Alamos Natl. Lab., Los Alamos, NM. 20 The proteins are more fully described, below, in Section 8.1.1.

      FIG. 8. A point mutation alters the conformation and anti-HIV activity of M41.

25       FIG. 9. Abrogation of DP178 anti-HIV activity. Cell fusion assays were carried out in the presence of 10 nM DP178 and various concentrations of M41Δ178 or M41PA178.

30       FIG. 10. Binding of DP178 to leucine zipper of gp41 analyzed by FAb-D ELISA.

      FIG. 11A-B. Models for a structural transition in the HIV-1 TM protein. Two models are proposed which indicate a structural transition from a native oligomer to a fusogenic state following a trigger event (possibly gp120 binding to CD4). Common 35

features of both models include (1) the native state is held together by noncovalent protein-protein interactions to form the heterodimer of gp120/41 and other interactions, principally through gp41 interactive sites, to form homo-oligomers on the virus surface of the gp120/41 complexes; (2) shielding of the hydrophobic fusogenic peptide at the N-terminus (F) in the native state; and (3) the leucine zipper domain (DP107) exists as a homo-oligomer coiled coil only in the fusogenic state. The major differences in the two models include the structural state (native or fusogenic) in which the DP107 and DP178 domains are complexed to each other. In the first model (FIG. 11A) this interaction occurs in the native state and in the second (FIG. 11B), it occurs during the fusogenic state. When triggered, the fusion complex in the model depicted in (A) is generated through formation of coiled-coil interactions in homologous DP107 domains resulting in an extended  $\alpha$ -helix. This conformational change positions the fusion peptide for interaction with the cell membrane. In the second model (FIG. 11B), the fusogenic complex is stabilized by the association of the DP178 domain with the DP107 coiled-coil.

FIG. 12. Motif design using heptad repeat positioning of amino acids of known coiled-coils.

FIG. 13. Motif design using proposed heptad repeat positioning of amino acids of DP107 and DP178.

FIG. 14. Hybrid motif design crossing GCN4 and DP107.

FIG. 15. Hybrid motif design crossing GCN4 and DP178.

FIG. 16. Hybrid motif design 107x178x4, crossing DP107 and DP178. This motif was found to be

the most consistent at identifying relevant DP107-like and DP178-like peptide regions.

FIG. 17. Hybrid motif design crossing GCN4, DP107, and DP178.

5       FIG. 18. Hybrid motif design ALLMOTI5 crossing GCN4, DP107, DP178, c-Fos c-Jun, c-Myc, and Flu Loop 36.

FIG. 19. PLZIP motifs designed to identify N-terminal proline-leucine zipper motifs.

10       FIG. 20. Search results for HIV-1 (BRU isolate) enveloped protein gp41. Sequence search motif designations: Spades (♠): 107x178x4; Hearts (♥) ALLMOTI5; Clubs (♣): PLZIP; Diamonds (♦): transmembrane region (the putative transmembrane domains were identified using a PC/Gene program  
15       designed to search for such peptide regions). Asterisk (\*): Lupas method. The amino acid sequences identified by each motif are bracketed by the respective characters. Representative sequences  
20       chosen based on 107x178x4 searches are underlined and in bold. DP107 and DP178 sequences are marked, and additionally double-underlined and italicized.

FIG. 21. Search results for human respiratory syncytial virus (RSV) strain A2 fusion glycoprotein F1. Sequence search motif designations  
25       are as in FIG. 20.

FIG. 22. Search results for simian immunodeficiency virus (SIV) enveloped protein gp41 (AGM3 isolate). Sequence search motif designations  
30       are as in FIG. 20.

FIG. 23. Search results for canine distemper virus (strain Onderstepoort) fusion glycoprotein 1. Sequence search motif designations  
are as in FIG. 20.

35

FIG. 24. Search results for newcastle disease virus (strain Australia-Victoria/32) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

5 FIG. 25. Search results for human parainfluenza 3 virus (strain NIH 47885) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

10 FIG. 26. Search results for influenza A virus (strain A/AICHI/2/68) hemagglutinin precursor HA2. Sequence search designations are as in FIG. 20.

FIG. 27A-D. Respiratory Syncytial Virus (RSV) peptide antiviral and circular dichroism data. FIG. 27A-B: Peptides derived from the F2 DP178/DP107-like region. Antiviral and CD data. FIG. 27C-D: 15 Peptides derived from the F1 DP107-like region. Peptide and CD data.

Antiviral activity (AV) is represented by the following qualitative symbols:

20 "-", negative antiviral activity;  
"+/-", antiviral activity at greater than 100 $\mu$ g/ml;  
"+", antiviral activity at between 50-100 $\mu$ g/ml;  
"++", antiviral activity at between 20-50 $\mu$ g/ml;  
25 "+++", antiviral activity at between 1-20 $\mu$ g/ml;  
"++++", antiviral activity at <1 $\mu$ g/ml.

CD data, referring to the level of helicity is represented by the following qualitative symbol:

30 "-", no helicity;  
"+", 25-50% helicity;  
"++", 50-75% helicity;  
"+++" 75-100% helicity.

35 IC<sub>50</sub> refers to the concentration of peptide necessary to produce only 50% of the number of syncytial relative to infected control cultures

containing no peptide.  $IC_{50}$  values were obtained using purified peptides only.

5       FIG. 28A-B. Respiratory Syncytial Virus (RSV) DP178-like region (F1) peptide antiviral and CD data. Antiviral symbols, CD symbols, and  $IC_{50}$  are as in FIG. 27A-D.  $IC_{50}$  values were obtained using purified peptides only.

10       FIG. 29A-B. Peptides derived from the HPIV3 F1 DP107-like region. Peptide antiviral and CD data. Antiviral symbols, CD symbols, and  $IC_{50}$  are as in FIG. 27A-D. Purified peptides were used to obtain  $IC_{50}$  values, except where the values are marked by an asterisk (\*), in which cases, the  $IC_{50}$  values were obtained using a crude peptide preparation.

15       FIG. 29C. HPIV3 peptide T-184 CD spectrum at 1°C in 0.1M NaCl 10mM  $KPO_4$ , pH 7.0. The data demonstrates the peptide's helical secondary structure ( $\theta_{222/208}=1.2$ ) over a wide range of concentrations (100-1500 $\mu$ M). This evidence is consistent with the peptide forming a helical coiled-coil structure.

20       FIG. 30A-B. Peptides derived from the HPIV3 F1 DP178-like region. Peptide antiviral and CD data. Antiviral symbols, CD symbols, and  $IC_{50}$  are as in FIG. 27A-D. Purified peptides were used to obtain  $IC_{50}$  values, except where the values are marked by an asterisk (\*), in which cases, the  $IC_{50}$  values were obtained using a crude peptide preparation.

25       FIG. 31. Motif search results for simian immunodeficiency virus (SIV) isolate MM251, enveloped polyprotein gp41. Sequence search designations are as in FIG. 20.

30       FIG. 32. Motif search results for Epstein-Barr Virus (Strain B95-8), glycoprotein gp110 precursor (designated gp115). BALF4. Sequence search designations are as in FIG. 20.

FIG. 33. Motif search results for Epstein-Barr Virus (Strain B95-8), BZLF1 trans-activator protein (designated EB1 or Zebra). Sequence search designations are as in FIG. 20. Additionally, "e" refers to a well known DNA binding domain and "+" refers to a well known dimerization domain, as defined by Flemington and Speck (Flemington, E. and Speck, S.H., 1990, Proc. Natl. Acad. Sci. USA 87:9459-9463).

FIG. 34. Motif search results for measles virus (strain Edmonston), fusion glycoprotein F1. Sequence search designations are as in FIG. 20.

FIG. 35. Motif search results for Hepatitis B Virus (Subtype AYW), major surface antigen precursor S. Sequence search designations are as in FIG. 20.

FIG. 36. Motif search results for simian Mason-Pfizer monkey virus, enveloped (TM) protein gp20. Sequence search designations are as in FIG. 20.

FIG. 37. Motif search results for *Pseudomonas aeruginosa*, fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

FIG. 38. Motif search results for *Neisseria gonorrhoeae* fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

FIG. 39. Motif search results for *Hemophilus influenzae* fimbrial protein. Sequence search designations are as in FIG. 20.

FIG. 40. Motif search results for *Staphylococcus aureus*, toxic shock syndrome toxin-1. Sequence search designations are as in FIG. 20.

FIG. 41. Motif search results for *Staphylococcus aureus* enterotoxin Type E. Sequence search designations are as in FIG. 20.

FIG. 42. Motif search results for *Staphylococcus aureus* enterotoxin A. Sequence search designations are as in FIG. 20.



FIG. 43. Motif search results for Escherichia coli, heat labile enterotoxin A. Sequence search designations are as in FIG. 20.

FIG. 44. Motif search results for human c-fos proto-oncoprotein. Sequence search designations  
5 are as in FIG. 20.

FIG. 45. Motif search results for human lupus KU autoantigen protein P70. Sequence search designations are as in FIG. 20.

FIG. 46. Motif search results for human  
10 zinc finger protein 10. Sequence search designations are as in FIG. 20.

FIG. 47. Measles virus (MeV) fusion protein DP178-like region antiviral and CD data. Antiviral symbols, CD symbols, and  $IC_{50}$  are as in FIG. 27A-D.  
15  $IC_{50}$  values were obtained using purified peptides.

FIG. 48. Simian immunodeficiency virus (SIV) TM (fusion) protein DP178-like region antiviral data. Antiviral symbols are as in FIG. 27A-D "NT", not tested.  
20

FIG. 49A-C. DP178-derived peptide antiviral data. The peptides listed herein were derived from the region surrounding the HIV-1 BRU isolate DP178 region (e.g., gp41 amino acid residues 615-717).

In instances where peptides contained DP178 point  
25 mutations, the mutated amino acid residues are shown with a shaded background. In instances in which the test peptide has had an amino and/or carboxy-terminal group added or removed (apart from the standard amido- and acetyl- blocking groups found on such peptides),  
30 such modifications are indicated. FIG. 49A: The column to the immediate right of the name of the test peptide indicates the size of the test peptide and points out whether the peptide is derived from a one  
35 amino acid peptide "walk" across the DP178 region.

The next column to the right indicates whether the test peptide contains a point mutation, while the column to its right indicates whether certain amino acid residues have been added to or removed from the DP178-derived amino acid sequence. FIG 49B: The  
5 column to the immediate right of the test peptide name indicates whether the peptide represents a DP178 truncation, the next column to the right points out whether the peptide contains a point mutation, and the  
10 column to its right indicates whether the peptide contains amino acids which have been added to or removed from the DP178 sequence itself. FIG. 49C: The column to the immediate right of the test peptide name indicates whether the test peptide contains a  
15 point mutation, while the column to its right indicates whether amino acid residues have been added to or removed from the DP178 sequence itself.  $IC_{50}$  is as defined in FIG. 27A-D, and  $IC_{50}$  values were obtained using purified peptides except where marked with an  
20 asterisk (\*), in which case the  $IC_{50}$  was obtained using a crude peptide preparation.

FIG. 50. DP107 and DP107 gp41 region truncated peptide antiviral data.  $IC_{50}$  as defined in FIG. 27A-D, and  $IC_{50}$  values were obtained using  
25 purified peptides except where marked with an asterisk (\*), in which case the  $IC_{50}$  was obtained using a crude peptide preparation.

FIG. 51A-B. Epstein-Barr virus Strain B95-8 BZLF1 DP178/DP107 analog region peptide walks and electrophoretic mobility shift assay results. The  
30 peptides (T-423 to T-446, FIG. 51A; T-447 to T-461, FIG. 51B) represent one amino acid residue "walks" through the EBV Zebra protein region from amino acid residue 173 to 246.

35

The amino acid residue within this region which corresponds to the first amino acid residue of each peptide is listed to the left of each peptide, while the amino acid residue within this region which corresponds to the last amino acid residue of each peptide is listed to the right of each peptide. The length of each test peptide is listed at the far right of each line, under the heading "Res".

"ACT" refers to a test peptide's ability to inhibit Zebra binding to its response element. "+" refers to a visible, but incomplete, abrogation of the response element/Zebra homodimer complex; "+++" refers to a complete abrogation of the complex; and "-" represents a lack of complex disruption.

FIG. 52A-B. Hepatitis B virus subtype AYW major surface antigen precursor S protein DP178/DP107 analog region and peptide walks. 52A depicts Domain I (S protein amino acid residues 174-220), which contains a potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain I. 52B depicts Domain II (S protein amino acid residues 233-291), which contains a second potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain II.

##### 5. DETAILED DESCRIPTION OF THE INVENTION

Described herein are peptides which may exhibit antifusogenic activity, antiviral capability, and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. The peptides described include, first, DP178 (SEQ ID NO:1), a gp41-derived 36 amino acid peptide and fragments and analogs of DP178.

In addition, the peptides of the invention described herein include peptides which are DP107 analogs. DP107 (SEQ ID NO:25) is a 38 amino acid peptide corresponding to residues 558 to 595 of the HIV-1<sub>LAI</sub> transmembrane (TM) gp41 protein. Such DP107 analogs may exhibit antifusogenic capability, antiviral activity or an ability to modulate intracellular processes involving coiled-coil structures.

Further, peptides of the invention include DP107 and DP178 are described herein having amino acid sequences recognized by the 107x178x4, ALLMOTI5, and PLZIP search motifs. Such motifs are also discussed.

Also described here are antifusogenic, antiviral, intracellular modulatory, and diagnostic uses of the peptides of the invention. Further, procedures are described for the use of the peptides of the invention for the identification of compounds exhibiting antifusogenic, antiviral or intracellular modulatory activity.

While not limited to any theory of operation, the following model is proposed to explain the potent anti-HIV activity of DP178, based, in part, on the experiments described in the Examples, *infra*. In the HIV protein, gp41, DP178 corresponds to a putative  $\alpha$ -helix region located in the C-terminal end of the gp41 ectodomain, and appears to associate with a distal site on gp41 whose interactive structure is influenced by the leucine zipper motif, a coiled-coil structure, referred to as DP107. The association of these two domains may reflect a molecular linkage or "molecular clasp" intimately involved in the fusion process. It is of interest that mutations in the C-terminal  $\alpha$ -helix motif of gp41 (*i.e.*, the D178 domain) tend to enhance the fusion ability of gp41, whereas mutations

in the leucine zipper region (i.e., the DP107 domain) decrease or abolish the fusion ability of the viral protein. It may be that the leucine zipper motif is involved in membrane fusion while the C-terminal  $\alpha$ -helix motif serves as a molecular safety to regulate the availability of the leucine zipper during virus-induced membrane fusion.

On the basis of the foregoing, two models are proposed of gp41-mediated membrane fusion which are schematically shown in FIG. 11A-B. The reason for proposing two models is that the temporal nature of the interaction between the regions defined by DP107 and DP178 cannot, as yet, be pinpointed. Each model envisions two conformations for gp41 - one in a "native" state as it might be found on a resting virion. The other in a "fusogenic" state to reflect conformational changes triggered following binding of gp120 to CD4 and just prior to fusion with the target cell membrane. The strong binding affinity between gp120 and CD4 may actually represent the trigger for the fusion process obviating the need for a pH change such as occurs for viruses that fuse within intracellular vesicles. The two major features of both models are: (1) the leucine zipper sequences (DP107) in each chain of oligomeric enveloped are held apart in the native state and are only allowed access to one another in the fusogenic state so as to form the extremely stable coiled-coils, and (2) association of the DP178 and DP107 sites as they exist in gp41 occur either in the native or fusogenic state. FIG. 11A depicts DP178/DP107 interaction in the native state as a molecular clasp. On the other hand, if one assumes that the most stable form of the enveloped occurs in the fusogenic state, the model in FIG. 11B can be considered.

When synthesized as peptides, both DP107 and DP178 are potent inhibitors of HIV infection and fusion, probably by virtue of their ability to form complexes with viral gp41 and interfere with its fusogenic process; e.g., during the structural transition of the viral protein from the native structure to the fusogenic state, the DP178 and DP107 peptides may gain access to their respective binding sites on the viral gp41, and exert a disruptive influence. DP107 peptides which demonstrate anti-HIV activity are described in Applicants' co-pending application Serial No. 08/264,531, filed June 23, 1994, which is incorporated by reference herein in its entirety.

As shown in the Examples, infra, a truncated recombinant gp41 protein corresponding to the ectodomain of gp41 containing both DP107 and DP178 domains (excluding the fusion peptide, transmembrane region and cytoplasmic domain of gp41) did not inhibit HIV-1 induced fusion. However, when a single mutation was introduced to disrupt the coiled-coil structure of the DP107 domain -- a mutation which results in a total loss of biological activity of DP107 peptides -- the inactive recombinant protein was transformed to an active inhibitor of HIV-1 induced fusion. This transformation may result from liberation of the potent DP178 domain from a molecular clasp with the leucine zipper, DP107 domain.

For clarity of discussion, the invention will be described primarily for DP178 peptide inhibitors of HIV. However, the principles may be analogously applied to other viruses, both enveloped and nonenveloped, and to other non-viral organisms.

#### 5.1. DP178 AND DP178-LIKE PEPTIDES

The DP178 peptide (SEQ ID:1) of the invention corresponds to amino acid residues 638 to 673 of the transmembrane protein gp41 from the HIV-1<sub>LAI</sub> isolate, and has the 36 amino acid sequence (reading from amino to carboxy terminus):

NH<sub>2</sub>-YTSLIHSLIEESQNQQEKNEQEELLELDKWASLWNWF-COOH (SEQ ID:1)

In addition to the full-length DP178 (SEQ ID:1) 36-mer, the peptides of the invention may include truncations of the DP178 (SEQ ID:1) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. Truncations of DP178 (SEQ ID:1) peptides may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide), as shown in Tables I and IA, below. Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group (-NH<sub>2</sub>) and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

TABLE I  
DP178 (SEQ ID:1) CARBOXY TRUNCATIONS

X-YTS-Z  
 X-YTSL-Z  
 X-YTSLI-Z  
 X-YTSLIH-Z  
 5 X-YTSLIHS-Z  
 X-YTSLIHSL-Z  
 X-YTSLIHSLI-Z  
 X-YTSLIHSLIE-Z  
 X-YTSLIHSLIEE-Z  
 X-YTSLIHSLIEES-Z  
 X-YTSLIHSLIEESQ-Z  
 10 X-YTSLIHSLIEESQN-Z  
 X-YTSLIHSLIEESQNNQ-Z  
 X-YTSLIHSLIEESQNNQQ-Z  
 X-YTSLIHSLIEESQNNQQE-Z  
 X-YTSLIHSLIEESQNNQQEK-Z  
 X-YTSLIHSLIEESQNNQQEKN-Z  
 X-YTSLIHSLIEESQNNQQEKNE-Z  
 X-YTSLIHSLIEESQNNQQEKNEQ-Z  
 15 X-YTSLIHSLIEESQNNQQEKNEQE-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEEL-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELL-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLE-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLEL-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLELD-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDK-Z  
 20 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKW-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWA-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWAS-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWASL-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWASLW-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWASLWN-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWASLWNW-Z  
 25 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWASLWNWF-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group,  
 including but not limited to carbobenzoxyl, dansyl, or  
 30 T-butyloxycarbonyl; an acetyl group; a 9-  
 fluorenylmethoxy-carbonyl (Fmoc) group; a  
 macromolecular carrier group including but not limited  
 to lipid-fatty acid conjugates, polyethylene glycol,  
 or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a  
 T-butyloxycarbonyl group; a macromolecular carrier  
 35 group including but not limited to lipid-fatty acid  
 conjugates, polyethylene glycol, or carbohydrates.



TABLE IA  
DP178 (SEQ ID:1) AMINO TRUNCATIONS

	X-NWF-Z
	X-WNWF-Z
	X-LWNWF-Z
5	X-SLWNWF-Z
	X-ASLWNWF-Z
	X-WASLWNWF-Z
	X-KWASLWNWF-Z
	X-DKWASLWNWF-Z
	X-LDKWASLWNWF-Z
	X-ELDKWASLWNWF-Z
10	X-LELDKWASLWNWF-Z
	X-LLELDKWASLWNWF-Z
	X-ELLELDKWASLWNWF-Z
	X-QELLELDKWASLWNWF-Z
	X-EQELLELDKWASLWNWF-Z
	X-NEQELLELDKWASLWNWF-Z
	X-KNEQELLELDKWASLWNWF-Z
	X-EKNEQELLELDKWASLWNWF-Z
15	X-QEKNEQELLELDKWASLWNWF-Z
	X-QQEKNEQELLELDKWASLWNWF-Z
	X-NQQEKNEQELLELDKWASLWNWF-Z
	X-QNQQEKNEQELLELDKWASLWNWF-Z
	X-SQNQQEKNEQELLELDKWASLWNWF-Z
	X-ESQNQQEKNEQELLELDKWASLWNWF-Z
	X-EESQNQQEKNEQELLELDKWASLWNWF-Z
	X-IEESQNQQEKNEQELLELDKWASLWNWF-Z
20	X-LIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-SLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-HSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-IHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-LIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-SLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-TSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
25	X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

The peptides of the invention also include DP178-like peptides. "DP178-like", as used herein, refers, first, to DP178 and DP178 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-178-like" refers to peptide sequences identified or recognized by the ALLMOTI5, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP178. The DP178-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP178-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP178-corresponding regions of HIV-1 and HIV-2. The amino acid conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP178 peptides of the invention. Utilizing the DP178 and DP178 analog sequences described herein, the skilled artisan can readily compile DP178 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids of similar charge, size, and/or

hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids possessing  
5 dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. The  
10 insertions may be made at the carboxy or amino terminal end of the DP178 or DP178 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that  
15 insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP178 (SEQ.ID:1) or DP178  
20 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to  
25 modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein  
30 regions either amino to or carboxy to the actual DP178 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP178  
35 region of the gp41 protein.

Deletions of DP178 (SEQ ID:1) or DP178 truncations are also within the scope of the invention. Such deletions consist of the removal of one or more amino acids from the DP178 or DP178-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP178 (SEQ.ID:1) or DP178 truncations, as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTIS or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are further described, below, in Section 5.3.

#### 5.2. DP107 AND DP107-LIKE PEPTIDES

Further, the peptides of the invention include peptides having amino acid sequences corresponding to DP107 analogs. DP107 is a 38 amino acid peptide which exhibits potent antiviral activity, and corresponds to residues 558 to 595 of HIV-1<sub>LAI</sub> transmembrane (TM) gp41 protein, as shown here:

NH<sub>2</sub>-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-COOH  
(SEQ ID:25)

In addition to the full-length DP107 (SEQ ID:25) 38-mer, the peptides of the invention may include truncations of the DP107 (SEQ ID:25) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes

involving coiled-coil peptide structures. Truncations of DP107 (SEQ ID:25) peptides may comprise peptides of between 3 and 38 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 38-mer polypeptide), as shown in Tables II and IIA, below.

5 Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group ( $-NH_2$ ) and "Z" may represent a carboxyl ( $-COOH$ ) group. Alternatively, "X" may represent a hydrophobic group, including but not

10 limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or

15 peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred

20 "X" or "Z" macromolecular group is a peptide group.

25

30

35

TABLE II  
DP107 (SEQ ID:25) CARBOXY TRUNCATIONS

```

X-NNL-Z
X-NNLL-Z
X-NNLLR-Z
5 X-NNLLRA-Z
X-NNLLRAI-Z
X-NNLLRAIE-Z
X-NNLLRAIEA-Z
X-NNLLRAIEAQ-Z
X-NNLLRAIEAQQ-Z
X-NNLLRAIEAQQH-Z
10 X-NNLLRAIEAQQHL-Z
X-NNLLRAIEAQQHLL-Z
X-NNLLRAIEAQQHLLQ-Z
X-NNLLRAIEAQQHLLQL-Z
X-NNLLRAIEAQQHLLQLT-Z
X-NNLLRAIEAQQHLLQLTV-Z
X-NNLLRAIEAQQHLLQLTVW-Z
X-NNLLRAIEAQQHLLQLTVWQ-Z
15 X-NNLLRAIEAQQHLLQLTVWQI-Z
X-NNLLRAIEAQQHLLQLTVWQIK-Z
X-NNLLRAIEAQQHLLQLTVWQIKQ-Z
X-NNLLRAIEAQQHLLQLTVWQIKQL-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQ-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQA-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQAR-Z
20 X-NNLLRAIEAQQHLLQLTVWQIKQLQARI-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQARIL-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQARILA-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAV-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVE-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVER-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERY-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYL-Z
25 X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLK-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKD-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-Z

```

The one letter amino acid code is used.

Additionally,

30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IIA  
DP178 (SEQ ID:25) AMINO TRUNCATIONS

	X-KDQ-	Z
	X-LKDQ-	Z
5	X-YLKDQ-	Z
	X-RYLKDQ-	Z
	X-ERYLKDQ-	Z
	X-VERYLKDQ-	Z
	X-AVERYLKDQ-	Z
	X-LAVERYLKDQ-	Z
	X-ILAVERYLKDQ-	Z
	X-RILAVERYLKDQ-	Z
10	X-ARILAVERYLKDQ-	Z
	X-QARILAVERYLKDQ-	Z
	X-LQARILAVERYLKDQ-	Z
	X-QLQARILAVERYLKDQ-	Z
	X-KQLQARILAVERYLKDQ-	Z
	X-IKQLQARILAVERYLKDQ-	Z
	X-QIKQLQARILAVERYLKDQ-	Z
15	X-WQIKQLQARILAVERYLKDQ-	Z
	X-VWQIKQLQARILAVERYLKDQ-	Z
	X-TVWQIKQLQARILAVERYLKDQ-	Z
	X-LTVWQIKQLQARILAVERYLKDQ-	Z
	X-QLTVWQIKQLQARILAVERYLKDQ-	Z
	X-LQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-LLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-HLLQLTVWQIKQLQARILAVERYLKDQ-	Z
20	X-QHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-QQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-AQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-EAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-IEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-AIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-RAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-LRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
25	X-LLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-NLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z

The one letter amino acid code is used.

Additionally,

30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

The peptides of the invention also include DP107-like peptides. "DP107-like", as used herein, refers, first, to DP107 and DP107 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-107-like" refers to peptide sequences identified or recognized by the ALLMOTI5, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP107. The DP107-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP107-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP107-corresponding regions of HIV-1 and HIV-2. The amino acid conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP107 peptides of the invention. Utilizing the DP107 and DP107 analog sequences described herein, the skilled artisan can readily compile DP107 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids of similar charge, size, and/or



hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids possessing  
5 dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. The  
10 insertions may be made at the carboxy or amino terminal end of the DP107 or DP107 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that  
15 insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP107 (SEQ.ID:25) or DP107  
20 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to  
25 modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein  
30 regions either amino to or carboxy to the actual DP107 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP107  
35 region of the gp41 protein.

Deletions of DP107 (SEQ ID:25) or DP178 truncations are also within the scope of the invention. Such deletions consist of the removal of one or more amino acids from the DP107 or DP107-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP107 (SEQ.ID:25) or DP107 truncations, as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

DP107 and DP107 truncations are more fully described in Applicants' co-pending U.S. Patent Application Ser. No. 08/374,666, filed January 27, 1995, and which is incorporated herein by reference in its entirety. DP107 analogs are further described, below, in Section 5.3.

### 5.3. DP107 and DP178 ANALOGS

Peptides corresponding to analogs of the DP178, DP178 truncations, DP107 and DP107 truncation sequences of the invention, described, above, in Sections 5.1 and 5.2 may be found in other viruses, including, for example, non-HIV-1<sub>LAI</sub> enveloped viruses, non-enveloped viruses and other non-viral organisms.

The term "analog", as used herein, refers to a peptide which is recognized or identified via the 107x178x4, ALLMOTI5 and/or PLZIP search strategies discussed below. Further, such peptides may exhibit antifusogenic capability, antiviral activity, or the

ability to modulate intracellular processes involving coiled-coil structures.

Such DP178 and DP107 analogs may, for example, correspond to peptide sequences present in TM proteins of enveloped viruses and may, additionally correspond  
5 to peptide sequences present in non enveloped and non-viral organisms. Such peptides may exhibit antifusogenic activity, antiviral activity, most particularly antiviral activity which is specific to the virus in which their native sequences are found,  
10 or may exhibit an ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are peptides whose amino acid sequences are comprised of the amino acid sequences of peptide regions of, for example, other (i.e., other  
15 than HIV-1<sub>LAI</sub>) viruses that correspond to the gp41 peptide region from which DP178 (SEQ ID:1) was derived. Such viruses may include, but are not limited to, other HIV-1 isolates and HIV-2 isolates. DP178 analogs derived from the corresponding gp41  
20 peptide region of other (i.e., non HIV-1<sub>LAI</sub>) HIV-1 isolates may include, for example, peptide sequences as shown below.

25 NH<sub>2</sub>-YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF-COOH (DP-185; SEQ ID:3);

NH<sub>2</sub>-YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF-COOH (SEQ ID:4);

30 NH<sub>2</sub>-YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF-COOH (SEQ ID:5).

SEQ ID:3 (DP-185), SEQ ID:4, and SEQ ID:5 are derived from HIV-1<sub>SF2</sub>, HIV-1<sub>RF</sub>, and HIV-1<sub>MN</sub> isolates, respectively. Underlined amino acid residues refer to those residues that differ from the corresponding  
35 position in the DP178 (SEQ ID:1) peptide. One such

DP178 analog, DP-185 (SEQ ID:3), is described in the Example presented in Section 6, below, where it is demonstrated that DP-185 (SEQ ID:3) exhibits antiviral activity. The DP178 analogs of the invention may also include truncations, as described above. Further, the  
5 analogs of the invention modifications such those described for DP178 analogs in Section 5.1., above. It is preferred that the DP178 analogs of the invention represent peptides whose amino acid sequences correspond to the DP178 region of the gp41  
10 protein, it is also contemplated that the peptides of the invention may, additionally, include amino sequences, ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP178  
15 amino acid sequence.

Striking similarities, as shown in FIG. 1, exist within the regions of HIV-1 and HIV-2 isolates which correspond to the DP178 sequence. A DP178 analog derived from the HIV-2<sub>NIH</sub> isolate has the 36 amino acid  
20 sequence (reading from amino to carboxy terminus):

NH<sub>2</sub>-LEANISQSLEQAQIQQEKMYELQKLNSWDVFTNWL-COOH (SEQ ID:7)

Table III and Table IV show some possible truncations  
25 of the HIV-2<sub>NIH</sub> DP178 analog, which may comprise peptides of between 3 and 36 amino acid residues (*i.e.*, peptides ranging in size from a tripeptide to a 36-mer polypeptide). Peptide sequences in these tables are listed from amino (left) to carboxy (right)  
30 terminus. "X" may represent an amino group (-NH<sub>2</sub>) and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-  
35 fluorenylmethoxy-carbonyl (Fmoc) group; or a

covalently attached macromolecular group, including  
but not limited to a lipid-fatty acid conjugate,  
polyethylene glycol, carbohydrate or peptide group.  
Further, "Z" may represent an amido group; a T-  
butoxycarbonyl group; or a covalently attached  
5 macromolecular group, including but not limited to a  
lipid-fatty acid conjugate, polyethylene glycol,  
carbohydrate or peptide group. A preferred "X" or "Z"  
macromolecular group is a peptide group.

10

15

20

25

30

35

TABLE III

HIV-2<sub>NH2</sub> DP178 analog carboxy truncations.

X-LEA-Z  
X-LEAN-Z  
X-LEANI-Z  
X-LEANIS-Z  
5 X-LEANISQ-Z  
X-LEANISQS-Z  
X-LEANISQSL-Z  
X-LEANISQSLE-Z  
X-LEANISQSLEQ-Z  
X-LEANISQSLEQA-Z  
X-LEANISQSLEQAQ-Z  
10 X-LEANISQSLEQAQI-Z  
X-LEANISQSLEQAQIQ-Z  
X-LEANISQSLEQAQIQQ-Z  
X-LEANISQSLEQAQIQQE-Z  
X-LEANISQSLEQAQIQQEK-Z  
X-LEANISQSLEQAQIQQEKN-Z  
X-LEANISQSLEQAQIQQEKNM-Z  
X-LEANISQSLEQAQIQQEKNMY-Z  
15 X-LEANISQSLEQAQIQQEKNMYE-Z  
X-LEANISQSLEQAQIQQEKNMYEL-Z  
X-LEANISQSLEQAQIQQEKNMYELQ-Z  
X-LEANISQSLEQAQIQQEKNMYELQK-Z  
X-LEANISQSLEQAQIQQEKNMYELQKL-Z  
X-LEANISQSLEQAQIQQEKNMYELQKLN-Z  
X-LEANISQSLEQAQIQQEKNMYELQKLNS-Z  
20 X-LEANISQSLEQAQIQQEKNMYELQKLNSW-Z  
X-LEANISQSLEQAQIQQEKNMYELQKLNSWD-Z  
X-LEANISQSLEQAQIQQEKNMYELQKLNSWDV-Z  
X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVF-Z  
X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFT-Z  
X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTN-Z  
X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNW-Z  
25 X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or  
30 T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a  
35 T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IV

HIV-2<sub>NIH2</sub> DP178 analog amino truncations.

	X-NWL-Z
	X-TNWL-Z
	X-FTNWL-Z
5	X-VFTNWL-Z
	X-DVFTNWL-Z
	X-WDVFTNWL-Z
	X-SWDVFTNWL-Z
	X-NSWDVFTNWL-Z
	X-LNSWDVFTNWL-Z
	X-KLNSWDVFTNWL-Z
	X-QKLNSWDVFTNWL-Z
10	X-LQKLNSWDVFTNWL-Z
	X-ELQKLNSWDVFTNWL-Z
	X-YELQKLNSWDVFTNWL-Z
	X-MYELQKLNSWDVFTNWL-Z
	X-NMYELQKLNSWDVFTNWL-Z
	X-KNMYELQKLNSWDVFTNWL-Z
	X-EKNMYELQKLNSWDVFTNWL-Z
15	X-QEKNMYELQKLNSWDVFTNWL-Z
	X-QQEKNMYELQKLNSWDVFTNWL-Z
	X-IQQEKNMYELQKLNSWDVFTNWL-Z
	X-QIQQEKNMYELQKLNSWDVFTNWL-Z
	X-AQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-QAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-EQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-LEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
20	X-SLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-QSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-SQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-ISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-NISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-ANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-EANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
25	X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

DP178 and DP107 analogs are recognized or identified, for example, by utilizing one or more of the 107x178x4, ALLMOTI5 or PLZIP computer-assisted search strategies described and demonstrated, below, in the Examples presented in Sections 9 through 16 and 19 through 25. The search strategy identifies additional peptide regions which are predicted to have structural and/or amino acid sequence features similar to those of DP107 and/or DP178.

The search strategies are described fully, below, in the Example presented in Section 9. While this search strategy is based, in part, on a primary amino acid motif deduced from DP107 and DP178, it is not based solely on searching for primary amino acid sequence homologies, as such protein sequence homologies exist within, but not between major groups of viruses. For example, primary amino acid sequence homology is high within the TM protein of different strains of HIV-1 or within the TM protein of different isolates of simian immunodeficiency virus (SIV). Primary amino acid sequence homology between HIV-1 and SIV, however, is low enough so as not to be useful. It is not possible, therefore, to find peptide regions similar to DP107 or DP178 within other viruses, or within non-viral organisms, whether structurally, or otherwise, based on primary sequence homology, alone.

Further, while it would be potentially useful to identify primary sequence arrangements of amino acids based on, for example, the physical chemical characteristics of different classes of amino acids rather than based on the specific amino acids themselves, such search strategies have, until now, proven inadequate. For example, a computer algorithm designed by Lupas et al. to identify coiled-coil propensities of regions within proteins (Lupas, A., et al., 1991 Science 252:1162-1164) is inadequate for



identifying protein regions analogous to DP107 or DP178.

Specifically, analysis of HIV-1 gp160 (containing both gp120 and gp41) using the Lupas algorithm does not identify the coiled-coil region within DP107. It does, however, identify a region within DP178 beginning eight amino acids N-terminal to the start of DP178 and ending eight amino acids from the C-terminus. The DP107 peptide has been shown experimentally to form a stable coiled coil. A search based on the Lupas search algorithm, therefore, would not have identified the DP107 coiled-coil region. Conversely, the Lupas algorithm identified the DP178 region as a potential coiled-coil motif. However, the peptide derived from the DP178 region failed to form a coiled coil in solution.

A possible explanation for the inability of the Lupas search algorithm to accurately identify coiled-coil sequences within the HIV-1 TM, is that the Lupas algorithm is based on the structure of coiled coils from proteins that are not structurally or functionally similar to the TM proteins of viruses, antiviral peptides (e.g. DP107 and DP178) of which are an object of this invention.

The computer search strategy of the invention, as demonstrated in the Examples presented below, in Sections 9 through 16 and 19 through 25, successfully identifies regions of proteins similar to DP107 or DP178. This search strategy was designed to be used with a commercially-available sequence database package, preferably PC/Gene.

A series of search motifs, the 107x178x4, ALLMOTI5 and PLZIP motifs, were designed and engineered to range in stringency from strict to broad, as discussed in this Section and in Section 9, with 107x178x4 being preferred. The sequences

identified via such search motifs, such as those listed in Tables V-XIV, below, potentially exhibit antifusogenic, such as antiviral, activity, may additionally be useful in the identification of antifusogenic, such as antiviral, compounds, and are  
5 intended to be within the scope of the invention.

Coiled-coiled sequences are thought to consist of heptad amino acid repeats. For ease of description, the amino acid positions within the heptad repeats are sometimes referred to as A through G, with the first  
10 position being A, the second B, etc. The motifs used to identify DP107-like and DP178-like sequences herein are designed to specifically search for and identify such heptad repeats. In the descriptions of each of the motifs described, below, amino acids enclosed by  
15 brackets , i.e., [], designate the only amino acid residues that are acceptable at the given position, while amino acids enclosed by braces, i.e., {}, designate the only amino acids which are unacceptable at the given heptad position. When a set of bracketed  
20 or braced amino acids is followed by a number in parentheses i.e., (), it refers to the number of subsequent amino acid positions for which the designated set of amino acids hold, e.g, a (2) means "for the next two heptad amino acid positions".

25 The ALLMOTI5 is written as follows:

{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-  
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-  
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-  
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-  
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-

30 Translating this motif, it would read: "at the first (A) position of the heptad, any amino acid residue except C, D, G, H, or P is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, or P is acceptable, at the fourth  
35 heptad position (D), any amino acid residue except C,

D, G, H, or P is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, or P is acceptable. This motif is designed to search for five consecutive heptad repeats (thus the repeat of the first line five times), meaning that it searches for 35-mer sized peptides. It may also be designed to search for 28-mers, by only repeating the initial motif four times. With respect to the ALLMOTI5 motif, a 35-mer search is preferred. Those viral (non-bacteriophage) sequences identified via such an ALLMOTI5 motif are listed in Table V, below, at the end of this Section. The viral sequences listed in Table V potentially exhibit antiviral activity, may be useful in the the identification of antiviral compounds, and are intended to be within the scope of the invention. In those instances wherein a single gene exhibits greater than one sequence recognized by the ALLMOTI5 search motif, the amino acid residue numbers of these sequences are listed under "Area 2", Area 3", etc. This convention is used for each of the Tables listed, below, at the end of this Section.

The 107x178x4 motif is written as follows:

[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-  
 [EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-  
 [EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-  
 [EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-

Translating this motif, it would read: "at the first (A) position of the heptad, only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, M or P is acceptable, at the fourth position (D), only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, M or P is acceptable. This motif is designed to search for

four consecutive heptad repeats (thus the repeat of the first line four times), meaning that it searches for 28-mer sized peptides. It may also be designed to search for 35-mers, by repeating the initial motif five times. With respect to the 107x178x4 motif, a  
5 28-mer search is preferred.

Those viral (non-bacteriophage) sequences identified via such a 107x178x4 motif are listed in Table VI, below, at the end of this Section, with those viral (non-bacteriophage) sequences listed in  
10 Table VII, below at the end of this Section, being preferred.

The 107x178x4 search motif was also utilized to identify non-viral procaryotic protein sequences, as listed in Table VIII, below, at the end of this  
15 Section. Further, this search motif was used to reveal a number of human proteins. The results of this human protein 107x178x4 search is listed in Table IX, below, at the end of this Section. The sequences listed in Tables VIII and IX, therefore, reveal  
20 peptides which may be useful as antifusogenic compounds or in the identification of antifusogenic compounds, and are intended to be within the scope of the invention.

The PLZIP series of motifs are as listed in FIG.  
25 19. These motifs are designed to identify leucine zipper coiled-coil like heptads wherein at least one proline residue is present at some predefined distance N-terminal to the repeat. These PLZIP motifs find regions of proteins with similarities to HIV-1 DP178  
30 generally located just N-terminal to the transmembrane anchor. These motifs may be translated according to the same convention described above. Each line depicted in FIG. 19 represents a single, complete search motif. "X" in these motifs refers to any amino  
35 acid residue. In instances wherein a motif contains

two numbers within parentheses, this refers to a variable number of amino acid residues. For example, X (1,12) is translated to "the next one to twelve amino acid residues, inclusive; may be any amino acid".

5       Tables X through XIV, below, at the end of this Section, list sequences identified via searches conducted with such PLZIP motifs. Specifically, Table X lists viral sequences identified via PCTLZIP, P1CTLZIP and P2CTLZIP search motifs, Table XI lists  
10       viral sequences identified via P3CTLZIP, P4CTLZIP, P5CTLZIP and P6CTLZIP search motifs, Table XII lists viral sequences identified via P7CTLZIP, P8CTLZIP and P9CTLZIP search motifs, Table XIII lists viral  
15       sequences identified via P12LZIPC searches and Table XIV lists viral sequences identified via P23TLZIPC search motifs. The viral sequences listed in these tables represent peptides which potentially exhibit  
20       antiviral activity, may be useful in the identification of antiviral compounds, and are intended to be within the scope of the invention.

      The Examples presented in Sections 17, 18, 26 and 27 below, demonstrate that viral sequences identified via the motif searches described herein identify  
25       substantial antiviral characteristics. Specifically, the Example presented in Section 17 describes peptides with anti-respiratory syncytial virus activity, the Example presented in Section 18 describes peptides  
30       with anti-parainfluenza virus activity, the Example presented in Section 26 describes peptides with anti-measles virus activity and the Example presented in Section 27 describes peptides with anti-simian  
      immunodeficiency virus activity.

      The DP107 and DP178 analogs may, further, contain any of the additional groups described for DP178,  
35       above, in Section 5.1. For example, these peptides

may include any of the additional amino-terminal groups as described above for "X" groups, and may also include any of the carboxy-terminal groups as described, above, for "Z" groups.

5        Additionally, truncations of the identified DP107 and DP178 peptides are among the peptides of the invention. Further, such DP107 and DP178 analogs and DP107/DP178 analog truncations may exhibit one or more amino acid substitutions, insertion, and/or deletions. The DP178 analog amino acid substitutions, insertions  
10        and deletions, are as described, above, for DP178-like peptides in Section 5.1. The DP-107 analog amino acid substitutions, insertions and deletions are also as described, above, for DP107-like peptides in Section  
15        5.2.

      Tables XV through XXII, below, present representative examples of such DP107/DP178 truncations. Specifically, Table XV presents Respiratory Syncytial Virus F1 region DP107 analog carboxy truncations, Table XVI presents Respiratory  
20        Syncytial Virus F1 region DP107 analog amino truncations, Table XVII presents Respiratory Syncytial Virus F1 region DP178 analog carboxy truncations, Table XVIII presents Respiratory Syncytial Virus F1 region DP178 analog amino truncations, Table XIX  
25        presents Human Parainfluenza Virus 3 F1 region DP178 analog carboxy truncations, Table XX presents Human Parainfluenza Virus 3 F1 region DP178 analog amino truncations, Table XXI presents Human Parainfluenza Virus 3 F1 region DP107 analog carboxy truncations and  
30        Table XXII presents Human Parainfluenza Virus 3 F1 region DP107 analog amino truncations. Further, Table XXIII, below, presents DP107/DP178 analogs and analog truncations which exhibit substantial antiviral activity. These antiviral peptides are grouped  
35        according to the specific virus which they inhibit,

including respiratory syncytial virus, human  
parainfluenza virus 3, simian immunodeficiency virus  
and measles virus.

5

10

15

20

25

30

35

TABLE V

ALLMOTIS SEARCH RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS















PCGENE	ALLNOTES	All Virus (no heterogeneity)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILENAME	PROTEIN	VIRUS	556-678	408-432						
PENK_SIVAG	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SINIAN IMMUNODEFICIENCY VIRUS (AGNI ISOLATE)	336-370	515-607	627-644	792-840				
PENK_SIVAI	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SINIAN IMMUNODEFICIENCY VIRUS (TYO-1 ISOLATE)	344-208	549-631	644-692	796-833				
PENK_SIVAT	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SINIAN IMMUNODEFICIENCY VIRUS (SIVCP22)	351-291	566-654	677-725	801-817				
PENK_SIVCB	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SINIAN IMMUNODEFICIENCY VIRUS (SINIAN4243 ISOLATE)	114-151	465-596	528-611	615-725	809-844			
PENK_SIVM1	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SINIAN IMMUNODEFICIENCY VIRUS (SINIAN4243 ISOLATE)	71-107	181-219	247-286					
PENK_SIVM2	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SINIAN IMMUNODEFICIENCY VIRUS (KAW ISOLATE)	464-505	549-612	618-724					
PENK_SIVM3	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SINIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	464-505	549-612	618-724					
PENK_SIVS4	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SINIAN IMMUNODEFICIENCY VIRUS (F36/SX/H4 ISOLATE)	466-509	517-616	618-724	812-853				
PENK_SIVSP	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SINIAN IMMUNODEFICIENCY VIRUS (PNU/C13 ISOLATE)	470-513	521-620	642-732	817-848				
PENK_SIVSH	ENVELOPE POLYPROTEIN PRECURSOR	SOURBEL MONKEY RETROVIRUS (SIVRV.11)	400-466							
PENK_SIVV1	ENV POLYPROTEIN	SINIAN RETROVIRUS SRV-1	409-475							
PENK_SIVV2	ENV POLYPROTEIN PRECURSOR	VISNA LENTIVIRUS (STRAIN 1514)	21-62	184-222	637-740	773-809				
PENK_SIVV3	ENV POLYPROTEIN PRECURSOR	VISNA LENTIVIRUS (STRAIN 15147 CLONE LV1-K31)	21-62	184-222	643-746	789-816				
PENK_SIVV4	ENV POLYPROTEIN PRECURSOR	VISNA LENTIVIRUS (STRAIN 15147 CLONE LV1-K33)	21-62	184-222	643-746	782-818				
PENK_SIVV5	ENV POLYPROTEIN PRECURSOR	AVIAN ERYTHROBLASTOSIS VIRUS (STRAIN E54)	106-140							
PENK_SIVV6	ENV POLYPROTEIN PRECURSOR	FOXP2 VIRUS (STRAIN TP-1)	190-224	533-557						
PENK_SIVV7	ENV POLYPROTEIN PRECURSOR	SHOPE FIBRINOLYTIC VIRUS (STRAIN KASZA)	37-71	267-340	350-387					
PENK_SIVV8	ENV POLYPROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	23-71	307-341						
PENK_SIVV9	ENV POLYPROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN NR)	23-71	307-341						
PENK_SIVV10	ENV POLYPROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	52-97	174-208						
PENK_SIVV11	ENV POLYPROTEIN PRECURSOR	VARIOLA VIRUS	52-97	174-208						
PENK_SIVV12	ENV POLYPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	80-114							
PENK_SIVV13	ENV POLYPROTEIN PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADAP)	89-141							
PENK_SIVV14	ENV POLYPROTEIN PRECURSOR	PSEUDORABIES VIRUS (STRAIN NIA-3)	82-120							
PENK_SIVV15	ENV POLYPROTEIN PRECURSOR	VARIOLA-ZOSTER VIRUS (STRAIN DUMAS)	109-157	342-383						
PENK_SIVV16	ENV POLYPROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 40	182-237							
PENK_SIVV17	ENV POLYPROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 41	182-237							
PENK_SIVV18	ENV POLYPROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 3	156-194							
PENK_SIVV19	ENV POLYPROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 7	176-210							
PENK_SIVV20	ENV POLYPROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 40	201-252							
PENK_SIVV21	ENV POLYPROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 41	201-252							
PENK_SIVV22	ENV POLYPROTEIN PRECURSOR	BOVINE ADENOVIRUS TYPE 3	181-215	585-626						
PENK_SIVV23	ENV POLYPROTEIN PRECURSOR	FBR MURINE OSTEOCARCINOMA VIRUS	131-169							
PENK_SIVV24	ENV POLYPROTEIN PRECURSOR	AVIAN RETROVIRUS NR24	109-152							
PENK_SIVV25	ENV POLYPROTEIN PRECURSOR	FBI MURINE OSTEOCARCINOMA VIRUS	155-193							
PENK_SIVV26	ENV POLYPROTEIN PRECURSOR	AVIAN SARCOMA VIRUS (STRAIN CT10)	57-101							
PENK_SIVV27	ENV POLYPROTEIN PRECURSOR	AVIAN ENDOGENOUS VIRUS EV-1	57-94							
PENK_SIVV28	ENV POLYPROTEIN PRECURSOR	AVIAN ENDOGENOUS ROUS-ASSOCIATED VIRUS-0	6-43							
PENK_SIVV29	ENV POLYPROTEIN PRECURSOR	AVIAN MYELOCYTOMA TOSIS VIRUS NC29	57-94							
PENK_SIVV30	ENV POLYPROTEIN PRECURSOR	AVIAN MYELOCYTOMA TOSIS VIRUS TBI	57-94							
PENK_SIVV31	ENV POLYPROTEIN PRECURSOR	AVIAN SARCOMA VIRUS (STRAIN UR3)	57-94							
PENK_SIVV32	ENV POLYPROTEIN PRECURSOR	AVIAN SARCOMA VIRUS (STRAIN Y21)	57-94							
PENK_SIVV33	ENV POLYPROTEIN PRECURSOR	BOVINE IMMUNODEFICIENCY VIRUS (ISOLATE 106)	1-41							
PENK_SIVV34	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (ISOLATE PETALLUM)	61-118							
PENK_SIVV35	ENV POLYPROTEIN PRECURSOR	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE PETALLUM)	76-110							
PENK_SIVV36	ENV POLYPROTEIN PRECURSOR	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE SAN DIEGO)	76-110							
PENK_SIVV37	ENV POLYPROTEIN PRECURSOR	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE TMD)	76-110							
PENK_SIVV38	ENV POLYPROTEIN PRECURSOR	FELINE LEUKEMIA VIRUS	496-537							
PENK_SIVV39	ENV POLYPROTEIN PRECURSOR	HUMAN SPINARETROVIRUS	130-186							
PENK_SIVV40	ENV POLYPROTEIN PRECURSOR	FELINE SARCOMA VIRUS (STRAIN MCDONOUGH)	499-534							



ACCENE	ALLNOTIS	All Virus (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
POAG_FUJ5V	GAG POLYPROTEIN	FUJINAMI SARCOMA VIRUS	57-94						
POAG_GALV	GAG POLYPROTEIN	GIBBON APE LEUKEMIA VIRUS	391-444						
POAG_HV1A2	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ARV25F2 ISOLATE)	87-131	294-328					
POAG_HV1B1	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BIII10 ISOLATE)	90-131	292-326					
POAG_HV1B5	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (III15 ISOLATE)	90-131	292-326					
POAG_HV1B8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (III15 ISOLATE)	90-131	292-326					
POAG_HV1C4	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-431 ISOLATE)	90-131	292-326					
POAG_HV1E1	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ELI ISOLATE)	93-131	292-326					
POAG_HV1H2	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (H102 ISOLATE)	90-131	292-326					
POAG_HV1J3	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (H11 ISOLATE)	87-131	292-326					
POAG_HV1J8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (JRCF ISOLATE)	87-131	292-326					
POAG_HV1MA	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (MAL ISOLATE)	90-131	292-326					
POAG_HV1N5	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (N1 ISOLATE)	87-131	292-326					
POAG_HV1N5	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NEW YORK-3 ISOLATE)	87-131	292-326					
POAG_HV1N5	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (N1 ISOLATE)	87-131	292-326					
POAG_HV1OY	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (OY1 ISOLATE)	87-131	292-326					
POAG_HV1P4	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (PV22 ISOLATE)	90-131	292-326					
POAG_HV1R8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RPHAT ISOLATE)	90-131	292-326					
POAG_HV1W2	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (VNU2 ISOLATE)	87-131	292-326					
POAG_HV1Z2	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2COC-214 ISOLATE)	292-326						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	292-326						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	93-137	320-357					
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	67-103	138-172					
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	80-131	138-172					
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	470-304						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	81-131	156-190					
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	81-131	156-190					
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	222-260						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	57-94						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	102-139						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	128-177						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	128-177						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	371-407						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	302-336						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	306-340						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	181-217						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	302-336						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	301-335						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	161-204						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	221-267						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	394-431						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	172-206						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	468-502						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	158-203						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	413-449						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	782-821						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	208-242						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	208-242						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	208-242						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	208-242						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	208-242						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	180-216						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	364-440						
POAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	378-454						











PGENE	ALLNOTIS	All Viruses (no bacteriophages)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7
FILENAME	PROTEIN	VIRUS	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7
PKF5_FUJ5	TYROSINE-PROTEIN KINASE TRANSFORMING PROT	FUJINAMI SARCONIA VIRUS	65-90		152-251				
PKITH_AMEV	THYMIDINE KINASE	ANISACTA MOOREI ENTOMOPHAGUS	47-81						
PKITH_CAPV	THYMIDINE KINASE	CAPRIPOX VIRUS (STRAIN KS-1)	28-82						
PKITH_EBV	THYMIDINE KINASE	EPSTEIN-BARR VIRUS (STRAIN B95-1)	228-262						
PKITH_HSV1	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	90-124		431-472				
PKITH_HSV2	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN CL101)	90-124						
PKITH_HSV3	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 3 / STRAIN IFEM)	90-124						
PKITH_HSV4	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 4 / STRAIN KOS)	90-124						
PKITH_HSV5	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 5 / STRAIN SC16)	90-124						
PKITH_HSV6	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN 311)	91-125						
PKITH_HSV7	THYMIDINE KINASE	BOVINE HERPES VIRUS TYPE 1 (STRAIN WC1)	616-663						
PKITH_HSV8	THYMIDINE KINASE	EQUINE HERPES VIRUS TYPE 1 (STRAIN 1942)	19-53		178-219				
PKITH_HSV9	THYMIDINE KINASE	EQUINE HERPES VIRUS TYPE 2 (STRAIN AD47)	19-53		178-210				
PKITH_HSV10	THYMIDINE KINASE	FELINE HERPES VIRUS (FELV) (STRAIN 1)	180-214						
PKITH_HSV11	THYMIDINE KINASE	MARMOSET HERPES VIRUS	32-86						
PKITH_HSV12	THYMIDINE KINASE	HERPES VIRUS SAIMIRI (STRAIN 11)	317-389						
PKITH_HSV13	THYMIDINE KINASE	HERPES VIRUS SAIMIRI (STRAIN NIA-3)	161-202						
PKITH_HSV14	THYMIDINE KINASE	PSEUDORABIES VIRUS (STRAIN NIA-3)	69-103						
PKITH_HSV15	THYMIDINE KINASE	AVIAN RETROVIRUS M102	190-224						
PKITH_HSV16	THYMIDINE KINASE	ICTALURID HERPES VIRUS 1	57-91		211-315				
PKITH_HSV17	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	487-528		597-631				
PKITH_HSV18	THYMIDINE KINASE	HERPES SIMPLEX VIRUS 1	11-45						
PKITH_HSV19	THYMIDINE KINASE	MORINE SARCONIA VIRUS M11	127-168						
PKITH_HSV20	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	127-168						
PKITH_HSV21	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN WR)	123-171						
PKITH_HSV22	THYMIDINE KINASE	VARIOLA VIRUS	142-181						
PKITH_HSV23	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	147-181						
PKITH_HSV24	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN WR)	169-203						
PKITH_HSV25	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	116-170						
PKITH_HSV26	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN L-197)	169-203						
PKITH_HSV27	THYMIDINE KINASE	VARIOLA VIRUS	111-145						
PKITH_HSV28	THYMIDINE KINASE	AVIAN SARCONIA VIRUS (STRAIN UR)	135-169						
PKITH_HSV29	THYMIDINE KINASE	AVIAN RETROVIRUS RPLJ0	174-223						
PKITH_HSV30	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN WR) (STRAIN COPENHAGEN)	441-475						
PKITH_HSV31	THYMIDINE KINASE	AVIAN SARCONIA VIRUS (STRAIN Y7)	223-264						
PKITH_HSV32	THYMIDINE KINASE	HUMAN ADENOVIRUS TYPE 2	191-232		408-442				
PKITH_HSV33	THYMIDINE KINASE	HUMAN ADENOVIRUS TYPE 3	199-233						
PKITH_HSV34	THYMIDINE KINASE	HUMAN ADENOVIRUS TYPE 4	228-284						
PKITH_HSV35	THYMIDINE KINASE	HUMAN ADENOVIRUS TYPE 5	144-179						
PKITH_HSV36	THYMIDINE KINASE	EPSTEIN-BARR VIRUS (STRAIN B95-1)	394-338						
PKITH_HSV37	THYMIDINE KINASE	SHOPE FIBROMA VIRUS (STRAIN KASZA)	54-152		627-656				
PKITH_HSV38	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	1-41		627-657				
PKITH_HSV39	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN WR)	1-41		627-657				
PKITH_HSV40	THYMIDINE KINASE	VARIOLA VIRUS	1-39		627-657				
PKITH_HSV41	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	72-137		245-286				
PKITH_HSV42	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN WR)	72-137		245-286				
PKITH_HSV43	THYMIDINE KINASE	VARIOLA VIRUS	72-137		245-286				
PKITH_HSV44	THYMIDINE KINASE	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	116-157		279-312				
PKITH_HSV45	THYMIDINE KINASE	ODONTOGLOSSUM KINGSPOT VIRUS	51-90						
PKITH_HSV46	THYMIDINE KINASE	PEPPER MILD MOTTLE VIRUS (STRAIN SPAIN)	26-66						
PKITH_HSV47	THYMIDINE KINASE	TOBACCO MILD GREEN MOSAIC VIRUS (TANV STRAIN US)	29-66						



PGENE	ALLNOTES	All Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PNCAP_NEA5Y	NUCLEOCAPSID PROTEIN	NEA5Y VIRUS (STRAIN YASAGATA-1)	383-411						
PNCAP_MOPEI	NUCLEOCAPSID PROTEIN	MOPEIA VIRUS	65-106	471-503					
PNCAP_MUNP1	NUCLEOCAPSID PROTEIN	MUNP5 VIRUS (STRAIN SBL-1)	214-235	500-514					
PNCAP_MUNPM	NUCLEOCAPSID PROTEIN	MUNP5 VIRUS (STRAIN MUYAHARA VACCINE)	214-235						
PNCAP_PHV	NUCLEOCAPSID PROTEIN	PROSPECT HILL VIRUS	1-35	405-74	317-392				
PNCAP_P11HC	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C19)	212-272	441-510					
PNCAP_P11HW	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN WASHINGTON1957)	212-272	441-510					
PNCAP_P11HT	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSHIIBA)	214-266	344-378					
PNCAP_P11B	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSHIIBA)	200-403	446-499					
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	HOVINE PARAINFLUENZA 3 VIRUS (STRAIN NHI 478B5)	83-135	308-366					
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 4A VIRUS (STRAIN TOSHIIBA)	58-94	191-267					
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 4B VIRUS (STRAIN TOSHIIBA)	58-94	191-267					
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 4B VIRUS (STRAIN 68-333)	65-112						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	PICHINDE ARENAY VIRUS	71-116	325-339					
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	PIRY VIRUS	1-35	405-74	317-392				
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	PUUMALA VIRUS (STRAIN HALLNAS 11)	1-35	405-74	317-392				
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	PUUMALA VIRUS (STRAIN SOTKANIO)	1-35	405-74	317-392				
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	PUUMALA VIRUS (STRAIN SOTKANIO)	91-141	248-303	344-398				
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	PNEUMONIA VIRUS OF MICE	131-167						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	RABIES VIRUS (STRAIN AVOI)	212-272	345-404					
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	SENDAL VIRUS (STRAIN 2/HOST MUTANTS)	212-272	345-404					
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	SENDAL VIRUS (STRAIN ENDERS)	212-272	345-404					
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	SENDAL VIRUS (STRAIN 2)	212-272	345-404					
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	SEOL VIRUS (STRAIN SR-11)	1-35	40-74	333-381				
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	SIMIAN VIRUS 41	212-267	372-406	418-466				
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	SOMCHUS YELLOW NET VIRUS	312-366						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	TASCARIBE VIRUS	50-84	230-264					
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	TOSCARIBE VIRUS	212-249						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	TOMATO SPOTTED WILT VIRUS (BRAZILIAN ISOLATE CPNIIHR)	79-120						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	TOMATO SPOTTED WILT VIRUS (HAWAIIAN ISOLATE)	79-120						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	TOMATO SPOTTED WILT VIRUS (STRAIN LJ)	79-120						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	UUKUNIEMI VIRUS	31-102						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	VIRAL HEMORRHAGIC SEPTICEMIA VIRUS (STRAIN 07-71)	249-323						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	VIRAL HEMORRHAGIC SEPTICEMIA VIRUS (STRAIN MAKALI)	143-180	249-323					
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	VESICULAR STOMATITIS VIRUS (SEROTYPE INDIANA / STRAIN C42-108)	67-115						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	VESICULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN 67-115)	42-115						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	VESICULAR STOMATITIS VIRUS (STRAIN SAN JUAN)	2-48						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE BEN)	7-41						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D194)	112-169						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ROD)	109-150						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE SBLISV)	108-149						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	96-140						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE AGM / CLONE CR 94)	232-267						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (F316/SNH4 ISOLATE)	9-43						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/BLACK DUCK/AUSTRALIA/702/71/47-81)	33-74						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/CANBERRA/HONGKONG/82)	50-91						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/CHICKENPENNSYLVANIA/1370/349-332)	349-332						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/CHICKENPENNSYLVANIA/8125/349-332)	349-332						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/CHICKENPENNSYLVANIA/49)	14-48						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/OWL PLAGUE VIRUS/SEYBOLD)	16-48						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/QUEENSLAND/1674)	10-47						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/QUEENSLAND/1674)	10-47						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/QUEENSLAND/1674)	5-44						
PNCAP_P11H4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/QUEENSLAND/1674)	50-91						













PCGENE	ALLNOTES	All Viruses (no Bacteriophages)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6
FILE NAME	PROTEIN	VIRUS	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6
PPOLN_RBDV	NON-STRUCTURAL POLYPROTEIN	ONYONG-ONYONG VIRUS (STRAIN GULLU)	899-933	1942-1986	2444-2502			
PPOLN_RAVN	NON-STRUCTURAL POLYPROTEIN	RABBIT HEMORRHAGIC DISEASE VIRUS	188-214	306-347	409-437	1652-1716		
PPOLN_RAVT	NON-STRUCTURAL POLYPROTEIN	ROSS RIVER VIRUS (STRAIN NB592)	891-919	1928-1962	2414-2467			
PPOLN_RUBVT	NON-STRUCTURAL POLYPROTEIN	ROSS RIVER VIRUS (STRAIN T44)	597-611	1083-1126				
PPOLN_SFV	NON-STRUCTURAL POLYPROTEIN	RUBELLA VIRUS (STRAIN THERIEN)	1506-1540	1531-1583	1720-1767	1862-1896		
PPOLN_SINDO	NON-STRUCTURAL POLYPROTEIN	SEXALIKI FOREST VIRUS	1094-1128	2138-2192				
PPOLN_EPMV	NON-STRUCTURAL POLYPROTEIN	SINDBIS VIRUS (SUBTYPE OCKELBO / STRAIN EDSBYN 82-3)	919-971	1491-1533	1961-1996	2442-2476		
PPOLN_EBAY	NON-STRUCTURAL POLYPROTEIN	SINDBIS VIRUS (STRAIN TROP)	1491-1533	1939-1994	2442-2476			
PPOLN_EEVV	RNA REPLICASE POLYPROTEIN	EGGPLANT MOSAIC VIRUS	899-933	1127-1161				
PPOLN_EEVV3	STRUCTURAL POLYPROTEIN	EASTERN EQUINE ENCEPHALITIS VIRUS	372-406	914-931				
PPOLN_EEVV1	STRUCTURAL POLYPROTEIN	EASTERN EQUINE ENCEPHALITIS VIRUS (STRAIN VAJ) [TEN BRO 372-407]	372-407	915-933				
PPOLN_EBVT	STRUCTURAL POLYPROTEIN	VENEZUELAN EQUINE ENCEPHALITIS VIRUS (STRAIN TC-81)	1216-1230					
PPOLN_IBDV1	STRUCTURAL POLYPROTEIN	VENEZUELAN EQUINE ENCEPHALITIS VIRUS (STRAIN TRINIDAD)	1216-1230					
PPOLN_IBDVA	STRUCTURAL POLYPROTEIN	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN 3270)	134-168	231-286	470-523			
PPOLN_IBDVC	STRUCTURAL POLYPROTEIN	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN AUSTRAL)	134-168	231-286	470-523			
PPOLN_IBDVE	STRUCTURAL POLYPROTEIN	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN CU-1)	134-168	231-286	470-523			
PPOLN_IBDVP	STRUCTURAL POLYPROTEIN	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN E)	134-168	231-286	470-523			
PPOLN_IBDVS	STRUCTURAL POLYPROTEIN	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN PG-98)	115-149	212-267	451-504			
PPOLN_IBNVI	STRUCTURAL POLYPROTEIN	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN STC)	134-168	249-283	470-523			
PPOLN_IPNV	STRUCTURAL POLYPROTEIN	INFECTIOUS PANCREATIC NECROSIS VIRUS (SEROTYPE JASPER)	69-103	723-785				
PPOLN_ONVGO	STRUCTURAL POLYPROTEIN	INFECTIOUS PANCREATIC NECROSIS VIRUS (STRAIN NI)	716-766					
PPOLN_RAV2	STRUCTURAL POLYPROTEIN	ONYONG-ONYONG VIRUS (STRAIN GULLU)	1204-1238					
PPOLN_RAVN	STRUCTURAL POLYPROTEIN	ROSS RIVER VIRUS (STRAIN 213970)	35-69					
PPOLN_RAVT	STRUCTURAL POLYPROTEIN	ROSS RIVER VIRUS (STRAIN NB592)	169-403	919-973				
PPOLN_RUBVH	STRUCTURAL POLYPROTEIN	ROSS RIVER VIRUS (STRAIN T44)	929-973					
PPOLN_RUBVA	STRUCTURAL POLYPROTEIN	RUBELLA VIRUS (VACCINE STRAIN HPV77)	999-1036					
PPOLN_RUBVT	STRUCTURAL POLYPROTEIN	RUBELLA VIRUS (VACCINE STRAIN RA370)	999-1036					
PPOLN_SINDO	STRUCTURAL POLYPROTEIN	RUBELLA VIRUS (STRAIN THERIEN)	999-1036					
PPOLN_SINDV	STRUCTURAL POLYPROTEIN	SINDBIS VIRUS (SUBTYPE OCKELBO / STRAIN EDSBYN 82-3)	362-396					
PPOLN_SINDW	STRUCTURAL POLYPROTEIN	SINDBIS VIRUS (STRAINS HRSP AND HRLP)	362-396					
PPOLN_WEEV	STRUCTURAL POLYPROTEIN	SINDBIS VIRUS (WILD TYPE 58 DERIVED FROM STRAIN ARJ19)	14-68					
PPOLN_BAEVM	STRUCTURAL POLYPROTEIN	WESTERN EQUINE ENCEPHALITIS VIRUS	913-947					
PPOLN_BLVAV	POL POLYPROTEIN	BABOON ENDOGENOUS VIRUS (STRAIN M7)	42-80	676-743	794-832	1001-1042		
PPOLN_BLV1	POL POLYPROTEIN	BOVINE LEUKEMIA VIRUS (AUSTRALIAN ISOLATE)	623-673					
PPOLN_CAEVC	POL POLYPROTEIN	BOVINE LEUKEMIA VIRUS (JAPANESE ISOLATE BLV-1)	623-673					
PPOLN_CAMVD	POL POLYPROTEIN	CAPRINE ARTHRITIS ENCEPHALITIS VIRUS (STRAIN COBK)	479-934					
PPOLN_COTMV	ENZYMATIC POLYPROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DH)	177-211					
PPOLN_EIAPV	POTATIVE POLYPROTEIN	COMBILINA YELLOW MOTTLE VIRUS	87-121	333-367	447-498	831-876	1310-1351	
PPOLN_EIAPV3	POL POLYPROTEIN	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE 1369)	511-568	1022-1036				
PPOLN_EIAPV1	POL POLYPROTEIN	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE CL2)	511-568	1022-1036				
PPOLN_FENVI	POL POLYPROTEIN	EQUINE INFECTIOUS ANEMIA VIRUS (ISOLATE WYOMING)	512-563	1021-1035				
PPOLN_FIVSD	POL POLYPROTEIN	FELINE ENDOGENOUS VIRUS ECEI	537-600	623-639	838-899			
PPOLN_FIVT2	POL POLYPROTEIN	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE PETALUMA)	429-473	606-663				
PPOLN_FIVT3	POL POLYPROTEIN	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE SAN DIEGO)	428-473	606-642				
PPOLN_FIVT4	POL POLYPROTEIN	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE Tm2)	428-473	595-662				
PPOLN_FIVT5	POL POLYPROTEIN	FIGWORT MOSAIC VIRUS (STRAIN DXS)	403-437					
PPOLN_FIVT6	POL POLYPROTEIN	HUMAN SPINARETROVIRUS (FOAMY VIRUS)	140-174	217-236	285-326			
PPOLN_HTL1A	POL POLYPROTEIN	GIBBON APE LEUKEMIA VIRUS	528-562	673-740				
PPOLN_HTL1C	POL POLYPROTEIN	HUMAN T-CELL LEUKEMIA VIRUS TYPE I (STRAIN ATK)	676-711					
PPOLN_HV1A2	POL POLYPROTEIN	HUMAN T-CELL LEUKEMIA VIRUS TYPE I (CARIBBEAN ISOLATE)	676-711					
PPOLN_HV1B1	POL POLYPROTEIN	HUMAN T-CELL LEUKEMIA VIRUS TYPE I (ARV25F2 ISOLATE)	501-537	606-664				
PPOLN_HV1B3	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH10 ISOLATE)	513-549	639-676				



















[illegible]

PGENE	ALLNOTIS	All Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILENAME	PROTEIN	VIRUS	443-491	497-538						AREA1
PTUN AVS1	DNA TERMINAL PROTEIN	HUMAN ADENOVIRUS TYPE 12	443-491	497-538						AREA1
PTNAF AVS4	TRANSFORMING PROTEIN JUN	AVIAN SARCOMA VIRUS (STRAIN 17)	210-284							
PTOP1 SFVKA	TRANSFORMING PROTEIN MAF	AVIAN MUSCULOPONEUROTIC FIBROSARCOMA VIRUS AS42	247-288	295-340						
PTOP2 SFVBT	DNA TOPOISOMERASE	SHOPE FIBROMA VIRUS (STRAIN KASZA)	177-183	269-310						
PTOP2 SFVMD	DNA TOPOISOMERASE II	AFRICAN SWINE FEVER VIRUS (STRAIN B471V)	146-180	481-515	601-642			1031-1093	1123-1162	
PTIS5 SNA5V	DNA TOPOISOMERASE II	AFRICAN SWINE FEVER VIRUS (ISOLATE MALAWI LIL 2001)	146-180	480-514	600-641			944-978	1031-1091	
PTVSY VZVDO	PDGF-RELATED TRANSFORMING PROTEIN P14-335	SRIMAN SARCOMA VIRUS	16-71							1122-1161
PUBIL NPVOP	THYMIDYLATE SYNTHASE	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	215-260							
PUL01 HCAVA	UBIQUITIN-LIKE PROTEIN	ORGANIA PSEUDOTISUCATA MOLLICAPSID POLYHEDROSIS VIRUS	431-480							
PUL03 HSYV1	HYPOTHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	169-203							
PUL03 HSYV2H	PROTEIN UL3	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	94-128							
PUL03 HSYV2H	PROTEIN UL3	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	94-128							
PUL04 HSYV1	GENE 60 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADH4P)	92-126							
PUL04 EBV	PROTEIN UL4	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	103-136							
PUL06 HCAVA	VRION PROTEIN BBRF1	EPSTEIN-BARR VIRUS (STRAIN B95-4)	104-145	311-347	376-410					
PUL06 HSYV1	HYPOTHETICAL PROTEIN UL6	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	216-250							
PUL06 HSYV2	VRION PROTEIN UL4	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	36-94	103-141	294-329	337-371	416-479			
PUL06 HSYV3A	VRION GENE 36 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADH4P)	62-170	337-413	448-503					
PUL06 VZVDO	VRION GENE 43 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	90-140	151-194	303-336	364-403				
PUL09 HCAVA	VRION GENE 34 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	87-131	330-409	704-738					
PUL09 HSYV2	HYPOTHETICAL PROTEIN UL8	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	6-50							
PUL09 VZVDO	ORIGIN OF REPLICATION BINDING PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADH4P)	174-208							
PUL11 HCAVA	ORIGIN OF REPLICATION BINDING PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	123-163							
PUL11 HCAVA	NONSENSE									
PUL14 HCAVA	HYPOTHETICAL PROTEIN UL13	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	47-81	185-227						
PUL14 HSYV2	HYPOTHETICAL PROTEIN UL14	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	303-340							
PUL14 PRVNO	HYPOTHETICAL GENE 48 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADH4P)	52-96	246-283						
PUL14 VZVDO	UL14 PROTEIN HOMOLOG	PSEUDORABIES VIRUS (STRAIN NIA-3)	43-93							
PUL16 HSYV2	HYPOTHETICAL GENE 46 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	61-103							
PUL17 HSYV6U	GENE 46 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADH4P)	266-300							
PUL21 HSYV2	PROTEIN 10R	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	219-280							
PUL21 HCAVA	GENE 40 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADH4P)	44-78	421-474						
PUL24 HCAVA	HYPOTHETICAL PROTEIN UL23	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	213-253							
PUL24 ILTVT	HYPOTHETICAL PROTEIN UL24	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	5-39							
PUL25 HCAVA	PROTEIN UL24 HOMOLOG	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE V8)	161-193							
PUL25 HSYV1	HYPOTHETICAL PROTEIN UL25	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	235-241	331-399						
PUL25 HSYV2	VRION PROTEIN UL25	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	370-411							
PUL31 HSYV3A	VRION PROTEIN UL31	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADH4P)	364-413							
PUL31 ILTVT	VRION GENE 19 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	28-92	183-231	365-408					
PUL31 VZVDO	64.1 KD VRION PROTEIN	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE V8)	38-84	165-208						
PUL31 HCAVA	VRION GENE 24 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	340-388							
PUL31 HSYV2	HYPOTHETICAL PROTEIN UL31	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	244-285							
PUL31 VZVDO	GENE 29 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADH4P)	131-187							
PUL31 HSYV2	GENE 27 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	163-197							
PUL31 VZVDO	MAJOR ENVELOPE GLYCOPROTEIN 200	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADH4P)	342-376							
PUL31 HCAVA	PROBABLE MAJOR ENVELOPE GLYCOPROTEIN 26	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	72-106	256-344						
PUL33 VZVDO	G-PROTEIN COUPLED RECEPTOR HOMOLOG UL33	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	94-135	309-352						
PUL34 EBV	GENE 23 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	29-63							
PUL34 HCAVA	BRF1 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-4)	159-200							
PUL34 HSYV1	HYPOTHETICAL PROTEIN UL34	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	113-147							
PUL37 HCAVA	VRION PROTEIN UL34	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	187-221							
PUL37 EBV	HYPOTHETICAL PROTEIN UL35	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	231-268							

FCGENE	ALLNOTIS	ALL Virus (no bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
FILE NAME	PROTEIN	VIRUS	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
PUL17_HSV11	PROTEIN BOLF1	EPSTEIN-BARR VIRUS (STRAIN B95-3)	705-742							
PUL17_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	833-891							
PUL17_HSV11	PROTEIN BOLF1	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD49)	82-137	311-345	614-648	713-730	781-822			
PUL17_HSV11	PROTEIN BOLF1	HERPESVIRUS SAIMIRI (STRAIN 11)	6-65	682-741						
PUL17_HSV11	PROTEIN BOLF1	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	719-733	786-827						
PUL17_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	10-51							
PUL17_HSV11	PROTEIN BOLF1	HOST SHUTOFF VIRION PROTEIN	330-366							
PUL17_HSV11	PROTEIN BOLF1	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	124-168	221-263						
PUL17_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	138-172							
PUL17_HSV11	PROTEIN BOLF1	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD49)	72-109							
PUL17_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	27-68							
PUL17_HSV11	PROTEIN BOLF1	EQUINE HERPESVIRUS TYPE 4 (STRAIN 1942)	312-363							
PUL17_HSV11	PROTEIN BOLF1	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	96-137							
PUL17_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	114-165	448-485	745-856					
PUL17_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	473-518							
PUL17_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	473-518							
PUL17_HSV11	PROTEIN BOLF1	BOVINE HERPESVIRUS TYPE 1 (STRAIN F)	561-612							
PUL17_HSV11	PROTEIN BOLF1	EQUINE HERPESVIRUS TYPE 4 (STRAIN 1942)	183-246	582-620	825-866					
PUL17_HSV11	PROTEIN BOLF1	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD49)	219-233	371-412	817-866					
PUL17_HSV11	PROTEIN BOLF1	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	84-135	156-209	664-701					
PUL17_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	155-189							
PUL17_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	118-169							
PUL17_HSV11	PROTEIN BOLF1	EQUINE HERPESVIRUS TYPE 4 (STRAIN 1942)	121-162							
PUL17_HSV11	PROTEIN BOLF1	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD49)	120-161							
PUL17_HSV11	PROTEIN BOLF1	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	122-163							
PUL17_HSV11	PROTEIN BOLF1	EPSTEIN-BARR VIRUS (STRAIN B95-3)	188-235							
PUL17_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	189-233							
PUL17_HSV11	PROTEIN BOLF1	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD49)	141-182	919-970						
PUL17_HSV11	PROTEIN BOLF1	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	445-483							
PUL17_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	101-142							
PUL17_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG32)	12-48							
PUL17_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	151-185							
PUL17_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	32-23							
PUL17_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	39-99							
PUL17_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	43-79							
PUL17_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	729-770							
PUL17_HSV11	PROTEIN BOLF1	HERPESVIRUS SAIMIRI (STRAIN 11)	366-400	322-616						
PUL17_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	357-391							
PUL17_HSV11	PROTEIN BOLF1	HERPESVIRUS SAIMIRI (STRAIN 11)	24-58							
PUL17_HSV11	PROTEIN BOLF1	EPSTEIN-BARR VIRUS (STRAIN B95-3)	107-144	188-222						
PUL17_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	79-116							
PUL17_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	101-145	174-216						
PUL17_HSV11	PROTEIN BOLF1	HERPESVIRUS SAIMIRI (STRAIN 11)	88-122							
PUL17_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	21-57	299-384						
PUL17_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	21-51	239-293						
PUL17_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	31-101							
PUL17_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	53-113							
PUL17_HSV11	PROTEIN BOLF1	HERPESVIRUS SAIMIRI (STRAIN 11)	45-100							
PUL17_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	6-40	758-792						
PUL17_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	1-56	170-171	330-364	439-492	541-575			





FCGENE	ALLMOTIS	FILE NAME	ALL VIMES (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PV1K_BWYF	50.8 KD PROTEIN	PV1K_BWYF	VIRUS	72-106							
PV1K_BWYF	51 KD PROTEIN	PV1K_BWYF	APPLE CHLOROTIC LEAF SPOT VIRUS	113-147	196-233	404-431					
PV1K_PLRV	51 KD PROTEIN	PV1K_PLRV	BEEET WESTERN YELLOW VIRUS (ISOLATE FL-1)	113-147	196-233	404-431					
PV1K_PLRV	56 KD PROTEIN	PV1K_PLRV	BEEET WESTERN YELLOW VIRUS (ISOLATE GRI)	47-81	431-472						
PV1K_BSMV	56 KD PROTEIN	PV1K_BSMV	POTATO LEAFROLL VIRUS (STRAIN 1)	47-81	431-472						
PV1K_BSMV	56 KD PROTEIN	PV1K_BSMV	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	47-81	431-472						
PV1K_BSMV	56 KD PROTEIN	PV1K_BSMV	BARLEY STRIPE MOSAIC VIRUS	128-162	323-371						
PV1K_BSMV	56.2 KD PROTEIN	PV1K_BSMV	BEEET WESTERN YELLOW VIRUS (ISOLATE FL-1)	48-52	314-348						
PV1K_PLRV	69.7 KD PROTEIN	PV1K_PLRV	POTATO LEAFROLL VIRUS (STRAIN 1)	98-144	409-443	514-548					
PV1K_PLRV	69.7 KD PROTEIN	PV1K_PLRV	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	98-144	409-443	514-548					
PV1K_PLRV	90.7 KD PROTEIN	PV1K_PLRV	ALFA MOSAIC VIRUS (STRAIN 435 / ISOLATE LEIDEN)	107-141							
PV1K_VACC	PROTEIN A4	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	32-66	231-275						
PV1K_VACC	PROTEIN A4	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	32-66	231-275						
PV1K_VACC	PROTEIN A4	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	32-66	231-275						
PV1K_VACC	PROTEIN A6	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	32-66	231-275						
PV1K_VACC	PROTEIN A6	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	32-66	231-275						
PV1K_VACC	PROTEIN A6	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	32-66	231-275						
PV1K_VACC	PROTEIN A6	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	32-66	231-275						
PV1K_VACC	PROTEIN A8	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	97-213	314-355						
PV1K_VACC	PROTEIN A8	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	97-213	314-355						
PV1K_VACC	PROTEIN A8	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	97-213	314-355						
PV1K_VACC	PROTEIN A8	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	97-213	314-355						
PV1K_VACC	PROTEIN A8	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	176-236							
PV1K_VACC	PROTEIN A8	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	176-236							
PV1K_VACC	PROTEIN A9	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	46-93							
PV1K_VACC	PROTEIN A9	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	46-93							
PV1K_VACC	PROTEIN A9	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	97-134	141-175	219-283					
PV1K_VACC	PROTEIN A9	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	97-134	141-175	219-283					
PV1K_VACC	PROTEIN A11	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	98-176	226-284						
PV1K_VACC	PROTEIN A11	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	98-176	226-284						
PV1K_VACC	PROTEIN A11	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	111-153							
PV1K_VACC	PROTEIN A12	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	111-153							
PV1K_VACC	56 KD ABORTIVE LATE PROTEIN	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	43-467							
PV1K_VACC	56 KD ABORTIVE LATE PROTEIN	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	43-467							
PV1K_VACC	56 KD ABORTIVE LATE PROTEIN	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	307-341	431-467						
PV1K_VACC	56 KD ABORTIVE LATE PROTEIN	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	307-341	431-467						
PV1K_VACC	PROTEIN A20	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	1-67							
PV1K_VACC	PROTEIN A20	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	1-67							
PV1K_VACC	PROTEIN A20	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	1-67							
PV1K_VACC	PROTEIN A20	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	1-67							
PV1K_VACC	PROTEIN A22	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	28-69							
PV1K_VACC	PROTEIN A22	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	28-69							
PV1K_VACC	PROTEIN A22	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	39-80							
PV1K_VACC	PROTEIN A22	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	39-80							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	95-143	171-207	235-289	344-382				
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	95-143	171-207	235-289	344-382				
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	95-143	171-207	235-289	344-382				
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	95-143	171-207	235-289	344-382				
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	88-126							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	88-126							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	217-231							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	217-231							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	63-97							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	63-97							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67	109-155						
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	26-67	109-155						
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	24-63							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	24-63							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-91							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	44-91							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-91							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	44-91							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	37-71							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	37-71							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	75-109							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	75-109							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	81-126							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	81-126							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	81-126							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	81-126							
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	62-96	143-184						
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	62-96	143-184						
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)	62-96	143-184						
PV1K_VACC	PROTEIN A23	PV1K_VACC	VACCINIA VIRUS (STRAIN WR)	62-96	143-184						



ALLNOTES  
Nucleic Search Results

PLGNAME	ALLNOTES	ALL Viruses (see bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PV491_VACC	PROTEIN A47	VARIOLA VIRUS	62-96	104-184					AREA1
PV492_VACC	PROTEIN A48	VACCINIA VIRUS (STRAIN COPENHAGEN)	3-40	126-160					
PV493_VACC	PROTEIN A49	VACCINIA VIRUS (STRAIN WR)	3-40	126-160					
PV494_VACC	PROTEIN A50	VARIOLA VIRUS	3-40	126-160					
PV495_VACC	PROTEIN A51	VACCINIA VIRUS (STRAIN COPENHAGEN)	91-122						
PV496_VACC	PROTEIN A52	VACCINIA VIRUS (STRAIN WR)	91-122						
PV497_VACC	GUANYLATE KINASE HOMOLOG	VACCINIA VIRUS (STRAIN COPENHAGEN)	124-168						
PV498_VACC	GUANYLATE KINASE HOMOLOG	VACCINIA VIRUS (STRAIN WR)	134-168						
PV499_VACC	AL1 PROTEIN	MAIZE STREAK VIRUS (KENYAN ISOLATE)	220-269						
PV500_VACC	AL1 PROTEIN	MAIZE STREAK VIRUS (NIGERIAN ISOLATE)	228-262						
PV501_VACC	AL1 PROTEIN	MAIZE STREAK VIRUS (SOUTH AFRICAN ISOLATE)	228-262						
PV502_VACC	AL1 PROTEIN	SQUASH LEAF CURL VIRUS	117-151						
PV503_VACC	AL1 PROTEIN	TOBACCO YELLOW DWARF VIRUS (STRAIN AUSTRALIA)	191-225						
PV504_VACC	AL1 PROTEIN	ADULTON MOSAIC VIRUS (ISOLATE WEST INDIA)	44-78	81-124					
PV505_VACC	AL1 PROTEIN	BEAN GOLDEN MOSAIC VIRUS	44-78	81-124					
PV506_VACC	AL1 PROTEIN	POTATY YELLOW MOSAIC VIRUS (ISOLATE VENEZUELA)	30-78	87-121					
PV507_VACC	AL1 PROTEIN	SQUASH LEAF CURL VIRUS	46-80	91-125					
PV508_VACC	AL1 PROTEIN	TOMATO GOLDEN MOSAIC VIRUS	44-78						
PV509_VACC	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN CH-1841)	22-70	84-127					
PV510_VACC	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DHI)	22-70						
PV511_VACC	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN BDC)	22-70	93-127					
PV512_VACC	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN NY8153)	22-70	93-127					
PV513_VACC	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN PV147)	22-70	93-127					
PV514_VACC	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN STRASBOURG)	22-70	93-130					
PV515_VACC	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN W760)	36-70						
PV516_VACC	APHID TRANSMISSION PROTEIN	CARNATION ETCHED RING VIRUS	99-138						
PV517_VACC	PROTEIN B1	VACCINIA VIRUS (STRAIN WR)	108-142						
PV518_VACC	PROTEIN B2	VACCINIA VIRUS (STRAIN COPENHAGEN)	89-123	331-372	496-530				
PV519_VACC	PROTEIN B3	VACCINIA VIRUS (STRAIN WR)	89-123	331-372					
PV520_VACC	PROTEIN B4	VARIOLA VIRUS	89-124	334-372	492-530				
PV521_VACC	PLAQUE-SIZE / HOST RANGE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN LC16ND)	234-298						
PV522_VACC	PLAQUE-SIZE / HOST RANGE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	234-298						
PV523_VACC	PLAQUE-SIZE / HOST RANGE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN LISTER)	234-298						
PV524_VACC	PLAQUE-SIZE / HOST RANGE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN WR)	234-298						
PV525_VACC	PROTEIN B5 PRECURSOR	VACCINIA VIRUS (STRAIN WR, AND (STRAIN COPENHAGEN))	28-62						
PV526_VACC	PROTEIN B6 PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-60						
PV527_VACC	PROTEIN B7	VACCINIA VIRUS (STRAIN WR)	337-375	491-532					
PV528_VACC	PROTEIN B8	VACCINIA VIRUS (STRAIN COPENHAGEN)	337-375	491-532					
PV529_VACC	PROTEIN B9	VARIOLA VIRUS	337-378	491-532					
PV530_VACC	SURFACE ANTIGEN 5 PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	82-121						
PV531_VACC	SURFACE ANTIGEN 5 PRECURSOR	VACCINIA VIRUS (STRAIN DAIEN I)	85-119						
PV532_VACC	SURFACE ANTIGEN 5 PRECURSOR	VACCINIA VIRUS (STRAIN WR)	85-119						
PV533_VACC	PROTEIN B10	VACCINIA VIRUS (STRAIN COPENHAGEN)	48-83						
PV534_VACC	PROTEIN B11	VACCINIA VIRUS (STRAIN WR)	61-95						
PV535_VACC	ILI PROTEIN	BEAN GOLDEN MOSAIC VIRUS	139-193						
PV536_VACC	ILI PROTEIN	SQUASH LEAF CURL VIRUS	139-193						
PV537_VACC	ILI PROTEIN	TOMATO GOLDEN MOSAIC VIRUS	139-193						
PV538_VACC	ILI PROTEIN	BEAN GOLDEN MOSAIC VIRUS	172-206						
PV539_VACC	ILI PROTEIN	SQUASH LEAF CURL VIRUS	20-61						
PV540_VACC	ILI PROTEIN	TOMATO GOLDEN MOSAIC VIRUS	25-59						
PV541_VACC	PROTEIN C1	VACCINIA VIRUS (STRAIN COPENHAGEN)	17-42	262-302	391-442				

PCGENE	ALLIOTIS	ALL Viruses (no bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PVC04_SFVKA	PROTEIN C3	VACCINIA VIRUS (STRAIN WR)	32-42	362-202	191-442					
PVC04_VACCC	PROTEIN C4	SHOPE FIBROMA VIRUS (STRAIN KASZA)	175-223	374-408						
PVC04_VACCV	PROTEIN C4	VACCINIA VIRUS (STRAIN COPENHAGEN)	12-46							
PVC04_VARY	PROTEIN C4	VACCINIA VIRUS (STRAIN WR)	12-46							
PVC03_SFVKA	PROTEIN C4	VARIOLA VIRUS	12-46							
PVC03_VACCC	HYPOTHEICAL PROTEIN C5	SHOPE FIBROMA VIRUS (STRAIN KASZA)	82-115							
PVC03_VACCV	PROTEIN C5	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-68							
PVC03_VARY	PROTEIN C5	VACCINIA VIRUS (STRAIN WR)	31-68							
PVC08_SFVKA	PROTEIN C5	VARIOLA VIRUS	32-70	73-121						
PVC09_SFVKA	HYPOTHEICAL PROTEIN C6	SHOPE FIBROMA VIRUS (STRAIN KASZA)	45-86							
PVC09_VACCC	HYPOTHEICAL PROTEIN C9	SHOPE FIBROMA VIRUS (STRAIN KASZA)	63-106							
PVC09_VACCV	PROTEIN C9	VACCINIA VIRUS (STRAIN COPENHAGEN)	82-116	168-226	289-323	575-612				
PVC10_VACCC	PROTEIN C9	VACCINIA VIRUS (STRAIN WR)	82-116	168-226	289-323	575-612				
PVC10_VACCV	PROTEIN C10	VACCINIA VIRUS (STRAIN COPENHAGEN)	136-180							
PVC10_VARY	PROTEIN C10	VACCINIA VIRUS (STRAIN WR)	136-176							
PVC12_SFVKA	PROTEIN C10	VARIOLA VIRUS	136-170							
PVC17_SFVKA	HYPOTHEICAL PROTEIN C12	SHOPE FIBROMA VIRUS (STRAIN KASZA)	2-36							
PVC16_VACCC	PROTEIN C13	SHOPE FIBROMA VIRUS (STRAIN KASZA)	3-66	117-182	189-240					
PVC17_VACCC	PROTEIN C13/32	VACCINIA VIRUS (STRAIN COPENHAGEN)	142-176							
PVC18_VACCC	PROTEIN C13/33	VACCINIA VIRUS (STRAIN COPENHAGEN)	100-155	323-339						
PVC19_SFVKA	PROTEIN C13/34	VACCINIA VIRUS (STRAIN COPENHAGEN)	40-98							
PVC19_VACCC	PROTEIN C19	SHOPE FIBROMA VIRUS (STRAIN KASZA)	56-97							
PVCAP_EBV	PROTEIN C13/35	VACCINIA VIRUS (STRAIN COPENHAGEN)	218-252							
PVCAP_HCNVA	MAJOR CAPSID PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8)	150-184	670-709						
PVCAP_HSV1	MAJOR CAPSID PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	136-174	191-225	260-294					
PVCAP_HSV2	MAJOR CAPSID PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	116-173	308-316						
PVCAP_HSVB	MAJOR CAPSID PROTEIN	HERPES SIMPLEX VIRUS	136-174	320-368	311-382					
PVCAP_HSVB	MAJOR CAPSID PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	150-184	304-352						
PVCAP_HSVB	MAJOR CAPSID PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	479-520	673-714	751-799					
PVCAP_HSVB	MAJOR CAPSID PROTEIN	PSEUDORABIES VIRUS (STRAIN INDIANA S)	101-160	292-326						
PVCAP_HSVB	MAJOR CAPSID PROTEIN	VARIOLA-ZOSTER VIRUS (STRAIN DUMAS)	128-198	316-350						
PVC03_FOWP1	DNA-BINDING PROTEIN	AUTOGORAPHA CALIFORNICA NUCLEAR POLYMERIZATION VIRUS	110-248							
PVC03_VACCC	92.6 KD PROTEIN	FOWLPOX VIRUS (STRAIN FP-1)	145-181							
PVC03_VACCV	PROTEIN D5	VACCINIA VIRUS (STRAIN COPENHAGEN)	123-157							
PVC03_VARY	PROTEIN D5	VACCINIA VIRUS (STRAIN WR)	123-157							
PVC09_VACCC	PROTEIN D5	VARIOLA VIRUS	123-157							
PVC09_VACCV	PROTEIN D9	VACCINIA VIRUS (STRAIN COPENHAGEN)	126-160							
PVC09_VARY	PROTEIN D9	VACCINIA VIRUS (STRAIN WR)	126-160							
PVC10_FOWP1	PROTEIN D9	VARIOLA VIRUS	126-160							
PVC10_SFVKA	PROTEIN D10	FOWLPOX VIRUS (STRAIN FP-1)	65-99	188-222						
PVC10_VARY	PROTEIN D10	SHOPE FIBROMA VIRUS (STRAIN KASZA)	4-32							
PVC10_VACCV	PROTEIN D10	VARIOLA VIRUS	67-103							
PVC10_VACCV	DNA-BINDING PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN CM-1841)	1-35							
PVC10_VACCV	DNA-BINDING PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DHI)	1-35							
PVC10_VACCV	DNA-BINDING PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN BDC)	1-35							
PVC10_VACCV	DNA-BINDING PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN NY153)	1-35							
PVC10_VACCV	DNA-BINDING PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN STRASBOURG)	1-35							
PVC10_VACCV	PROTEIN E3	VACCINIA VIRUS (STRAIN COPENHAGEN)	282-316							
PVC10_VACCV	PROTEIN E3	VACCINIA VIRUS (STRAIN WR)	282-316							
PVC10_VACCV	PROTEIN E3	VARIOLA VIRUS	282-316							
PVC10_VACCV	PROTEIN E3	VACCINIA VIRUS (STRAIN COPENHAGEN)	17-61							
PVC10_VACCV	PROTEIN E3	VACCINIA VIRUS (STRAIN WR)	17-61							







































PCGENE	ALLNOTIS	ALL VITUS (no Brucella phage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
ELUSANIE	PROTEIN	VIRUS								
PV40_EBV	INNER CORE PROTEIN VP3	SINIAN I1 ROTAVIRUS (STRAIN SAI1)	26-76							
PV40_HSV1	CAPSID PROTEIN P40	EPSTEIN-BARR VIRUS (STRAIN D95-8) (HUMAN HERPESVIRUS 4)	431-467	311-365	451-492	662-696				
PV40_HSV2	CAPSID PROTEIN P40	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	206-237	599-633						
PV40_ILTVT	CAPSID PROTEIN P40	EQUINE HERPESVIRUS TYPE 1 (STRAIN AIMP) (EIV-1)	180-245							
PV40_SINVC	CAPSID PROTEIN P40	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE V8)	1-35	509-557						
PV40_VZV	CAPSID PROTEIN P40	SINIAN CYTOMEGALOVIRUS (STRAIN COLUBUS)	457-488							
PV41_NPVAC	CAPSID PROTEIN P40	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS) (VZV)	167-246	486-532						
PV41_ROT51	STRUCTURAL GLYCOPROTEIN GP1	AUTOGRAPIA CALIFORNICA NUCLEAR POLYOMEDROSIS VIRUS (112-166)								
PV42_ROT51	OUTER CAPSID PROTEIN VP4	SINIAN I1 ROTAVIRUS (STRAIN SAI1)	1-33	484-518	518-610					
PV4A_VACCC	OUTER CAPSID PROTEIN VP4	SINIAN I1 ROTAVIRUS (STRAIN SAI1)	1-35	217-518	511-646					
PV4A_VACCC	MAJOR CORE PROTEIN P4A PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	355-359	718-763	794-838	857-891				
PV4A_VARV	MAJOR CORE PROTEIN P4A PRECURSOR	VACCINIA VIRUS (STRAIN W8)	282-296	355-359	718-763	794-838	857-891			
PV4B_FOVPV	MAJOR CORE PROTEIN P4B PRECURSOR	VARIOLA VIRUS	355-389	719-764	795-839	858-892				
PV4B_VACCC	MAJOR CORE PROTEIN P4B PRECURSOR	FOWLPOX VIRUS	131-172	296-310						
PV4B_VARV	MAJOR CORE PROTEIN P4B PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	3-37	125-163	249-283					
PV4B_BTIV10	MAJOR CORE PROTEIN P4B PRECURSOR	VACCINIA VIRUS (STRAIN W8)	3-37	125-163	249-283					
PV4B_BTIV11	VP4 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	579-617	619-653						
PV4B_BTIV12	VP4 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	569-607	609-643						
PV4B_NCDV	VP4 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 2 / ISOLATE USA)	569-607	609-643						
PV4B_RDV	OUTER CAPSID PROTEIN VP4	NEBRASKA CALF DIARRHEA VIRUS (STRAIN NCDV-LINCOLN)	484-518	528-670						
PV4B_ROT84	NONSTRUCTURAL PROTEIN PNS4	RICE DWARF VIRUS (RDV)	388-437	444-478	627-679					
PV4B_ROT8C	OUTER CAPSID PROTEIN VP4	BOVINE ROTAVIRUS (SEROTYPE 6 / STRAIN B641)	1-33	112-146	338-379	484-518	528-633			
PV4B_ROT8D	OUTER CAPSID PROTEIN VP4	BOVINE ROTAVIRUS (STRAIN C486)	1-35	484-518	528-630					
PV4B_ROT8E	OUTER CAPSID PROTEIN VP4	BOVINE ROTAVIRUS (STRAIN UK)	1-35	112-146	338-379	484-518	528-633			
PV4B_ROT8I	OUTER CAPSID PROTEIN VP4	EQUINE ROTAVIRUS (STRAIN H-2)	1-35	112-146	227-274	345-379	484-518	528-633		
PV4B_ROT8J	OUTER CAPSID PROTEIN VP4	ROTAVIRUS (GROUP B / STRAIN IDIR)	117-151	476-519	337-378	483-517	510-645			
PV4B_ROT8K	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN 1076)	1-35	236-273	337-378	483-517	527-632			
PV4B_ROT8L	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN RV-5)	1-35	236-273	337-378	483-517	527-632			
PV4B_ROT8M	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN 694)	1-35	112-146	237-274	338-379	484-518	531-646		
PV4B_ROT8N	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN DS1)	1-35	236-273	337-378	483-517	527-632			
PV4B_ROT8O	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN KU)	1-35	237-274	345-379	484-518	528-588			
PV4B_ROT8P	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN L76)	1-35	236-273	337-378	483-517	527-632			
PV4B_ROT8Q	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 5 / STRAIN M17)	1-35	337-378	483-517	510-645				
PV4B_ROT8R	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 6 / STRAIN P)	1-35	237-274	338-379	484-518	531-645			
PV4B_ROT8S	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 7 / STRAIN RV)	1-35	91-146	227-274					
PV4B_ROT8T	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 8 / STRAIN ST. THOMAS J)	1-35	236-273	337-378	483-517	530-644			
PV4B_ROT8U	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 9 / STRAIN VA70)	1-35	237-273	344-378	483-517	527-632			
PV4B_ROT8V	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN VA)	1-35	237-273	344-378	483-517	527-632			
PV4B_ROT8W	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (SEROTYPE 3 / STRAIN OSU)	112-146	484-518	528-679					
PV4B_ROT8X	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (GROUP C / STRAIN COWDEN)	6-40	127-161	241-278	293-334	380-614			
PV4B_ROT8Y	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (STRAIN GOTTFRIED)	1-35	236-273	337-378	483-517	530-564	569-638		
PV4B_ROT8Z	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (STRAIN YAL)	1-35	112-146	237-274	484-518	528-629			
PV4B_ROT9	OUTER CAPSID PROTEIN VP4	RIESUS ROTAVIRUS	1-38	484-518	528-630	338-379	484-532	531-646		
PV4B_ROT9S	OUTER CAPSID PROTEIN VP4	SINIAN I1 ROTAVIRUS (STRAIN SAI1-FEN)	1-35							
PV4B_WTV	DE OUTER CAPSID PROTEIN VP4	SINIAN I1 ROTAVIRUS (STRAIN SAI1-SEN)	1-35	237-274	345-379	484-518	531-646			
PV21_AHSV4	NONSTRUCTURAL PROTEIN PNS4	WOUND TUMOR VIRUS (WTV)	28-62	565-621						
PV3_BSD	OUTER CAPSID PROTEIN VP3	AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 4 / STRAIN VACC)	7-58	113-229						
PV3_BTIV10	OUTER CAPSID PROTEIN VP3	BROADHAVEN VIRUS (BDV)	45-46	98-226						



GENE	ALLIOTIS	ALL Viruses (no bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
FILENAME	PROTEIN	VIRUS	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
PIPR_SINVL	32 KD POLYMERAL ENVELOPE PROTEIN	ORIGIN PSEUDOTUBICATA MULTICAPSID POLYMERAL VIRUS (J1-201)	206-265							
PIPR_HVIA2	VPR PROTEIN	SINIAN INKUNODEFICIENCY VIRUS (N78 ISOLATE) (SIV-NAC)	78-115							
PIPR_HVIB1	VPU PROTEIN	HUMAN INKUNODEFICIENCY VIRUS TYPE I (ARV25F2 ISOLATE) (I)								
PIPR_HVIB2	VPU PROTEIN	HUMAN INKUNODEFICIENCY VIRUS TYPE I (B1110 ISOLATE) (III)	4-72							
PIPR_HVIB3	VPU PROTEIN	HUMAN INKUNODEFICIENCY VIRUS TYPE I (B1118 ISOLATE) (III)	5-72							
PIPR_HVIB4	VPU PROTEIN	HUMAN INKUNODEFICIENCY VIRUS TYPE I (BRUJ ISOLATE) (III)	4-72							
PIPR_HVIB5	VPU PROTEIN	HUMAN INKUNODEFICIENCY VIRUS TYPE I (CDC-451 ISOLATE) (III)	3-40							
PIPR_HVIB6	VPU PROTEIN	HUMAN INKUNODEFICIENCY VIRUS TYPE I (ELI ISOLATE) (IIIV)	6-40							
PIPR_HVIB7	VPU PROTEIN	HUMAN INKUNODEFICIENCY VIRUS TYPE I (HXB2 ISOLATE) (III)	5-72							
PIPR_HVIB8	VPU PROTEIN	HUMAN INKUNODEFICIENCY VIRUS TYPE I (HXB3 ISOLATE) (III)	2-50							
PIPR_HVIB9	VPU PROTEIN	HUMAN INKUNODEFICIENCY VIRUS TYPE I (HXB4 ISOLATE) (III)	4-59							
PIPR_HVIB10	VPU PROTEIN	HUMAN INKUNODEFICIENCY VIRUS TYPE I (HXB5 ISOLATE) (III)	5-50							
PIPR_HVIB11	VPU PROTEIN	HUMAN INKUNODEFICIENCY VIRUS TYPE I (HXB6 ISOLATE) (III)	4-40							
PIPR_HVIB12	VPU PROTEIN	HUMAN INKUNODEFICIENCY VIRUS TYPE I (HXB7 ISOLATE) (III)	4-72							
PIPR_HVIB13	VPU PROTEIN	HUMAN INKUNODEFICIENCY VIRUS TYPE I (HXB8 ISOLATE) (III)	1-39							
PIPR_HVIB14	VPU PROTEIN	HUMAN INKUNODEFICIENCY VIRUS TYPE I (HXB9 ISOLATE) (III)	4-59							
PIPR_HVIB15	VPU PROTEIN	HUMAN INKUNODEFICIENCY VIRUS TYPE I (HXB10 ISOLATE) (III)	6-40							
PIPR_HVIB16	VPU PROTEIN	CHIMPANZEE INKUNODEFICIENCY VIRUS (SIV(CP23)) (CIV)	21-78							
PIPR_HVIB17	VPU PROTEIN	HUMAN INKUNODEFICIENCY VIRUS TYPE I (ISOLATE D203.7) (I)	42-85							
PIPR_HVIB18	VPU PROTEIN	BARLEY STRIPE MOSAIC VIRUS (BSMV)	40-74	857-898						
PIPR_HVIB19	ALPHA-A PROTEIN	SINIAN 11 ROTAVIRUS (STRAIN SA11)	248-287							
PIPR_HVIB20	NONSTRUCTURAL PROTEIN NCVP2	BOVINE ROTAVIRUS (GROUP C / STRAIN SHINTOKU)	6-44							
PIPR_HVIB21	VPA PROTEIN	ROTAVIRUS (GROUP B / STRAIN ADV) (ADULT DIARRHEA ROT)	109-144							
PIPR_HVIB22	VPA PROTEIN	ROTAVIRUS (GROUP B / STRAIN IDIR)	24-58	64-103						
PIPR_HVIB23	VPA PROTEIN	ROTAVIRUS (GROUP C / STRAIN BRISTOL)	9-43							
PIPR_HVIB24	VPA PROTEIN	ROTAVIRUS (GROUP C / STRAIN COWDEN)	9-43							
PIPR_HVIB25	VPA PROTEIN	BOVINE ROTAVIRUS (STRAIN KN-4)	2-36	212-230						
PIPR_HVIB26	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (STRAIN UK)	88-153	199-236						
PIPR_HVIB27	NONSTRUCTURAL PROTEIN NCVP3	PORCINE ROTAVIRUS (SEROTYPE 3 / STRAIN OSU)	88-162	202-236						
PIPR_HVIB28	NONSTRUCTURAL PROTEIN NCVP3	SINIAN 11 ROTAVIRUS (STRAIN SA11)	88-153	199-236						
PIPR_HVIB29	NONSTRUCTURAL PROTEIN NS2/VP9	BOVINE ROTAVIRUS (STRAIN UK)	2-70	75-119	160-226					
PIPR_HVIB30	NONSTRUCTURAL PROTEIN NCVP4	SINIAN 11 ROTAVIRUS (STRAIN SA11)	2-46	144-212	217-235					
PIPR_HVIB31	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (SEROTYPE 6 / STRAIN B641)	2-54	282-320						
PIPR_HVIB32	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (STRAIN A3)	2-54	282-320						
PIPR_HVIB33	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (SEROTYPE 6 / STRAIN 61A)	2-54	282-320						
PIPR_HVIB34	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (STRAIN A44)	2-54	282-320						
PIPR_HVIB35	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (SEROTYPE 10 / STRAIN B223)	2-54	282-320						
PIPR_HVIB36	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (STRAIN KK3)	2-54	282-320						
PIPR_HVIB37	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (STRAIN NC4V)	2-54	282-320						
PIPR_HVIB38	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (SEROTYPE 7 / STRAIN T449)	2-54	282-320						
PIPR_HVIB39	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (STRAIN UK)	2-54	282-320						
PIPR_HVIB40	GLYCOPROTEIN VP7	CHICKEN ROTAVIRUS A (SEROTYPE 7 / STRAIN C112)	235-226							
PIPR_HVIB41	GLYCOPROTEIN VP7	EQUINE ROTAVIRUS (STRAIN L333)	282-320							
PIPR_HVIB42	GLYCOPROTEIN VP7 PRECURSOR	ROTAVIRUS (GROUP B / STRAIN ADV) (ADULT DIARRHEA ROT)	41-77							
PIPR_HVIB43	GLYCOPROTEIN VP7 PRECURSOR	ROTAVIRUS (GROUP B / STRAIN IDIR)	45-79							
PIPR_HVIB44	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN RV-4)	2-43	282-320						
PIPR_HVIB45	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 7 / STRAIN RK9)	282-320							
PIPR_HVIB46	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 7 / STRAIN IUS)	282-320							
PIPR_HVIB47	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 6 / STRAIN B17)	2-43	282-320						
PIPR_HVIB48	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 7 / STRAIN DS1)	282-320							
PIPR_HVIB49	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 7 / STRAIN HNI26)	282-320							

GENE	ALLNOTES	ALLNOTES (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
GLYNAME	PROTEIN	VIRUS								
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (STRAIN L-26)	1-35	282-320						
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN NJ7)	2-43	282-320						
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN MO AND STRAIN DJ)	2-43	282-320						
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN P)	282-320							
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN RV)	282-320							
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN S)	282-320							
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN ST THOMAS J)	18-56	208-242	282-320					
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN VA70)	18-56	208-242	282-320					
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	2-43	282-320						
PV309_ROT101	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 3 / STRAIN AT76)	282-320							
PV309_ROT101	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 3 / STRAIN CRV-4)	282-320							
PV309_ROT101	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 4 / STRAIN OSU)	2-56	208-242	282-320					
PV309_ROT101	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 5 / STRAIN OSU)	282-320							
PV309_ROT101	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 5 / STRAIN TFR-1)	282-320							
PV309_ROT101	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 4 / STRAIN BEN-144)	18-56	208-242	282-320					
PV309_ROT101	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE K)	18-56	208-242	282-320					
PV309_ROT101	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 4 / STRAIN BAH-1)	1-35	282-320						
PV309_ROT101	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (STRAIN YN)	282-320							
PV309_ROT101	GLYCOPROTEIN VP7	RUESUS ROTAVIRUS	282-320							
PV309_ROT101	GLYCOPROTEIN VP7	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	282-320							
PV309_ROT101	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (STRAIN NCDV)	71-161							
PV309_ROT101	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (GROUP C / STRAIN SIINTOKU)	17-58							
PV309_ROT101	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (STRAIN UK)	71-161							
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (STRAIN A31)	71-162							
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (STRAIN A67 CLONE 2)	71-162							
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (STRAIN A67 CLONE 6)	71-162							
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (GROUP C / STRAIN BRISTOL)	121-158							
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	71-136							
PV309_ROT101	GLYCOPROTEIN VP7	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	71-162							
PV309_ROT101	GLYCOPROTEIN VP7	ROTAVIRUS (GROUP B / STRAIN ADRV) (ADULT DIARRHEA ROTAVIRUS)	96-130							
PV309_ROT101	GLYCOPROTEIN VP7	ROTAVIRUS (GROUP B / STRAIN IDIR)	9-68							
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN RV-5)	100-145							
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN 69A)	107-144							
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE G / STRAIN D37)	107-144							
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN DS1)	111-145							
PV309_ROT101	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	111-145							
PV309_ROT101	GLYCOPROTEIN VP7	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	111-145							
PV309_ROT101	GLYCOPROTEIN VP7	TONATO BLACK RING VIRUS (STRAIN C) (TBRV)	217-265							
PV309_ROT101	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN SBL-1) AND MUMPS VIRUS (STRAIN SBL)	9-46							
PV309_ROT101	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN EDINGBOURGH 2) AND (STRAIN EDINGBOURGH 4)	13-47							
PV309_ROT101	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN EDINGBOURGH 4)	13-47							
PV309_ROT101	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN MATSUYAMA)	13-51							
PV309_ROT101	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN BELFAST)	13-52							
PV309_ROT101	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN ENDERS)	9-46							
PV309_ROT101	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN ERLY-LYNN)	9-46							
PV309_ROT101	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN KILHAM)	9-51							
PV309_ROT101	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN BRISTOL 1)	13-55							
PV309_ROT101	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN NITAHARA VACCINE)	13-51							
PV309_ROT101	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN TAKAHASHI)	13-47							
PV309_ROT101	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN URABE VACCINE A19)	13-47							
PV309_ROT101	GLYCOPROTEIN VP7	REOVIRUS (TYPE 2 / STRAIN DEARING)	8-122	121-175	222-259					
PV309_ROT101	GLYCOPROTEIN VP7	REOVIRUS (TYPE 2 / STRAIN D5/ONE5)	1-178							

PCGENE	ALLIOTIS	ALLIOTIS (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PROTEIN	PROTEIN	PROTEIN	3-107	112-198						
PROTEIN	PROTEIN	PROTEIN	350-384							
PROTEIN	PROTEIN	PROTEIN	350-384							
PROTEIN	PROTEIN	PROTEIN	85-119							
PROTEIN	PROTEIN	PROTEIN	7-45							
PROTEIN	PROTEIN	PROTEIN	318-332							
PROTEIN	PROTEIN	PROTEIN	317-331							
PROTEIN	PROTEIN	PROTEIN	318-332							
PROTEIN	PROTEIN	PROTEIN	318-332							
PROTEIN	PROTEIN	PROTEIN	186-220							
PROTEIN	PROTEIN	PROTEIN	120-138							
PROTEIN	PROTEIN	PROTEIN	86-120							
PROTEIN	PROTEIN	PROTEIN	86-120							
PROTEIN	PROTEIN	PROTEIN	395-629							
PROTEIN	PROTEIN	PROTEIN	417-451							
PROTEIN	PROTEIN	PROTEIN	468-502							
PROTEIN	PROTEIN	PROTEIN	11-45							
PROTEIN	PROTEIN	PROTEIN	98-136							
PROTEIN	PROTEIN	PROTEIN	226-267							
PROTEIN	PROTEIN	PROTEIN	588-622							
PROTEIN	PROTEIN	PROTEIN	4-38							
PROTEIN	PROTEIN	PROTEIN	104-138							
PROTEIN	PROTEIN	PROTEIN	16-80							
PROTEIN	PROTEIN	PROTEIN	4-65							
PROTEIN	PROTEIN	PROTEIN	35-59							
PROTEIN	PROTEIN	PROTEIN	10-96							
PROTEIN	PROTEIN	PROTEIN	13-87							
PROTEIN	PROTEIN	PROTEIN	4-38							
PROTEIN	PROTEIN	PROTEIN	4-38							
PROTEIN	PROTEIN	PROTEIN	13-50							
PROTEIN	PROTEIN	PROTEIN	13-50							
PROTEIN	PROTEIN	PROTEIN	40-77							
PROTEIN	PROTEIN	PROTEIN	43-77							
PROTEIN	PROTEIN	PROTEIN	16-67							
PROTEIN	PROTEIN	PROTEIN	2-36							
PROTEIN	PROTEIN	PROTEIN	5-19							
PROTEIN	PROTEIN	PROTEIN	119-166							
PROTEIN	PROTEIN	PROTEIN	1-35							
PROTEIN	PROTEIN	PROTEIN	1-45							
PROTEIN	PROTEIN	PROTEIN	102-136							
PROTEIN	PROTEIN	PROTEIN	73-107							
PROTEIN	PROTEIN	PROTEIN	17-180							
PROTEIN	PROTEIN	PROTEIN	17-154							
PROTEIN	PROTEIN	PROTEIN	7-97							
PROTEIN	PROTEIN	PROTEIN	100-141							
PROTEIN	PROTEIN	PROTEIN	210-278							
PROTEIN	PROTEIN	PROTEIN	115-149							
PROTEIN	PROTEIN	PROTEIN	1-51							
PROTEIN	PROTEIN	PROTEIN	56-94							
PROTEIN	PROTEIN	PROTEIN	81-123							
PROTEIN	PROTEIN	PROTEIN	503-537							
PROTEIN	PROTEIN	PROTEIN	46-83							
PROTEIN	PROTEIN	PROTEIN	74-115							
PROTEIN	PROTEIN	PROTEIN	184-221							

GENE	ALL NOTIS	ALL VIRENS (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
ELCNAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF4 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	59-70							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF5 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	1-37	61-95						
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF6 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	115-149							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF7 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	144-178							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF10 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	142-253							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF11 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	4-47	117-153						
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF12 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	122-163							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF13 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	458-506							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF14 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	147-188							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF15 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	160-204							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF16 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	176-211							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF17 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	34-78	95-139						
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF18 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	24-58	181-222						
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF19 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	16-38							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF20 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	39-81							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF21 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	64-125							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF22 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	94-147							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF23 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	33-77							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF24 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	100-134							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF25 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	14-54							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF26 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	70-127							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF27 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	21-67	89-130						
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF28 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	6-51							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF29 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	78-122							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF30 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	1-43							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF31 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	1-43							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF32 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	4-28	281-315						
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF33 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	4-89							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF34 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	33-72							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF35 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	31-101	106-157						
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF36 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	51-101	106-157						
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF37 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	49-111	197-231						
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF38 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	49-111	197-231						
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF39 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	1-63							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF40 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	116-153							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF41 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	25-66							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF42 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	9-61							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF43 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	1-57	62-96	149-183					
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF44 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	191-264							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF45 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	134-175							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF46 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	232-286	404-442						
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF47 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	1-45							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF48 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	96-130							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF49 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	96-177							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF50 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	390-424							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF51 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	170-204							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF52 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	29-63							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF53 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	3-37							
POWPOX_F0WPM	HYPOTHETICAL BANHI-ORF54 PROTEIN	POWPOX VIRUS (ISOLATE IP-4)(HJNUSNCIII)	78-112							



PCGENE	ALLNOTIS	All Virus (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
QUKXAJE	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PYVBI_VACCC	HYPOTHETICAL 79 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENIAGEN)	23-57							
PYVCC_VACCC	HYPOTHETICAL 74 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENIAGEN)	5-39							
PYVDB_VACCC	HYPOTHETICAL 92 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENIAGEN)	11-48							
PYVDB_VACCV	HYPOTHETICAL 83 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENIAGEN)	29-80							
PYVDC_VACCV	HYPOTHETICAL 83 KD PROTEIN	VACCINIA VIRUS (STRAIN WR)	46-80							
PYVGB_VACCC	HYPOTHETICAL 73 KD PROTEIN	VACCINIA VIRUS (STRAIN WR)	7-41							
PYVIA_VACCC	HYPOTHETICAL 84 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENIAGEN)	10-51							
	HYPOTHETICAL 81 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENIAGEN)	9-53							



TABLE VI

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS









PGCENE	10717144	All Virus (no bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PROTEIN	PROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	549-608								
ENV POLYPROTEIN	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (F216S/II4 ISOLATE)	281-308	642-669		691-718					
ENV POLYPROTEIN	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (PB/IOC11 ISOLATE)	286-313	554-595							
ENV POLYPROTEIN	ENV POLYPROTEIN	SOURREC MONKEY RETROVIRUS (SMRV-1H)	400-462								
ENV POLYPROTEIN	ENV POLYPROTEIN	SIMIAN RETROVIRUS SRV-1	409-471								
ENV POLYPROTEIN	ENV POLYPROTEIN	SIMIAN RETROVIRUS (STRAIN 1514)	773-800								
ENV POLYPROTEIN	ENV POLYPROTEIN	VISNA LENTIVIRUS (STRAIN 1514/ CLONE LV1-1K51)	22-62	780-807							
ENV POLYPROTEIN	ENV POLYPROTEIN	VISNA LENTIVIRUS (STRAIN 1514/ CLONE LV1-1K52)	22-62	782-809							
ENV POLYPROTEIN	ENV POLYPROTEIN	FOXPVIRUS (STRAIN FP-1)	190-224								
EARLY TRANS FACTOR 70 KD SUBUNIT	EARLY TRANS FACTOR 70 KD SUBUNIT	SHOPE FIBROMA VIRUS (STRAIN KASZA)	306-340	469-496	550-587						
EARLY TRANS FACTOR 70 KD SUBUNIT	EARLY TRANS FACTOR 70 KD SUBUNIT	VACCINIA VIRUS (STRAIN COPENHAGEN)	307-341	470-497							
EARLY TRANS FACTOR 70 KD SUBUNIT	EARLY TRANS FACTOR 70 KD SUBUNIT	VACCINIA VIRUS (STRAIN WPA)	307-341	470-497							
EARLY TRANSCRIPTION FACTOR B2	EARLY TRANSCRIPTION FACTOR B2	VACCINIA VIRUS (STRAIN COPENHAGEN)	66-97	174-210	302-332						
EARLY TRANSCRIPTION FACTOR B2	EARLY TRANSCRIPTION FACTOR B2	VACCINIA VIRUS (STRAIN COPENHAGEN)	66-97	174-210	302-332						
ALKALINE EXONUCLEASE	ALKALINE EXONUCLEASE	VARIOLA VIRUS	109-139								
41.4 KD FIBER PROTEIN	41.4 KD FIBER PROTEIN	VARIOLA VIRUS	179-237								
41.4 KD FIBER PROTEIN	41.4 KD FIBER PROTEIN	HUMAN ADENOVIRUS TYPE 40	178-216								
FIBER PROTEIN	FIBER PROTEIN	HUMAN ADENOVIRUS TYPE 41	308-335								
FIBER PROTEIN	FIBER PROTEIN	HUMAN ADENOVIRUS TYPE 40	324-351	446-473							
FIBER PROTEIN	FIBER PROTEIN	HUMAN ADENOVIRUS TYPE 41	339-366	461-488							
FIBER PROTEIN	FIBER PROTEIN	BOVINE ADENOVIRUS TYPE 1	178-145	184-191							
FIBER PROTEIN	FIBER PROTEIN	MOUSE ADENOVIRUS TYPE 1	275-305	335-352							
V-FOS/FOX TRANSFORMING PROTEIN	V-FOS/FOX TRANSFORMING PROTEIN	FBX MURINE OSTEOSARCOMA VIRUS	116-147								
P33-V-FOS TRANSFORMING PROTEIN	P33-V-FOS TRANSFORMING PROTEIN	AVIAN RETROVIRUS NK24	162-193								
P33-V-FOS TRANSFORMING PROTEIN	P33-V-FOS TRANSFORMING PROTEIN	AVIAN RETROVIRUS NK24	270-297								
GAO POLYPROTEIN	GAO POLYPROTEIN	FEI MURINE NECROSIS VIRUS	144-171								
GAO POLYPROTEIN	GAO POLYPROTEIN	EQUINE INFECTIOUS ANEMIA VIRUS (ISOLATE WYONING)	621-648								
GAO POLYPROTEIN	GAO POLYPROTEIN	HUMAN SPIDARETROVIRUS	447-474								
GAO POLYPROTEIN	GAO POLYPROTEIN	GIBBON APE LEUKAEMIA VIRUS	396-442								
GAO POLYPROTEIN	GAO POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ARV25F2 ISOLATE)	91-118								
GAO POLYPROTEIN	GAO POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (H1 ISOLATE)	91-118								
GAO POLYPROTEIN	GAO POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (N1 ISOLATE)	87-118								
GAO POLYPROTEIN	GAO POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE BEN)	88-115								
GAO POLYPROTEIN	GAO POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D194)	88-115								
GAO POLYPROTEIN	GAO POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE NIH-2)	88-115								
GAO POLYPROTEIN	GAO POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	88-115								
RETROVIRUS-RELATED GAG POLYPROTEIN	RETROVIRUS-RELATED GAG POLYPROTEIN	HAMSTER INTRACISTERNAL A-PARTICLE	270-297								
RETROVIRUS-RELATED GAG POLYPROTEIN	RETROVIRUS-RELATED GAG POLYPROTEIN	MOUSE INTRACISTERNAL A-PARTICLE	31-60	69-103	232-259						
RETROVIRUS-RELATED GAG POLYPROTEIN	RETROVIRUS-RELATED GAG POLYPROTEIN	MOUSE INTRACISTERNAL A-PARTICLE	96-130								
RETROVIRUS-RELATED GAG POLYPROTEIN	RETROVIRUS-RELATED GAG POLYPROTEIN	MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6)	84-131	156-187							
RETROVIRUS-RELATED GAG POLYPROTEIN	RETROVIRUS-RELATED GAG POLYPROTEIN	MOUSE MAMMARY TUMOR VIRUS (STRAIN C3H)	84-131								
RETROVIRUS-RELATED GAG POLYPROTEIN	RETROVIRUS-RELATED GAG POLYPROTEIN	MOUSE MAMMARY TUMOR VIRUS (STRAIN GR)	84-131	156-187							
MAJOR COAT PROTEIN	MAJOR COAT PROTEIN	SIMIAN NASOPHARYNGEAL VIRUS (NPMV)	222-260								
MAJOR COAT PROTEIN	MAJOR COAT PROTEIN	SACCHAROMYCES CEREVISIAE VIRUS L-A	497-531	624-651							
GAO POLYPROTEIN	GAO POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE AGM1 / CLONE GRU-1)	473-507								
GAO POLYPROTEIN	GAO POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K6W ISOLATE)	88-115								
GAO POLYPROTEIN	GAO POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (STM1 ISOLATE)	88-115								
GAO POLYPROTEIN	GAO POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (STM1 ISOLATE)	88-115								
GAO POLYPROTEIN	GAO POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (F216S/II4 ISOLATE)	88-115								
GAO POLYPROTEIN	GAO POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (PB/IOC11 ISOLATE)	88-115								
GAO POLYPROTEIN	GAO POLYPROTEIN	SIMIAN SARCOMA VIRUS	397-443								
GAO POLYPROTEIN	GAO POLYPROTEIN	SIMIAN RETROVIRUS SRV-1	222-261								
PROBABLE HELICASE	PROBABLE HELICASE	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	184-211	321-348							
PROBABLE HELICASE	PROBABLE HELICASE	HERPESVIRUS SAIMIRI (STRAIN 11)	418-449								
PROBABLE HELICASE	PROBABLE HELICASE	VARIOLA VIRUS (STRAIN DUMAS)	490-517	701-728							
HEMAGGLUTININ-ESTERASE PRECURSOR	HEMAGGLUTININ-ESTERASE PRECURSOR	BOVINE CORONAVIRUS (STRAIN F13)	308-242								
HEMAGGLUTININ-ESTERASE PRECURSOR	HEMAGGLUTININ-ESTERASE PRECURSOR	BOVINE CORONAVIRUS (STRAIN LY-138)	308-242								
HEMAGGLUTININ-ESTERASE PRECURSOR	HEMAGGLUTININ-ESTERASE PRECURSOR	BOVINE CORONAVIRUS (STRAIN MEBUS)	308-242								













PGCENE	10117144	All Viruses (no bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
ELFAMK	PROTEIN	CRIMINAL-CONGO HEMORRHAGIC FEVER VIRUS (ISOLATE C60011)	221-271								
PNCAP CCIVV	NUCLEOCAPSID PROTEIN	CANINE DISTEMPER VIRUS (STRAIN ONDUSUPOORT)	140-174								
PNCAP CDVO	NUCLEOCAPSID PROTEIN	CHANDIPURA VIRUS (STRAIN 183314)	40-74								
PNCAP CHAV	NUCLEOCAPSID PROTEIN	CANINE ENTERIC CORONAVIRUS (STRAIN K378)	191-227								
PNCAP CVCAC	NUCLEOCAPSID PROTEIN	PORCINE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAIN PURO)	191-227								
PNCAP CVPFV	NUCLEOCAPSID PROTEIN	PORCINE RESPIRATORY CORONAVIRUS (STRAIN B6131004 / BRITISH ISOLAT)	191-227								
PNCAP CYPH8	NUCLEOCAPSID PROTEIN	PORCINE RESPIRATORY CORONAVIRUS (STRAIN R14)	191-227								
PNCAP CYPH8	NUCLEOCAPSID PROTEIN	DUGBE VIRUS	238-265								
PNCAP DUGBV	NUCLEOCAPSID PROTEIN	FELINE INFECTIOUS PERITONITIS VIRUS (STRAIN 79-1146)	182-209								
PNCAP FIPV	NUCLEOCAPSID PROTEIN	HAZARA VIRUS (ISOLATE C280)	6-33	236-283							
PNCAP HAZV1	NUCLEOCAPSID PROTEIN	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B7 STRAIN 18337)	4-31	74-108	112-141						
PNCAP HRSV1	NUCLEOCAPSID PROTEIN	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	4-31								
PNCAP HRSV2	NUCLEOCAPSID PROTEIN	LASSA VIRUS (STRAIN GA391)	64-99	147-174							
PNCAP LASS1	NUCLEOCAPSID PROTEIN	LASSA VIRUS (STRAIN JOSIAH)	64-99	467-504							
PNCAP LYCVA	NUCLEOCAPSID PROTEIN	LYMPHOCTIC CHORIOMENINGITIS VIRUS (STRAIN ARASTRONG)	64-97								
PNCAP MAGV	NUCLEOCAPSID PROTEIN	MAGUARI VIRUS	41-68	192-219							
PNCAP MOPE1	NUCLEOCAPSID PROTEIN	MOPEIA VIRUS	64-99								
PNCAP P11HC	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C39)	377-404	433-482							
PNCAP P11HW	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN WASHINGTON/1957)	377-404	444-488							
PNCAP P11H4	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NIH 14785)	376-403								
PNCAP P1PV	NUCLEOCAPSID PROTEIN	PUNTA TORO PHLEBOVIRUS	1-30								
PNCAP PUDMH	NUCLEOCAPSID PROTEIN	PUDMALA VIRUS (STRAIN HALLNAS D1)	2-29								
PNCAP PUDMS	NUCLEOCAPSID PROTEIN	PUDMALA VIRUS (STRAIN SOTKANIO)	2-29								
PNCAP PYM	NUCLEOCAPSID PROTEIN	PNEUMONIA VIRUS OF MICE	91-120								
PNCAP RABVA	NUCLEOCAPSID PROTEIN	RABIES VIRUS (STRAIN AVO1)	133-167								
PNCAP RABVP	NUCLEOCAPSID PROTEIN	RABIES VIRUS (STRAIN PV)	133-167								
PNCAP RABVS	NUCLEOCAPSID PROTEIN	RABIES VIRUS (STRAIN SAD B19)	133-167								
PNCAP SEND1	NUCLEOCAPSID PROTEIN	SENDAI VIRUS (STRAIN Z7/HIST MUTANTS)	161-404								
PNCAP SEND2	NUCLEOCAPSID PROTEIN	SENDAI VIRUS (STRAIN ENDERS)	161-404								
PNCAP SEND3	NUCLEOCAPSID PROTEIN	SENDAI VIRUS (STRAIN Z)	161-404								
PNCAP SF3V	NUCLEOCAPSID PROTEIN	SANDLEY FEVER SICILIAN VIRUS	4-31								
PNCAP SV41	NUCLEOCAPSID PROTEIN	SIMIAN VIRUS 41	507-514								
PNCAP TACY	NUCLEOCAPSID PROTEIN	TACARIBE VIRUS	50-77								
PNCAP TOSV	NUCLEOCAPSID PROTEIN	TOSCANA VIRUS	6-33								
PNCAP UUR	NUCLEOCAPSID PROTEIN	UUKUNEMAI VIRUS	68-102								
PNCAP VHSV0	NUCLEOCAPSID PROTEIN	VIRAL HEMORRHAGIC SEPTICEMIA VIRUS (STRAIN 02-71)	284-314								
PNCAP VHSV4	NUCLEOCAPSID PROTEIN	VIRAL HEMORRHAGIC SEPTICEMIA VIRUS (STRAIN NAKAI1)	149-176	284-314							
PNCAP VSVIG	NUCLEOCAPSID PROTEIN	VESICULAR STOMATITIS VIRUS (SEROTYPE INDIANA / STRAIN GLASGOW)	56-83								
PNCAP VSVJ0	NUCLEOCAPSID PROTEIN	VESICULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN OGDEN)	67-94	318-363							
PNCAP VSVJ1	NUCLEOCAPSID PROTEIN	VESICULAR STOMATITIS VIRUS (STRAIN SAN JUAN)	56-83								
PNEF HYV1	NEGATIVE FACTOR	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ELI ISOLATE)	81-119								
PNEF HYV2	NEGATIVE FACTOR	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE)	81-119								
PNEF STV1	NEGATIVE FACTOR	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ZAIRE 6 ISOLATE)	86-124								
PNEF STV2	NEGATIVE FACTOR	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE AGM / CLONE GR1-1)	96-137								
PNRAM IADBA	NEURAMINIDASE	INFLUENZA A VIRUS (STRAIN A/BLACK DUCK/VAUS/STR/14/02/78)	47-81								
PNRAM IACAO	NEURAMINIDASE	INFLUENZA A VIRUS (STRAIN A/CANAL/MONGOLIA/82)	33-64								
PNRAM IACHI	NEURAMINIDASE	INFLUENZA A VIRUS (STRAIN A/CHILE/7/83)	16-43	50-91							
PNRAM IADAI	NEURAMINIDASE	INFLUENZA A VIRUS (STRAIN A/DUCK/VALBERT/2/876)	31-81								
PNRAM IADGE	NEURAMINIDASE	INFLUENZA A VIRUS (STRAIN A/DUCK/GERMANY/49)	31-81								
PNRAM IADPW	NEURAMINIDASE	INFLUENZA A VIRUS (STRAIN A/OWL PLAGE VIRUS/WEYBRIDGE)	10-48	53-80	197-224						
PNRAM IAHCO	NEURAMINIDASE	INFLUENZA A VIRUS (STRAIN A/QUEBEC/CM/1674)	197-224	386-413							
PNRAM IAKRI	NEURAMINIDASE	INFLUENZA A VIRUS (STRAIN A/QUEBEC/KENTUCKY/1/81)	3-44	46-76	164-400						
PNRAM IAKXE	NEURAMINIDASE	INFLUENZA A VIRUS (STRAIN A/KIEV/5/979)	50-81								
PNRAM IALEN	NEURAMINIDASE	INFLUENZA A VIRUS (STRAIN A/ENIGRAD/4/41)	50-81								
PNRAM IAMEI	NEURAMINIDASE	INFLUENZA A VIRUS (STRAIN A/MEPHIS/1/71/H-ABELLANY/42N)	16-43	50-81							
PNRAM IAPAR	NEURAMINIDASE	INFLUENZA A VIRUS (STRAIN A/PARROT/ST/187/73)	16-43	30-81							
PNRAM IAPUE	NEURAMINIDASE	INFLUENZA A VIRUS (STRAIN A/PUERTO RICO/04)	16-43								



PCGENE	1071784	All Viruses (no bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PPOLG ENCV	GENOME POLYPROTEIN	ENCEPHALOMYOCARDITIS VIRUS	70-108	1484-1518	1522-1563							
PPOLG ENCVB	GENOME POLYPROTEIN	ENCEPHALOMYOCARDITIS VIRUS (STRAIN EN-C-NONDIABETIC)	70-97	1486-1520	1524-1563							
PPOLG ENCVB	GENOME POLYPROTEIN	ENCEPHALOMYOCARDITIS VIRUS (STRAIN EN-C-DIABETIC)	70-97	1486-1520	1524-1563							
PPOLG ENMG	GENOME POLYPROTEIN	MENGO ENCEPHALOMYOCARDITIS VIRUS (STRAIN 17A)	70-108									
PPOLG ENMG	GENOME POLYPROTEIN	MENGO ENCEPHALOMYOCARDITIS VIRUS	3-41									
PPOLG ENMG	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN A10-41)	302-329	1119-1146								
PPOLG ENMG	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN A12)	301-328	1119-1146								
PPOLG ENMG	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAINS OIK AND OIII5)	1119-1146									
PPOLG ENMG	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN CI-SANTA PAU [C-S1])	101-128									
PPOLG ENMG	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE 1)	702-729									
PPOLG ENMG	GENOME POLYPROTEIN	HOG CHOLERA VIRUS (STRAIN ALFORT)	699-726	1193-1232	1301-1333	1434-1461	1608-1695	1406-1440				
PPOLG ENMG	GENOME POLYPROTEIN	HOG CHOLERA VIRUS (STRAIN BRESIA)	699-726	1193-1232	1301-1333	1434-1461	1608-1695	1406-1440				
PPOLG ENMG	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE BK)	702-729	1045-1072								
PPOLG ENMG	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE II)	702-729	1045-1072								
PPOLG ENMG	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE IIC-16)	374-401	2089-2116								
PPOLG ENMG	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE IIC-18)	1049-1076	2089-2116								
PPOLG ENMG	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE JAPANESE)	374-401	2089-2116								
PPOLG ENMG	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE IIC-17)	702-729	1045-1072								
PPOLG ENMG	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE TAIWANE)	702-729	1045-1072								
PPOLG ENMG	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN 2A)	202-237	1021-1048	1117-1149	1454-1481						
PPOLG ENMG	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN 41C)	202-237	1021-1048	1117-1149	1454-1481						
PPOLG ENMG	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN 1B)	202-237	1021-1048	1117-1149	1454-1481						
PPOLG ENMG	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN CR26)	202-237	1021-1048	1117-1149	1454-1481						
PPOLG ENMG	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN CA 76)	182-216									
PPOLG ENMG	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN IN-175)	202-237	1021-1048	1103-1149							
PPOLG ENMG	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN LA)	202-237	1021-1048	1103-1149							
PPOLG ENMG	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN NIBD)	202-237	1021-1048	1103-1149							
PPOLG ENMG	GENOME POLYPROTEIN	SIMIAN HEPATITIS A VIRUS (STRAIN AGM-27)	207-241	1023-1032	1115-1192							
PPOLG ENMG	GENOME POLYPROTEIN	SIMIAN HEPATITIS A VIRUS (STRAIN CY-143)	201-237									
PPOLG ENMG	GENOME POLYPROTEIN	HUMAN RHINOVIRUS 14	17-44	359-386	652-679	1877-1904						
PPOLG ENMG	GENOME POLYPROTEIN	HUMAN RHINOVIRUS 18	1132-1159	1853-1882								
PPOLG ENMG	GENOME POLYPROTEIN	HUMAN RHINOVIRUS 2	1135-1152	1532-1593								
PPOLG ENMG	GENOME POLYPROTEIN	HUMAN RHINOVIRUS 89	883-910	1141-1168	1566-1607	1862-1889						
PPOLG ENMG	GENOME POLYPROTEIN	AVIAN ENTEROVIRUS 70 (STRAIN 167071)	876-910									
PPOLG ENMG	STRUCTURAL POLYPROTEIN	AVIAN ENTEROVIRUS 70 (STRAIN 167071)	231-277									
PPOLG ENMG	GENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN OII)	214-248	983-1010	2796-2823							
PPOLG ENMG	GENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN SA-14)	214-248	983-1010	2796-2823							
PPOLG ENMG	GENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN SA(V))	214-248	983-1010	2796-2823							
PPOLG ENMG	GENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN JAOKA5912)	141-175	911-938								
PPOLG ENMG	GENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN HAKAYAMA)	980-1007									
PPOLG ENMG	GENOME POLYPROTEIN	KUNIN VIRUS (STRAIN M0461C)	431-463	1634-1661								
PPOLG ENMG	GENOME POLYPROTEIN	LANGAT VIRUS (STRAIN TP21)	431-463	1634-1661								
PPOLG ENMG	GENOME POLYPROTEIN	LANGAT VIRUS (STRAIN YELANTSEV)	431-463									
PPOLG ENMG	GENOME POLYPROTEIN	LOUPING ILL VIRUS	151-185									
PPOLG ENMG	GENOME POLYPROTEIN	LOUPING ILL VIRUS (STRAIN SB 26)	151-185									
PPOLG ENMG	GENOME POLYPROTEIN	MOSQUITO CELL FUSING AGENT	671-698	3036-3083	3103-3130							
PPOLG ENMG	GENOME POLYPROTEIN	MAIZE DWARF MOSAIC VIRUS	10-37									
PPOLG ENMG	GENOME POLYPROTEIN	MURRAY VALLEY ENCEPHALITIS VIRUS	312-236									
PPOLG ENMG	GENOME POLYPROTEIN	ORANTHOGALUM MOSAIC VIRUS	24-51	946-973								
PPOLG ENMG	GENOME POLYPROTEIN	PEPPER MOTTLE VIRUS (CALIFORNIA ISOLATE)	377-404	704-738	831-858	900-927	1167-1201	1485-1512	1787-1814	2433-2464		
PPOLG ENMG	GENOME POLYPROTEIN	POLIOVIRUS TYPE 1 (STRAIN MATHONEY)	1060-1100	1901-1931								
PPOLG ENMG	GENOME POLYPROTEIN	POLIOVIRUS TYPE 1 (STRAIN SABIN)	620-697	1063-1101	1903-1933							
PPOLG ENMG	GENOME POLYPROTEIN	POLIOVIRUS TYPE 2 (STRAIN LANSING)	1061-1099	1901-1931								
PPOLG ENMG	GENOME POLYPROTEIN	POLIOVIRUS TYPE 2 (STRAIN W-2)	1061-1099	1901-1931								
PPOLG ENMG	GENOME POLYPROTEIN	POLIOVIRUS TYPE 3 (STRAIN 2117)	1060-1098	1900-1930								
PPOLG ENMG	GENOME POLYPROTEIN	POLIOVIRUS TYPE 3 (STRAINS PILEON37 AND PILEON 12A [11])	1060-1098	1900-1930								
PPOLG ENMG	GENOME POLYPROTEIN	PLUM POX POTYVIRUS (STRAIN D)	921-948	1498-1523	2771-2798							
PPOLG ENMG	GENOME POLYPROTEIN	PLUM POX POTYVIRUS (STRAIN EL AMAR)	1146-1187									

FILE NAME	10211714	ALL Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PROTEIN											
PPOL PPVNA	GENOME POLYPROTEIN	PLUM POX POTYVIRUS (ISOLATE NAT)	920-947	1497-1524	2770-2800						
PPOL PPVNA	GENOME POLYPROTEIN	PLUM POX POTYVIRUS (STRAIN RANKOVIC)	920-947	1497-1524	2770-2797						
PPOL PPVNA	GENOME POLYPROTEIN	PAPAYA RINGSPOOT VIRUS (STRAIN P / MUTANT IIA)	500-527								
PPOL PPVNA	GENOME POLYPROTEIN	PAPAYA RINGSPOOT VIRUS (STRAIN P / MUTANT IIA 5-1)	391-418								
PPOL PPVNA	GENOME POLYPROTEIN	PAPAYA RINGSPOOT VIRUS (STRAIN W)	489-516								
PPOL PPVNA	GENOME POLYPROTEIN	PEA SEED-BORNE MOSAIC VIRUS (STRAIN DPT01)	271-315	1132-1177	1510-1537						
PPOL PPVNA	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN C) (PVY)	433-460	701-735							
PPOL PPVNA	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN HUNGARIAN)	218-245	433-460	701-735	1486-1513	1777-1811				
PPOL PPVNA	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN N)	433-460	701-735	1486-1513						
PPOL PPVNA	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN O)	433-460	701-735							
PPOL PPVNA	GENOME POLYPROTEIN	PARSNIP YELLOW FLECK VIRUS (ISOLATE P-121)	1124-1151	2702-2734							
PPOL PPVNA	GENOME POLYPROTEIN	SUGARCANE MOSAIC VIRUS (STRAIN SC)	10-37								
PPOL PPVNA	GENOME POLYPROTEIN	SWINE VESICULAR DISEASE VIRUS (STRAIN IJ) 76)	1024-1060								
PPOL PPVNA	GENOME POLYPROTEIN	TICK-DORNE ENCEPHALITIS VIRUS (STRAIN SOPHIN)	87-121	214-272	1032-1061	1265-1292	2007-2036				
PPOL PPVNA	GENOME POLYPROTEIN	BORNE ENCEPHALITIS VIRUS (WESTERN SUBTYPE)	1632-1659								
PPOL PPVNA	GENOME POLYPROTEIN	TOBACCO ETCH VIRUS	845-872	1148-1175	1416-1443	1773-1800					
PPOL PPVNA	GENOME POLYPROTEIN	THEILER'S MURINE ENCEPHALOMYELITIS VIRUS (STRAIN DEAN 8386)	79-117	200-227							
PPOL PPVNA	GENOME POLYPROTEIN	THEILER'S MURINE ENCEPHALOMYELITIS VIRUS (STRAIN DA)	90-117	200-227							
PPOL PPVNA	GENOME POLYPROTEIN	THEILER'S MURINE ENCEPHALOMYELITIS VIRUS (STRAIN GDVII)	90-117	200-227							
PPOL PPVNA	GENOME POLYPROTEIN	TURNIP MOSAIC VIRUS	232-262	773-800							
PPOL PPVNA	GENOME POLYPROTEIN	TOBACCO VEIN MOTTLE VIRUS	406-433	670-704	2708-2742						
PPOL PPVNA	GENOME POLYPROTEIN	WATERMELON MOSAIC VIRUS II	202-229								
PPOL PPVNA	GENOME POLYPROTEIN	WEST NILE VIRUS	210-254	3385-3412							
PPOL PPVNA	GENOME POLYPROTEIN	YELLOW FEVER VIRUS (STRAIN I7D)	436-463								
PPOL PPVNA	GENOME POLYPROTEIN	YELLOW FEVER VIRUS (STRAIN PASTEUR 17D-204)	436-463								
PPOL PPVNA	GENOME POLYPROTEIN	ZUCCHINI YELLOW MOSAIC VIRUS	69-96								
PPOL PPVNA	GENOME POLYPROTEIN	POLIOVIRUS TYPE I (STRAIN MAHONEY)	1003-1101	1901-1913							
PPOL PPVNA	GENOME POLYPROTEIN	VENEZUELAN EQUINE ENCEPHALITIS VIRUS (STRAIN TRINIDAD DONKEY)	1402-1463	1894-1921							
PPOL PPVNA	GENOME POLYPROTEIN	FELINE CALICIVIRUS (STRAIN CF168 FIV)	443-472								
PPOL PPVNA	GENOME POLYPROTEIN	FELINE CALICIVIRUS (STRAIN F9)	1014-1061								
PPOL PPVNA	GENOME POLYPROTEIN	HEPATITIS E VIRUS (STRAIN BURMA)	219-246	349-376							
PPOL PPVNA	GENOME POLYPROTEIN	HEPATITIS E VIRUS (STRAIN MEXICO)	219-246	349-376							
PPOL PPVNA	GENOME POLYPROTEIN	HEPATITIS E VIRUS (STRAIN MYANMAR)	219-246	349-376							
PPOL PPVNA	GENOME POLYPROTEIN	HEPATITIS E VIRUS (STRAIN PAKISTAN)	218-245	348-375							
PPOL PPVNA	GENOME POLYPROTEIN	MIDDELBURG VIRUS	935-982								
PPOL PPVNA	GENOME POLYPROTEIN	ONYOM-ONYOM VIRUS (STRAIN GULU)	2453-2480								
PPOL PPVNA	GENOME POLYPROTEIN	RABBIT HEMORRHAGIC DISEASE VIRUS	311-347	1637-1684							
PPOL PPVNA	GENOME POLYPROTEIN	ROSS RIVER VIRUS (STRAIN NB992)	1037-1084	1472-1504	2418-2445						
PPOL PPVNA	GENOME POLYPROTEIN	RUBELLA VIRUS (STRAIN T48)	146-173	1087-1114							
PPOL PPVNA	GENOME POLYPROTEIN	SEMLIKI FOREST VIRUS	2060-2087								
PPOL PPVNA	GENOME POLYPROTEIN	SINDBIIS VIRUS (SUBTYPE OCKELBO / STRAIN EDSBYN 82-5)	1154-1181								
PPOL PPVNA	GENOME POLYPROTEIN	WESTERN EQUINE ENCEPHALITIS VIRUS	916-970								
PPOL PPVNA	GENOME POLYPROTEIN	AVIAN INFECTION BURSAL DISEASE VIRUS (STRAIN 5270)	4-31								
PPOL PPVNA	GENOME POLYPROTEIN	AVIAN INFECTION BURSAL DISEASE VIRUS (STRAIN AUSTRALIAN 602-71)	231-238								
PPOL PPVNA	GENOME POLYPROTEIN	AVIAN INFECTION BURSAL DISEASE VIRUS (STRAIN CU-1)	231-238								
PPOL PPVNA	GENOME POLYPROTEIN	AVIAN INFECTION BURSAL DISEASE VIRUS (STRAIN E)	231-238								
PPOL PPVNA	GENOME POLYPROTEIN	AVIAN INFECTION BURSAL DISEASE VIRUS (STRAIN PDG-98)	212-239								
PPOL PPVNA	GENOME POLYPROTEIN	AVIAN INFECTION BURSAL DISEASE VIRUS (STRAIN STC)	231-238								
PPOL PPVNA	GENOME POLYPROTEIN	ONYOM-ONYOM VIRUS (STRAIN GULU)	356-393								
PPOL PPVNA	GENOME POLYPROTEIN	ROSS RIVER VIRUS (STRAIN NB992)	919-973								
PPOL PPVNA	GENOME POLYPROTEIN	SINDBIIS VIRUS (SUBTYPE OCKELBO / STRAIN EDSBYN 82-5)	1138-1165								
PPOL PPVNA	GENOME POLYPROTEIN	WESTERN EQUINE ENCEPHALITIS VIRUS	920-947								
PPOL PPVNA	GENOME POLYPROTEIN	BABOON ENDOGENOUS VIRUS (STRAIN M7)	675-706	715-742							















PCGENE	1071714	All Virus (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	EXOTIN	VIRUS									
PUL37 HSV1	PROTEIN UL37	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	470-497	831-884							
PUL37 HSVB	GENE 33 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD49)	315-749	987-1014							
PUL37 HSVSA	GENE 63 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	31-65	643-737							
PUL37 VZV0	GENE 21 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	107-134	485-512	976-1003						
PUL41 VZV0	HOST SHUTOFF VIRION PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	330-364								
PUL42 HSV11	DNA-BINDING PROTEIN UL42	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	231-258								
PUL43 VZV0	GENE 13 MEMBRANE PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	129-156	312-340							
PUL47 HCMVA	PROTEIN UL47	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	114-148	488-485	763-790	802-853					
PUL47 HSV11	VIRION PROTEIN UL47	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	488-515								
PUL47 HSVIF	VIRION PROTEIN UL47	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN F)	190-217								
PUL47 HSVEA	97 KD ALPHA TRANS-INDUCING PROTEIN	EQUINE HERPESVIRUS TYPE 4	159-186								
PUL50 HCMVA	PROTEIN UL50	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	185-212	787-814							
PUL53 EBV	PROB DNA REPLICATION PROTEIN BSLF1	EPSTEIN-BARR VIRUS (STRAIN B95-8)	191-220	943-970							
PUL53 HSVB	DNA REPLICATION PROTEIN UL52	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD49)	130-157								
PUL53 HSVSA	PROB DNA REP GENE 34 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	301-337								
PUL53 VZV0	PROB DNA REP GENE 6 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	74-101								
PUL59 HCMVA	HYPOTHETICAL PROTEIN UL59	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	65-92								
PUL70 HCMVA	PROB DNA REP PROTEIN UL70	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	5-73								
PUL73 HCMVA	UL73 GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	9-36								
PUL73 HSVSA	HYPOTHETICAL GENE 53 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	45-79								
PUL74 HCMVA	HYPOTHETICAL PROTEIN UL74	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	409-436								
PUL77 EBV	HYPOTHETICAL PROTEIN BICRF1	EPSTEIN-BARR VIRUS (STRAIN B95-8)	516-563	729-768							
PUL77 HSVB	HYPOTHETICAL PROTEIN 3R	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	582-609								
PUL77 HSVSA	HYPOTHETICAL GENE 34 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	107-144	168-196							
PUL92 EBV	HYPOTHETICAL PROTEIN BDLF4	EPSTEIN-BARR VIRUS (STRAIN B95-8)	92-122								
PUL92 HSVSA	HYPOTHETICAL GENE 31 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	26-53	314-381							
PUL93 HCMVA	PROTEIN UL93	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	37-71								
PUL93 HSVB	HYPOTHETICAL PROTEIN UL93	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	73-100	105-134							
PUL93 HSVSA	VIRION PROTEIN UL104	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	4-31	443-477							
PUL99 HCMVA	HYPOTHETICAL PROTEIN UL119	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	90-124								
PULD0 HCMVA	HYPOTHETICAL PROTEIN UL130	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	135-176								
PUN0 HSVSA	URACIL-DNA GLYCOSYLASE	HERPESVIRUS SAIMIRI (STRAIN 11)	81-115								
PUN0 SEVKA	URACIL-DNA GLYCOSYLASE	SHOPE FIBROMA VIRUS (STRAIN KASZA)	85-116	129-156							
PUN0 VACCC	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	85-116	129-156							
PUN0 VACCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN WR)	85-116	129-156							
PUN0 YARV	URACIL-DNA GLYCOSYLASE	VARIOLA VIRUS	85-116								
PUS89 HCMVA	HYPOTHETICAL PROTEIN HQLF3	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	20-47								
PUS14 HCMVA	HYPOTHETICAL PROTEIN HVL4	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	273-308								
PUS18 HCMVA	MEMBRANE PROTEIN HWL5	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	191-218								
PV121 ASFLL	LIS 121-1 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS57)	2-29								
PV137 ASFLL	LIS 137 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS57)	702-729								
PV137 ASFLL	LIS 137 PROTEIN	AFRICAN SWINE FEVER VIRUS (ISOLATE LEIDEN)	2-29								
PV137 ASFLL	LIS 137 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS57)	39-86								
PV143 NPVAC	HELICASE	TOBACCO RATTLE VIRUS (STRAIN PLB)	496-560	945-972							
PV16K TRVPS	16 KD PROTEIN	AUTOGRAPIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	75-113								
PV1A BMY	1A PROTEIN	TOBACCO RATTLE VIRUS (STRAIN PSG)	23-54	710-737	840-868						
PV1A CMV	1A PROTEIN	BROME MOSAIC VIRUS	22-58	384-411	836-863	892-919					
PV1A CMYFN	1A PROTEIN	COWPEA CHLOROTIC MOTTLE VIRUS	249-276								
PV1A CMVO	1A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN FNY)	11-38								
PV1A CMVQ	1A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN O)	11-38	664-902							
PV1A PSVI	1A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN Q)	11-38								
PV1A TAV	1A PROTEIN	PEANUT STUNT VIRUS (STRAIN J)	4-38	372-599							
PV23K NPVAC	23 KD PROTEIN	TOMATO ASPERM VIRUS	11-38	271-298	376-403	857-884					
PV29K PEBV	29.6 KD PROTEIN	AUTOGRAPIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	4-31								
PV29K TRVSV	29 KD PROTEIN	PEA EARLY BROWNING VIRUS	140-170								
PV29K TRVSV	29 KD PROTEIN	TOBACCO RATTLE VIRUS	170-197								

PCGENE	107178.4	All Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
FILENAME	PROTEIN	VIRUS	48-75									
PV3K TRVC	39 KD PROTEIN	TOBACCO RATTLE VIRUS (STRAIN TCN)	101-124									
PV3A BMY	2A PROTEIN	BROAD LEAF MOTTLE VIRUS	178-205									
PV3A CCMV	2A PROTEIN	COWPEA CLIMOTIC MOTTLE VIRUS	792-819									
PV3A CMVN	2A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN FNY)	712-751									
PV3A PSV	2A PROTEIN	PEANUT STUNT VIRUS (STRAIN I)	313-352									
PV3A TAV	2A PROTEIN	TOMATO ASPERNY VIRUS	722-756									
PV3K HCMVE	30 KD MAJOR EARLY PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN EISENHARDT)	194-221									
PV3K TRVC	29.1 KD PROTEIN	TOBACCO RATTLE VIRUS (STRAIN TCN)	130-160									
PV3P ADE41	31 KD PHOSPHOPROTEIN	HUMAN ADENOVIRUS TYPE 41	15-42									
PV3B ASF7	K162 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	35-102									
PV3B ASF7	D163 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	5-30									
PV3A BMY	3A PROTEIN	BROME MOSAIC VIRUS	11-38									
PV3A CMVN	3A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN FNY)	222-232									
PV3A CMVN	3A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN I)	212-232									
PV3A CMVO	3A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN O)	222-232									
PV3A CMVY	3A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN Y)	222-232									
PV3A BVH	3A PROTEIN	AVIAN INFECTIONOUS BRONCHITIS VIRUS (STRAIN HEALING 11)	25-57									
PV3A BVH	3A PROTEIN	AVIAN INFECTIONOUS BRONCHITIS VIRUS (STRAIN ES/18/166)	29-56									
PV3B BVH	3B PROTEIN	AVIAN INFECTIONOUS BRONCHITIS VIRUS (STRAIN BEALJETTE)	6-33									
PV3K BYDVP	50 KD PROTEIN	BARLEY YELLOW DWARF VIRUS (ISOLATE PA)	119-146									
PV3K BMY	51 KD PROTEIN	BEEF WESTERN YELLOW VIRUS (ISOLATE FL-4)	113-147									
PV3K BMY	51 KD PROTEIN	BEEF WESTERN YELLOW VIRUS (ISOLATE GR1)	113-147									
PV3K PLV1	50 KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN I)	124-151									
PV3K PLVW	50 KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	124-151									
PV3K BMY	51 KD PROTEIN	BARLEY STRIPE MOSAIC VIRUS	128-155									
PV3K PLV1	60.7 KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN I)	110-140									
PV3K PLVW	60.7 KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	110-140									
PV3K AMYLE	90 KD PROTEIN	ALPHA MOSAIC VIRUS (STRAIN 42/7 ISOLATE LEIDEN)	107-114									
PV3K VACC	PROTEIN A6	VACCINIA VIRUS (STRAIN COPENHAGEN)	157-216									
PV3K VACC	PROTEIN A6	VACCINIA VIRUS (STRAIN WR)	156-215									
PV3K VACC	PROTEIN A6	VARIOLA VIRUS	157-216									
PV3K VACC	PROTEIN A6	VACCINIA VIRUS (STRAIN COPENHAGEN)	176-208									
PV3K VACC	PROTEIN A8	VARIOLA VIRUS	176-208									
PV3K VACC	PROTEIN A8	VARIOLA VIRUS	60-95									
PV3K VACC	PROTEIN A9	VACCINIA VIRUS (STRAIN COPENHAGEN)	219-283									
PV3K VACC	PROTEIN A11	VARIOLA VIRUS	220-284									
PV3K VACC	PROTEIN A11	VARIOLA VIRUS	440-467									
PV3K VACC	PROTEIN A20	VACCINIA VIRUS (STRAIN COPENHAGEN)	8-67									
PV3K VACC	PROTEIN A20	VARIOLA VIRUS	8-67									
PV3K VACC	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	45-72									
PV3K VACC	PROTEIN A22	VARIOLA VIRUS	56-83									
PV3K VACC	PROTEIN A23	VACCINIA VIRUS (STRAIN COPENHAGEN)	95-144									
PV3K VACC	PROTEIN A23	VARIOLA VIRUS	95-144									
PV3K VACC	PROTEIN A23	VACCINIA VIRUS (STRAIN WR)	22-49									
PV3K VACC	PROTEIN A23	VARIOLA VIRUS	22-49									
PV3K VACC	PROTEIN A30	VACCINIA VIRUS (STRAIN WR)	12-55									
PV3K VACC	PROTEIN A31	VACCINIA VIRUS (STRAIN COPENHAGEN)	88-115									
PV3K VACC	PROTEIN A31	VARIOLA VIRUS	88-122									
PV3K VACC	PROTEIN A34	VACCINIA VIRUS (STRAIN COPENHAGEN)	87-114									
PV3K VACC	PROTEIN A34	VARIOLA VIRUS	87-114									
PV3K VACC	PROTEIN A34	VACCINIA VIRUS (STRAIN WR)	87-114									
PV3K VACC	PROTEIN A34	VARIOLA VIRUS	87-114									
PV3K VACC	PROTEIN A36 PRECURSOR	VACCINIA VIRUS (STRAIN WR)	120-155									
PV3K VACC	PROTEIN A31	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV3K VACC	PROTEIN A31	VACCINIA VIRUS (STRAIN WR)	44-81									
PV3K VACC	PROTEIN A31	VARIOLA VIRUS	44-81									
PV3K VACC	PROTEIN A39	VACCINIA VIRUS (STRAIN COPENHAGEN)	37-71									



PCGENE	1071784	All Viruses (no bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	VIRUS	209-216	484-515							
PVC04 SFVXA	PROTEIN C4	SHOPE FIBROMA VIRUS (STRAIN KASZA)	12-46								
PVC04 VACCC	PROTEIN C4	VACCINIA VIRUS (STRAIN COPENIAGEN)	12-46								
PVC04 VACCV	PROTEIN C4	VACCINIA VIRUS (STRAIN WR)	12-46								
PVC04 VARV	PROTEIN C4	VARIOLA VIRUS	12-46								
PVC03 SFVXA	HYPOTHEICAL PROTEIN C5	SHOPE FIBROMA VIRUS (STRAIN KASZA)	85-123	152-179							
PVC03 VACCC	PROTEIN C5	VACCINIA VIRUS (STRAIN COPENIAGEN)	38-65								
PVC03 VACCV	PROTEIN C5	VACCINIA VIRUS (STRAIN WR)	38-65								
PVC03 VARV	PROTEIN C5	VARIOLA VIRUS	38-65								
PVC01 VACCV	PROTEIN C7	VACCINIA VIRUS (STRAIN WR)	80-111								
PVC01 VARV	PROTEIN C7	VARIOLA VIRUS	80-111								
PVC09 VACCC	PROTEIN C9	VACCINIA VIRUS (STRAIN COPENIAGEN)	42-69	82-116	178-205	232-279	289-333	372-405			
PVC09 VACCV	PROTEIN C9	VACCINIA VIRUS (STRAIN WR)	42-69	82-116	178-205	232-279	289-333	372-405			
PVC09 VARV	PROTEIN C9	VARIOLA VIRUS	136-180								
PVC10 VACCC	PROTEIN C10	VACCINIA VIRUS (STRAIN COPENIAGEN)	136-180								
PVC10 VACCV	PROTEIN C10	VACCINIA VIRUS (STRAIN WR)	136-180								
PVC10 VARV	PROTEIN C10	VARIOLA VIRUS	136-180								
PVC11 SFVXA	PROTEIN C13	SHOPE FIBROMA VIRUS (STRAIN KASZA)	3-30	19-66	117-182	206-240					
PVC11 VACCC	PROTEIN C13	VACCINIA VIRUS (STRAIN COPENIAGEN)	111-153								
PVC11 VACCV	PROTEIN C13	VACCINIA VIRUS (STRAIN WR)	40-74								
PVC11 VARV	PROTEIN C13	VARIOLA VIRUS	36-97								
PVC18 SFVXA	PROTEIN C19	SHOPE FIBROMA VIRUS (STRAIN KASZA)	72-99								
PVC18 VACCC	PROTEIN C19	VACCINIA VIRUS (STRAIN COPENIAGEN)	399-126								
PVC18 VACCV	PROTEIN C19	VACCINIA VIRUS (STRAIN WR)	847-874								
PVC18 VARV	PROTEIN C19	VARIOLA VIRUS	769-799								
PVC21 EBY	MAJOR CAPSID PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-1)	136-170	335-382							
PVC21 HSVA	MAJOR CAPSID PROTEIN	HERPES SIMPLEX VIRUS (TYPE 67 STRAIN UGANDA-1102)	88-115	199-248							
PVC21 HSVA	MAJOR CAPSID PROTEIN	HERPES VIRUS SAMIRI (STRAIN 11)	87-114								
PVC01 NPVAC	DNA-BINDING PROTEIN	AUTOGRAPIA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS	133-165								
PVC04 ADE02	MINOR CORE PROTEIN	HUMAN ADENOVIRUS TYPE 2	88-115								
PVC04 ADE03	MINOR CORE PROTEIN	HUMAN ADENOVIRUS TYPE 3	87-114								
PVC05 FOWP1	92.6 KD PROTEIN	FOWLPOX VIRUS (STRAIN FP-1)	6-33	184-211	221-248						
PVC05 VACCC	PROTEIN D5	VACCINIA VIRUS (STRAIN COPENIAGEN)	240-267	333-360							
PVC05 VACCV	PROTEIN D5	VACCINIA VIRUS (STRAIN WR)	240-267								
PVC05 VARV	PROTEIN D5	VARIOLA VIRUS	240-267								
PVC09 VACCC	PROTEIN D9	VACCINIA VIRUS (STRAIN COPENIAGEN)	123-150								
PVC09 VACCV	PROTEIN D9	VACCINIA VIRUS (STRAIN WR)	123-150								
PVC09 VARV	PROTEIN D9	VARIOLA VIRUS	123-160								
PVC10 SFVXA	PROTEIN D10	SHOPE FIBROMA VIRUS (STRAIN KASZA)	18-33								
PVC10 CERV	DNA-BINDING PROTEIN	CARNATION ETCHED RING VIRUS	2-35								
PVC02 VARV	PROTEIN E2	VARIOLA VIRUS	287-322								
PVC06 VACCC	PROTEIN E6	VACCINIA VIRUS (STRAIN COPENIAGEN)	89-116	437-464							
PVC06 VACCV	PROTEIN E6	VACCINIA VIRUS (STRAIN WR)	89-116	437-464							
PVC06 VARV	PROTEIN E6	VARIOLA VIRUS	89-116	437-464							
PVE1 HPV18	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 18	60-87								
PVE1 HPV2A	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 2A	21-48								
PVE1 HPV3J	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 3J	180-207								
PVE1 HPV39	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 39	103-130								
PVE1 HPV41	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	55-89								
PVE1 HPV42	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 42	25-59								
PVE1 HPV47	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	146-173								
PVE1 HPV57	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 57	21-48								
PVE16 NPVAC	EARLY 21.9 KD PROTEIN	AUTOGRAPIA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS	72-113								
PVE2 CRPVK	PROBABLE E3 PROTEIN	COTTONTAIL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN KAN SAS)	5-34								
PVE2 HPV05	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 5	17-51								
PVE2 HPV1J	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 1J	157-184	314-361							
PVE2 HPV16	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 16	61-105	312-342							
PVE2 HPV18	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 18	113-340								
PVE2 HPV1A	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 1A	159-186								
PVE2 HPV2A	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 2A	159-193								
PVE2 HPV3J	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 3J	304-331								



PCGENE	1071214	All Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	VIRUS	158-192	321-334							
PVE1 HPV33	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 33	7-34	321-337							
PVE2 HPV39	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 39	17-51	148-175	276-303						
PVE3 HPV41	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	137-184								
PVE4 HPV51	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 51	168-193								
PVE5 HPV53	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 53	2-36	309-336							
PVE6 HPV58	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 58	17-51								
PVE7 HPV5B	PROBABLE E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 5B	120-150								
PVE8 PAPV6	PROBABLE E2 PROTEIN	EUROPEAN ELK PAPILLOMAVIRUS	267-294	327-361							
PVE9 PCPVI	E2 PROTEIN	PGHAY CHIMPANZEE PAPILLOMAVIRUS TYPE 1	202-229								
PVEA HPV03	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 3	81-108								
PVEB HPV11	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 11	66-93								
PVEC HPV16	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 16	59-86								
PVED HPV18	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 18	75-102								
PVEE HPV21	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 21	63-97								
PVEF HPV31	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 31	202-229								
PVEG HPV5B	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 5B	30-60								
PVEH HPV11	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 11	30-60								
PVEI HPV6B	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 6B	30-60								
PVEJ HPV6C	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 6C	30-60								
PVEK HPV33	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 33	27-54								
PVEL HPV3B	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 3B	11-41								
PVEM PCPVI	PROBABLE E4 PROTEIN	PGHAY CHIMPANZEE PAPILLOMAVIRUS TYPE 1	35-62								
PVEN HPV11	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 11	75-102								
PVEO HPV31	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 31	69-96								
PVEP HPV39	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 39	71-102								
PVEQ HPV41	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	119-146								
PVER HPV43	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 43	75-102								
PVES HPV51	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 51	72-99								
PVEU HPVME	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE ME10	71-102								
PVEV HPVAC	EARLY M4 KD PROTEIN	HUMAN PAPILLOMAVIRUS TYPE ME10	630-647								
PVEW GYTN	VIRAL ENHANCING FACTOR	TRICHOPLUSIA NI GRANULOSIS VIRUS	411-418								
PVEY DRYT1	ENVELOPE GLYCOPROTEIN PRECURSOR	DIORBI VIRUS (STRAIN INDIAN/VI11/01)	318-366								
PVENY EAV	ENVELOPE GLYCOPROTEIN	EQUINE ARTERITIS VIRUS	120-147								
PVENY THOGV	ENVELOPE GLYCOPROTEIN PRECURSOR	THOGOTO VIRUS	313-347								
PVET0 VACCC	PROTEIN F3	VACCINIA VIRUS (STRAIN COPENHAGEN)	71-110	185-212							
PVET0 VACCV	PROTEIN F3	VACCINIA VIRUS (STRAIN WR)	71-110	185-212							
PVET0 VACCP	38 KD MAJOR MEMBRANE PRO PRECURSOR	VACCINIA VIRUS (STRAIN L-1VP)	33-60								
PVET0 VACCV	38 KD MAJOR MEMBRANE PRO PRECURSOR	VACCINIA VIRUS (STRAIN WR)	33-60								
PVET0 VARV	PROTEIN F6	VARIOLA VIRUS	10-44								
PVET1 VACCC	PROTEIN F11	VACCINIA VIRUS (STRAIN COPENHAGEN)	274-321								
PVET1 VACCP	PROTEIN F11	VACCINIA VIRUS (STRAIN L-1VP)	270-317								
PVET1 VARV	PROTEIN F11	VARIOLA VIRUS	274-321								
PVET2 VACCC	PROTEIN F12	VACCINIA VIRUS (STRAIN COPENHAGEN)	10-37	113-140	354-381						
PVET2 VACCP	PROTEIN F12	VACCINIA VIRUS (STRAIN L-1VP)	10-37	113-140	354-381						
PVET3 VARV	PROTEIN F16	VARIOLA VIRUS	10-37	202-216	354-381						
PVET4 VACCC	PROTEIN F16	VACCINIA VIRUS (STRAIN COPENHAGEN)	35-62	132-179							
PVET4 VACCP	PROTEIN F16	VACCINIA VIRUS (STRAIN L-1VP)	35-62	132-179							
PVET5 VARV	PROTEIN F16	VARIOLA VIRUS	35-62	149-179							
PVET6 FOWPV	PROTEIN F4	FOWLPOX VIRUS	146-173								
PVET7 ORFNZ	10 KD FUSION PROTEIN	ORF VIRUS (STRAIN NZ2)	59-86								
PVET8 VACCC	14 KD FUSION PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	37-64								
PVET9 VACCC	KD FUSION PROTEIN	VACCINIA VIRUS (STRAIN WR)	37-64								
PVET0 VACCC	PROTEIN G1	VACCINIA VIRUS (STRAIN COPENHAGEN)	225-232	301-315							
PVET1 VACCV	PROTEIN G1	VACCINIA VIRUS (STRAIN WR)	164-191	240-274							
PVET2 VARV	PROTEIN G1	VARIOLA VIRUS	235-252	301-315							
PVET3 VACCV	ISATIN-B-TSC DEF PROTEIN	VACCINIA VIRUS (STRAIN WR)	96-123								
PVET4 VARV	ISATIN-B-TSC DEF PROTEIN	VARIOLA VIRUS	96-123								



PCGENE	10117144	All Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PVG01 HSVED	GENE 3 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AHA1P)	146-176								
PVG01 HSVEX	GENE 3 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN KENTUCKY A)	146-176								
PVG03 VACC	PROTEIN G3	VACCINIA VIRUS (STRAIN COPENHAGEN)	48-75	131-161	235-289	355-389					
PVG03 VARCV	PROTEIN G3	VARIOLA VIRUS	48-75	124-161	235-289	355-389					
PVG07 HSVI	HYPOTHETICAL GENE 7 MEMB PRO	ICTALURID HERPESVIRUS 1	71-98								
PVG09 VACC	PROTEIN F1	VACCINIA VIRUS (STRAIN COPENHAGEN)	108-238								
PVG09 VACC	PROTEIN F1	VACCINIA VIRUS (STRAIN VIR)	271-301								
PVG09 VARV	PROTEIN F1	VARIOLA VIRUS	108-238								
PVG12 SPVIR	GENE 12 PROTEIN	SPIROPLASMA VIRUS SPV1-RAA2 B	11-45								
PVG17 HSVI	HYPOTHETICAL GENE 17 PROTEIN	ICTALURID HERPESVIRUS 1	177-204								
PVG18 HSVI	HYPOTHETICAL GENE 18 PROTEIN	ICTALURID HERPESVIRUS 1	174-208								
PVG1 SPVIR	CAPSID PROTEIN	SPIROPLASMA VIRUS SPV1-RAA2 B	260-287								
PVG1 SPV4	CAPSID PROTEIN	SPIROPLASMA VIRUS 4	282-314	381-410	668-705	766-824					
PVG2 HSVI	HYPOTHETICAL GENE 32 PROTEIN	ICTALURID HERPESVIRUS 1	373-400	581-622	668-705	766-824					
PVG4 HSVI	HYPOTHETICAL GENE 44 PROTEIN	ICTALURID HERPESVIRUS 1	311-58								
PVG8 HSVI	HYPOTHETICAL GENE 28 PROTEIN	AMSACTA MOOREI ENTOMOPHOXVIRUS	233-290	497-528							
PVG8 AMEPV	HYPOTHETICAL G3R PROTEIN	AMSACTA MOOREI ENTOMOPHOXVIRUS	311-64	91-118							
PVG2 SPVIR	GENE 2 PROTEIN	SPIROPLASMA VIRUS SPV1-RAA2 B	285-226								
PVG1 SPV4	GENE 2 PROTEIN	SPIROPLASMA VIRUS 4	146-173	175-205	262-310						
PVG1 HSVI	HYPOTHETICAL GENE 34 PROTEIN	ICTALURID HERPESVIRUS 1	95-122								
PVG17 HSVI	HYPOTHETICAL GENE 37 PROTEIN	ICTALURID HERPESVIRUS 1	442-469								
PVG19 HSVI	HYPOTHETICAL GENE 39 PROTEIN	ICTALURID HERPESVIRUS 1	651-678	1088-1115							
PVG1 AMEPV	HYPOTHETICAL GIL PROTEIN	AMSACTA MOOREI ENTOMOPHOXVIRUS	2-29								
PVG1 SPVIR	GENE 3 PROTEIN	SPIROPLASMA VIRUS SPV1-RAA2 B	15-49								
PVG1 SPV4	GENE 3 PROTEIN	SPIROPLASMA VIRUS 4	18-52	87-148							
PVG4 HSVI	HYPOTHETICAL GENE 45 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	118-163								
PVG4 HSVI	PROBABLE MAJOR GLYCOPROTEIN	ICTALURID HERPESVIRUS 1	42-109	346-373	497-524	973-1007					
PVG4 HSVI	HYPOTHETICAL GENE 48 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	360-394								
PVG4 AMEPV	GPR PROTEIN	AMSACTA MOOREI ENTOMOPHOXVIRUS	4-31								
PVG4 SPVIR	GENE 4 PROTEIN	SPIROPLASMA VIRUS SPV1-RAA2 B	116-146								
PVG1 HSVI	HYPOTHETICAL GENE 31 MEMBRANE PROTEIN	ICTALURID HERPESVIRUS 1	14-61	87-114							
PVG3 HSVI	HYPOTHETICAL GENE 32 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	47-74								
PVG6 HSVI	HYPOTHETICAL GENE 56 PROTEIN	ICTALURID HERPESVIRUS 1	582-609								
PVG1 SPVIR	GENE 5 PROTEIN	SPIROPLASMA VIRUS SPV1-RAA2 B	65-92								
PVG1 SPV4	GENE 5 PROTEIN	SPIROPLASMA VIRUS 4	56-83								
PVG3 HSVI	HYPOTHETICAL GENE 63 PROTEIN	ICTALURID HERPESVIRUS 1	550-584								
PVG4 HSVI	HYPOTHETICAL GENE 64 PROTEIN	ICTALURID HERPESVIRUS 1	475-504								
PVG3 HSVI	HYPOTHETICAL GENE 65 PROTEIN	ICTALURID HERPESVIRUS 1	1273-1254								
PVG6 HSVI	HYPOTHETICAL GENE 66 PROTEIN	ICTALURID HERPESVIRUS 1	362-406								
PVG7 HSVI	HYPOTHETICAL GENE 67 PROTEIN	ICTALURID HERPESVIRUS 1	1342-1369								
PVG4 HSVI	HYPOTHETICAL GENE 68 PROTEIN	ICTALURID HERPESVIRUS 1	261-288								
PVG7 HSVI	HYPOTHETICAL GENE 72 PROTEIN	ICTALURID HERPESVIRUS 1	447-481								
PVG1 HSVI	HYPOTHETICAL GENE 73 PROTEIN	ICTALURID HERPESVIRUS 1	318-422								
PVG6 HSVI	HYPOTHETICAL GENE 76 PROTEIN	ICTALURID HERPESVIRUS 1	200-227								
PVG7 SPV4	GENE 7 PROTEIN	SPIROPLASMA VIRUS 4	14-44								
PVG1 HSVI	F1 PROTEIN	AVIAN INFECTION BRONCHITIS VIRUS	1230-1260	2408-2435							
PVG1 HSVI	F2 GLYCOPROTEIN PRECURSOR	BOVINE CORONA VIRUS (STRAIN F15)	399-426	642-676	1022-1084	1278-1305					
PVG2 HSVI	F3 GLYCOPROTEIN PRECURSOR	BOVINE CORONA VIRUS (STRAIN L9)	399-426	642-676	1022-1084	1278-1305					
PVG3 HSVI	F4 GLYCOPROTEIN PRECURSOR	BOVINE CORONA VIRUS (STRAIN L13)	399-426	642-676	1022-1084	1278-1305					
PVG4 HSVI	F5 GLYCOPROTEIN PRECURSOR	BOVINE CORONA VIRUS (STRAIN MEUBS)	399-426	642-676	1022-1084	1278-1305					
PVG5 HSVI	F6 GLYCOPROTEIN PRECURSOR	BOVINE CORONA VIRUS (STRAIN QUEBEC)	399-426	642-676	1022-1084	1278-1305					
PVG6 HSVI	F7 GLYCOPROTEIN PRECURSOR	BOVINE CORONA VIRUS (STRAIN VACCINE)	399-426	642-676	1022-1084	1278-1305					
PVG7 HSVI	F8 GLYCOPROTEIN PRECURSOR	HUMAN CORONA VIRUS (STRAIN 229E)	710-99	109-131	1056-1112						
PVG8 HSVI	F9 GLYCOPROTEIN PRECURSOR	MURINE CORONA VIRUS MHV (STRAIN WILD TYPE 4)	643-684	1030-1092							
PVG9 HSVI	F10 GLYCOPROTEIN PRECURSOR	MURINE CORONA VIRUS MHV (STRAIN A39)	76-63	591-632	978-1040						
PVG10 HSVI	F11 GLYCOPROTEIN PRECURSOR	MURINE CORONA VIRUS MHV (STRAIN A39)	643-684	1030-1092							
PVG11 HSVI	F12 GLYCOPROTEIN PRECURSOR	MURINE CORONA VIRUS MHV (STRAIN JRM)	502-543	1889-551							















PGCENE	10711784	All Viruses (no bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	VIRUS									
PVP10 RGDV	NONSTRUCTURAL PROTEIN PMS10	RICE GALL DWARF VIRUS	205-232								
PVP10 WTV	NONSTRUCTURAL PROTEIN PMS10	WOUND TUMOR VIRUS	151-181	227-234							
PVP11 RDV	NONSTRUCTURAL PROTEIN PMS11	RICE DWARF VIRUS	53-80								
PVP11 WTV	NONSTRUCTURAL PROTEIN PMS12	WOUND TUMOR VIRUS	81-108								
PVP11 WTVN1	NONSTRUCTURAL PROTEIN PMS12	WOUND TUMOR VIRUS (STRAIN NI)	81-108								
PVP19 ANCV	CORE PROTEIN P19	ARTICHOKE MOTTLED CRINKLE VIRUS	71-100								
PVP19 BSVC	CORE PROTEIN P19	TOMATO BUSHY STUNT VIRUS (STRAIN CHERRY)	71-100								
PVP21 HSVA	PROBABLE CAPSID PROTEIN VP21	HERPESVIRUS SAIMIRI (STRAIN 11)	2-29								
PVP26 HSVD	CAPSID PROTEIN VP26	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB41)	36-63								
PVP26 HSVA	CAPSID PROTEIN VP26	HERPESVIRUS SAIMIRI (STRAIN 11)	48-75								
PVP2 HSVA	OUTER CAPSID PROTEIN VP2	AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 4 / STRAIN VACCINE)	271-304	410-437	632-662	907-934					
PVP2 BTY12	OUTER CAPSID PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE USA)	815-846								
PVP2 BTY1A	OUTER CAPSID PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 1 / ISOLATE AUSTRALIA)	898-923								
PVP2 BTY1A	OUTER CAPSID PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 1 / ISOLATE AUSTRALIA)	119-146								
PVP2 BTY1A	OUTER CAPSID PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 1 / ISOLATE AUSTRALIA)	72-103	415-453							
PVP2 BTY1A	OUTER CAPSID PROTEIN VP2	EPIZOOTIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1)	19-94	524-554							
PVP2 BTY1A	OUTER CAPSID PROTEIN VP2	BOVINE ROTAVIRUS (STRAIN RF)	70-101	531-567							
PVP2 ROTB	RNA-BINDING PROTEIN VP2	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	32-99	178-156	518-543	705-746					
PVP2 ROTB	RNA-BINDING PROTEIN VP2	PORCINE ROTAVIRUS (GROUP C / STRAIN COWDEN)	36-96								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	19-75								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	AFRICAN SWINE FEVER VIRUS (STRAIN E-75)	19-75								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	AFRICAN SWINE FEVER VIRUS (STRAIN DA715)	19-75								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	EBOLA VIRUS	81-119								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	MARBURG VIRUS (STRAIN MUGEN)	80-107	231-238							
PVP2 ROTB	RNA-BINDING PROTEIN VP2	MARBURG VIRUS (STRAIN POPP)	80-107	231-238							
PVP2 ROTB	RNA-BINDING PROTEIN VP2	AUTOGRAHA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS	270-297								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	BOVINE MORBID NUCLEAR POLYIHDROSIS VIRUS	68-102								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	VACCINIA VIRUS (STRAIN WR)	178-205								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	AUTOGRAHA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS	134-161	264-291							
PVP2 ROTB	RNA-BINDING PROTEIN VP2	ORGYIA PSEUDOTOGATA MULTICAPSID POLYIHDROSIS VIRUS	263-290								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 4 / STRAIN VACCINE)	132-159								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	214-232								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE USA)	214-232								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE AUSTRALIA)	214-232								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	EPIZOOTIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1)	209-243	798-832							
PVP2 ROTB	RNA-BINDING PROTEIN VP2	EPIZOOTIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 2 / STRAIN AUSTRALIA)	798-832								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	GRAPEVINE FANLEAF VIRUS	99-133								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	PORCINE ROTAVIRUS (GROUP C / STRAIN COWDEN)	39-66	379-384							
PVP2 ROTB	RNA-BINDING PROTEIN VP2	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	26-67	350-377	431-497	619-692					
PVP2 ROTB	RNA-BINDING PROTEIN VP2	EPSTEIN-BARR VIRUS (STRAIN B93-4)	440-470								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	HERPESVIRUS SAIMIRI (STRAIN 11)	205-232	344-372							
PVP2 ROTB	RNA-BINDING PROTEIN VP2	INFECTIOUS LARYNGITIS VIRUS (STRAIN THORNE V882)	515-549								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	174-208	495-522							
PVP2 ROTB	RNA-BINDING PROTEIN VP2	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	8-35	589-619							
PVP2 ROTB	RNA-BINDING PROTEIN VP2	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	8-35	584-622							
PVP2 ROTB	RNA-BINDING PROTEIN VP2	VACCINIA VIRUS (STRAIN COPENHAGEN)	48-75								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	VACCINIA VIRUS (STRAIN WR)	48-75								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	VARIOLA VIRUS	48-75								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	FOWLPOX VIRUS	80-110								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	VACCINIA VIRUS (STRAIN COPENHAGEN)	7-37								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	VACCINIA VIRUS (STRAIN WR)	7-37								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	VARIOLA VIRUS	7-37								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	34-61	576-603							
PVP2 ROTB	RNA-BINDING PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 13 / ISOLATE USA)	34-61	576-603							
PVP2 ROTB	RNA-BINDING PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 2 / ISOLATE USA)	34-61	576-603							
PVP2 ROTB	RNA-BINDING PROTEIN VP2	NEBRASKA CALF DIARRHEA VIRUS (STRAIN NCDV-LINCOLN)	553-632								
PVP2 ROTB	RNA-BINDING PROTEIN VP2	BOVINE ROTAVIRUS (SEROTYPE 6 / STRAIN B641)	595-629								



PCGENE	1011/784	All Viruses (no bacteriophages)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
FILE NAME	PROTEIN	VIRUS	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PVP4 ROTB	OUTER CAPSID PROTEIN VP4	BOVINE ROTAVIRUS (STRAIN C46)	8-35	584-622							
PVP4 ROTBC	OUTER CAPSID PROTEIN VP4	BOVINE ROTAVIRUS (STRAIN UK)	595-629								
PVP4 ROTBU	OUTER CAPSID PROTEIN VP4	EQUINE ROTAVIRUS (STRAIN H-2)	112-146	235-269	552-629						
PVP4 ROTBI	OUTER CAPSID PROTEIN VP4	ROTAVIRUS (GROUP B / STRAIN IDIR)	5-32								
PVP4 ROTGI	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN 076)	8-35	572-628							
PVP4 ROTHI	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN RV-5)	8-35	279-306	565-621						
PVP4 ROTJ	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN 694)	8-35	112-139	584-629						
PVP4 ROTK	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN 694)	8-35	279-306	565-621						
PVP4 ROTL	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN US1)	8-35	279-306	565-621						
PVP4 ROTM	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN K8)	8-35	111-118							
PVP4 ROTN	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN KU)	8-35	77-104	279-306	577-621					
PVP4 ROTL	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN L26)	8-35	279-306	565-621						
PVP4 ROTM	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN K37)	8-35	572-610							
PVP4 ROTN	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN MCN1)	8-35	573-628							
PVP4 ROTP	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN P)	8-35	577-621							
PVP4 ROTR	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN RV)	8-35	105-135	235-262						
PVP4 ROTI	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN ST. THOMAS 3)	8-35	572-627							
PVP4 ROTJ	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN VA10)	8-35	279-306	590-617						
PVP4 ROTK	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	8-35	577-621							
PVP4 ROTL	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (SEROTYPE 3 / STRAIN OSU)	112-146	584-625							
PVP4 ROTM	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (GROUP C / STRAIN COWDEN)	5-33	115-161	293-310						
PVP4 ROTN	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (STRAIN GOTTFRIED)	8-35	572-628	584-625						
PVP4 ROTP	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (STRAIN YN)	8-35	584-622							
PVP4 ROTQ	OUTER CAPSID PROTEIN VP4	RHESUS ROTAVIRUS	8-35	589-619							
PVP4 ROTR	OUTER CAPSID PROTEIN VP4	SIMIAN 11 ROTAVIRUS (STRAIN SA11-FEM)	8-35	130-157	584-622						
PVP4 ROTS	OUTER CAPSID PROTEIN VP4	SIMIAN 11 ROTAVIRUS (STRAIN SA11-SEM)	8-35	130-157	584-622						
PVP4 ROTU	OUTER CAPSID PROTEIN VP4	AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 4 / STRAIN VACCINE)	113-183	191-218							
PVP4 ROTV	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	51-80	99-126							
PVP4 ROTW	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	51-80	92-126							
PVP4 ROTX	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 13 / ISOLATE USA)	51-80	89-126							
PVP4 ROTY	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE AUSTRALIA)	51-80	89-126							
PVP4 ROTZ	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE SOUTH AFRICA)	51-80	92-126	148-182						
PVP4 ROT1	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 2 / ISOLATE USA)	51-80	89-126							
PVP4 ROT2	OUTER CAPSID PROTEIN VP5	EPIDEMIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1)	31-80	191-218	399-426						
PVP4 ROT3	OUTER CAPSID PROTEIN P5	WOUND TUMOR VIRUS	648-653								
PVP4 ROT4	OUTER CAPSID PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	161-193								
PVP4 ROT5	OUTER CAPSID PROTEIN P5	MAIZE ROUGH DWARF VIRUS	153-202								
PVP4 ROT6	OUTER CAPSID PROTEIN P5	AUTOGRAFA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	36-63								
PVP4 ROT7	OUTER CAPSID PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	157-189								
PVP4 ROT8	OUTER CAPSID PROTEIN P5	ORGANIA PSEUDOTUSGATA MULTICAPSID POLYEDROSIS VIRUS	45-72								
PVP4 ROT9	OUTER CAPSID PROTEIN P5	AUTOGRAFA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	44-81								
PVP4 ROT10	OUTER CAPSID PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	157-189								
PVP4 ROT11	OUTER CAPSID PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	157-189								
PVP4 ROT12	OUTER CAPSID PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE USA)	157-189								
PVP4 ROT13	OUTER CAPSID PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE SOUTH AFRICA)	161-193								
PVP4 ROT14	OUTER CAPSID PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 2 / ISOLATE USA)	133-172								
PVP4 ROT15	OUTER CAPSID PROTEIN P5	RICE DWARF VIRUS	10-37	354-381							
PVP4 ROT16	OUTER CAPSID PROTEIN P5	AUTOGRAFA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	413-440								
PVP4 ROT17	OUTER CAPSID PROTEIN P5	HERPESVIRUS SAMIRI (STRAIN 11)	181-208	929-977							
PVP4 ROT18	OUTER CAPSID PROTEIN P5	AUTOGRAFA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	44-78	370-397							
PVP4 ROT19	OUTER CAPSID PROTEIN P5	EPIDEMIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1)	16-43								
PVP4 ROT20	OUTER CAPSID PROTEIN P5	WOUND TUMOR VIRUS	458-485								
PVP4 ROT21	OUTER CAPSID PROTEIN P5	AUTOGRAFA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	101-142	260-298							
PVP4 ROT22	OUTER CAPSID PROTEIN P5	ORGANIA PSEUDOTUSGATA MULTICAPSID POLYEDROSIS VIRUS	132-159								
PVP4 ROT23	OUTER CAPSID PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	105-132								
PVP4 ROT24	OUTER CAPSID PROTEIN P5	FOWLPOX VIRUS	211-238								



PCGENE	10717814	All Viruses (no bacteriophages)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
ELK-NASIE	PROTEIN	VIRUS	13-40	111-145						
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN RV-5)	13-40	111-145						
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN DS1)	13-40	111-145						
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	111-145							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	RABBIT ROTAVIRUS (STRAIN ALABAMA)	111-145							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	111-146							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS	9-46							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN MATSUJAMA)	12-41							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN BELFAST)	9-41							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN ENDERS)	9-46							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN JER-YL-LYN)	9-46							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN KILIAN)	9-46							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN BRISTOL 1)	9-46							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN MTHAARA VACCINE)	12-41							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN RV)	9-41							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN URABE VACCINE A49)	12-41							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 3 / STRAIN DEARING)	26-63	71-122	127-168	222-239				
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 2 / STRAIN D510N5)	4-104	130-193						
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 1 / STRAIN LANG)	4-52	35-104	112-160					
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 1 / STRAIN DEARING)	350-384							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 2 / STRAIN D510N5)	289-316							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 3 / STRAIN DEARING)	90-117							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 1 / STRAIN LANG)	50-77							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	CAPRIPOX VIRUS (STRAIN INS-1)	124-158							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SHOPE FIBROMA VIRUS (STRAIN KASZA)	250-277							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8)	234-290							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	417-451							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	HERPES SIMPLEX VIRUS (TYPE 8 / STRAIN LGANIDA-1 [n2])	176-203							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	ICTALURID HERPESVIRUS 1	310-377							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	394-421							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	THERMOPROTEUS TENAX VIRUS 1 (STRAIN VT1)	169-196							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	THERMOPROTEUS TENAX VIRUS 1 (STRAIN KKA1)	169-196							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	HUMAN PARAINFLUENZA 4A VIRUS (STRAIN TOSIIB4)	4-38							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	35-65							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	4-61							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	30-78							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	TOBACCO YELLOW DWARF VIRUS (STRAIN AUSTRALIA)	53-87							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	AUTOGRAFIA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	85-112							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	59-86							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	5-39							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	AUTOGRAFIA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	80-107							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	77-111							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	9-36	119-153						
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MAIZE STREAK VIRUS (NIGERIAN ISOLATE)	34-61							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MAIZE STREAK VIRUS (SOUTH-AFRICAN ISOLATE)	34-61							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	76-103							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	93-164							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	118-148							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	24-97							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	231-267							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	AUTOGRAFIA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	133-184							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	122-149							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	56-94							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	81-121	546-573	658-700					
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	13-40							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	FOWLPOX VIRUS (ISOLATE HP-318[MUNICH])	74-108	152-179	184-218					
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	FOWLPOX VIRUS (ISOLATE HP-318[MUNICH])	62-89							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	FOWLPOX VIRUS (ISOLATE HP-318[MUNICH])	162-197	214-241						

PCGENE	1021/104	FILENAME	PROTEIN	ALL Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PYB12_FOWPM		HYPOTHETICAL BAMB-ORF12 PROTEIN		VIRUS	11-38								
PYB13_FOWPM		HYPOTHETICAL BAMB-ORF13 PROTEIN		FOWLPOX VIRUS (ISOLATE IP-431(MUNICH))	128-167								
PYB13_FOWPM		BEL-3 PROTEIN		HUMAN SPONARETROVIRUS	87-116								
PYDHI_HSV57		HYPOTH 21.1 KD IN DIFR 3 REGION		HERPESVIRUS SAIMIRI (STRAIN 484-72)	161-188								
PYDHI_HSV58		HYPOTH 21.2 KD IN DIFR 3 REGION		HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 484)	52-82								
PYDHI_HSV59		HYPOTH 21.3 KD IN DIFR 3 REGION		HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 484)	51-83								
PYF36_FOWP1		HYPOTHETICAL 25.9 KD PROTEIN		FOWLPOX VIRUS (STRAIN F8-1)	8-35								
PYF36_FOWP1		HYPOTHETICAL 30.9 KD PROTEIN		FOWLPOX VIRUS (STRAIN F8-1)	170-204								
PYH22_VACCV		HYPOTH 21.7 KD IN DIFR 3 PRO		VACCINIA VIRUS (STRAIN WR)	37-64	95-126	144-171						
PYH22_VACCV		HYPOTH HOST RANGE 27.4 KD PRO		VACCINIA VIRUS (STRAIN WR)	31-58	179-206							
PYK84_EBV		HYPOTHETICAL BKRF2 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN B95-8)	90-121								
PYK84_EBV		HYPOTHETICAL BKRF4 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN B95-8)	19-53								
PYL15_ADE41		HYPOTH 12.4 KD IN 31 KD REGION		HUMAN ADENOVIRUS TYPE 41	47-86								
PYL15_ADE41		HYPOTHETICAL BLRF1 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN B95-8)	27-54								
PYOR1_COTMV		HYPOTHETICAL 23 KD PROTEIN		COMELINA YELLOW MOTTLE VIRUS	94-143								
PYOR2_COTMV		HYPOTHETICAL 13 KD PROTEIN		COMELINA YELLOW MOTTLE VIRUS	35-76								
PYOR3_WCMVM		HYPOTHETICAL 13 KD PROTEIN		WHITE CLOVER MOSAIC VIRUS (STRAIN M)	64-94								
PYOR3_WCMVM		HYPOTHETICAL 13 KD PROTEIN		WHITE CLOVER MOSAIC VIRUS (STRAIN O)	65-95								
PYOR3_ADEG1		HYPOTHETICAL 31.3 KD PROTEIN		AVIAN ADENOVIRUS GALI (STRAIN PHELP5)	92-119								
PYOR4_TTV1		HYPOTHETICAL 8.1 KD PROTEIN		THERMOPROTEUS TENAX VIRUS I (STRAIN KRA1)	23-57								
PYOR4_TTV1		HYPOTHETICAL 24.8 KD PROTEIN		THERMOPROTEUS TENAX VIRUS I (STRAIN KRA1)	15-42								
PYOR4_TTV1		HYPOTHETICAL 7.3 KD PROTEIN		THERMOPROTEUS TENAX VIRUS I (STRAIN KRA1)	3-31								
PYOR4_TTV1		HYPOTHETICAL 12.1 KD PROTEIN		THERMOPROTEUS TENAX VIRUS I (STRAIN KRA1)	4-40								
PYF12_RTBVP		HYPOTHETICAL P12 PROTEIN		RICE TUNGRO BACILLIFORM VIRUS	44-71								
PYF12_RTBVP		HYPOTHETICAL P12 PROTEIN		RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES)	44-71								
PYF24_RTBVP		HYPOTHETICAL P24 PROTEIN		RICE TUNGRO BACILLIFORM VIRUS	59-101	106-157							
PYF24_RTBVP		HYPOTHETICAL P24 PROTEIN		RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES)	51-101	106-157							
PYF46_RTBVP		HYPOTHETICAL P46 PROTEIN		RICE TUNGRO BACILLIFORM VIRUS	58-107	197-231							
PYF46_RTBVP		HYPOTHETICAL P46 PROTEIN		RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES)	58-107	197-231							
PYF63_NPVAC		HYPOTH PRO P6.3 5 REGION		AUTOGRAPIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	44-71								
PYF63_NPVAC		HYPOTH 4.0 KD IN P6.3 5 REGION		ORGANIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS	325-352								
PYF63_NPVAC		HYPOTH 23.6 KD IN POLYHEDRIN 5 REGION		AUTOGRAPIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	116-153								
PYF63_NPVAC		HYPOTHETICAL 17.0 KD PROTEIN		INFECTIOUS PANCREATIC NECROSIS VIRUS (STRAIN NI)	5-32	59-96	156-183						
PYQ1_AMEPV		HYPOTHETICAL PROTEIN IN TK 3 REGION		HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN GS)	208-235								
PYF31_HSV60		HYPOTHETICAL PROTEIN RF1		HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN GS)	233-257	268-299							
PYF31_HSV60		HYPOTHETICAL PROTEIN RF2		HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN GS)	141-168								
PYF31_HSV60		HYPOTHETICAL PROTEIN RF3		HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN GS)	404-441								
PYF31_HSV60		HYPOTHETICAL PROTEIN RF4		HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN GS)	10-45								
PYF31_HSV60		REPETITIVE PROTEIN ORF2		CHLO RUDESCENT VIRUS	7-34								
PYVAG_VACCV		HYPOTHETICAL 9.3 KD PROTEIN		VACCINIA VIRUS (STRAIN COPENHAGEN)	81-112								
PYVAG_VACCV		HYPOTHETICAL 14.5 KD PROTEIN		VACCINIA VIRUS (STRAIN COPENHAGEN)	29-77								
PYVDB_VACCV		HYPOTHETICAL 8.3 KD PROTEIN		VACCINIA VIRUS (STRAIN COPENHAGEN)	46-77								
PYVDB_VACCV		HYPOTHETICAL 8.3 KD PROTEIN		VACCINIA VIRUS (STRAIN WR)	20-50								
PYVDB_VACCV		HYPOTHETICAL 7.2 KD PROTEIN		VACCINIA VIRUS (STRAIN WR)	10-44								
PYVDB_VACCV		HYPOTHETICAL 8.4 KD PROTEIN		VACCINIA VIRUS (STRAIN COPENHAGEN)	152-179								
PYF12_EBV		HYPOTHETICAL BZLF1 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN B95-8)									

TABLE VII

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

(PREFERRED VIRAL SEQUENCES)

3  
—

Accession	Protein	All Virus (no better description)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
POL MLVAK	POL POLYPROTEIN	AKA MURINE LEUKEMIA VIRUS	453-460								
PENY MLVAV	ENV POLYPROTEIN	AKY MURINE LEUKEMIA VIRUS	517-544								
POL MLVAV	POL POLYPROTEIN	AKY MURINE LEUKEMIA VIRUS	805-832								
PATYC AVIM2	MYC TRANSFORMING PROTEIN	AVIAN MYELOCYTOMATOSIS VIRUS CHII	232-266	375-402							
PATYC AVIM0	MYC TRANSFORMING PROTEIN	AVIAN MYELOCYTOMATOSIS VIRUS IIBI	233-267	376-403							
PATYC AVIMC	MYC TRANSFORMING PROTEIN	AVIAN MYELOCYTOMATOSIS VIRUS NC19	233-267	376-403							
VLI EPVL	PROBABLE LI PROTEIN	AVIAN PAPILLOMA VIRUS EPV-L	38-65								
PVGLB HSVB1	GLYCOPROTEIN 1 PRECURSOR	BOVINE HERPESVIRUS TYPE 1	427-454								
PURQ HSVB3	RIBONUCLEOPROTEIN REDUCT SMALL CHA	BOVINE HERPESVIRUS TYPE 1 (STRAIN 34)	90-117								
PVGLB HSVB2	GLYCOPROTEIN B-1 PRECURSOR	BOVINE HERPESVIRUS TYPE 2 (STRAIN BMV)	447-474								
PENY BLV06	ENV POLYPROTEIN	BOVINE IMMUNODEFICIENCY VIRUS (ISOLATE 106)	17-44	344-603	631-695						
PENY BLV73	ENV POLYPROTEIN	BOVINE IMMUNODEFICIENCY VIRUS (ISOLATE 127)	17-44	573-632	660-724						
PENY BLVAF	ENV POLYPROTEIN	BOVINE LEUKEMIA VIRUS (AMERICAN ISOLATE FLK)	304-377								
PENY BLVAV	ENV POLYPROTEIN	BOVINE LEUKEMIA VIRUS (AMERICAN ISOLATE VDM)	304-377								
PENY BLVAU	ENV POLYPROTEIN	BOVINE LEUKEMIA VIRUS (AUSTRALIAN ISOLATE)	304-377								
PENY BLVB2	ENV POLYPROTEIN	BOVINE LEUKEMIA VIRUS (BELGIUM ISOLATE LDB35)	304-377								
PENY BLVB5	ENV POLYPROTEIN	BOVINE LEUKEMIA VIRUS (JAPANESE ISOLATE BLV-1)	304-377								
PHEMA PJIB	HEMAGGLUTININ-NEURAMINIDASE	BOVINE PARAINFLUENZA 3 VIRUS	66-93								
PRAP PJIB	RNA POLYMERASE ALPHA SUBUNIT	BOVINE PARAINFLUENZA 3 VIRUS	34-91	255-282	285-314						
PVGLF PJIB	FUSION GLYCOPROTEIN PRECURSOR	BOVINE PARAINFLUENZA 3 VIRUS	115-182	207-241	459-497						
PVMA1 PJIB	MATRIX PROTEIN	BOVINE PARAINFLUENZA 3 VIRUS	201-231								
PRPP BRSA	RNA POLYMERASE ALPHA SUBUNIT	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A1908)	99-133								
PVGLF BRSA	FUSION GLYCOPROTEIN PRECURSOR	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A1908)	38-65	154-202	216-243	441-469	486-531				
PVMA2 BRSA	MATRIX GLYCOPROTEIN M2	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A1908)	124-152								
PVMA1 BRSA	MATRIX PROTEIN	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A1908)	219-246								
PVGLF BRSA	FUSION GLYCOPROTEIN PRECURSOR	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A1908)	38-65	154-202	216-243	441-471	488-533				
PVGLF BRSA	MAJOR SURFACE GLYCOPROTEIN O	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN COPENHAGEN)	92-123								
PVGLF BRSA	FUSION GLYCOPROTEIN PRECURSOR	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN COPENHAGEN)	38-65	154-202	216-243	441-471	488-533				
PENY MLVCB	ENV POLYPROTEIN	CAS-BAC MURINE LEUKEMIA VIRUS	510-539								
PENY SIVCZ	ENV POLYPROTEIN	CHIMPANZEE IMMUNODEFICIENCY VIRUS	160-187	253-289	316-346	526-584	637-654				
PVPU SIVCZ	VPU PROTEIN	CHIMPANZEE IMMUNODEFICIENCY VIRUS	51-78								
PVLA SIVCZ	POL POLYPROTEIN	CHIMPANZEE IMMUNODEFICIENCY VIRUS (SIVCP2)	242-269	636-685							
PVLA SIVCZ	PROBABLE E1 PROTEIN	COTTONTAIL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN KANSAS)	5-34								
VLI CUPVK	PROBABLE LI PROTEIN	COTTONTAIL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN KANSAS)	331-333								
PVLA DEN15	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 1 (STRAIN 16681)	1558-1855	2890-2935	2989-3016						
PVLA DEN16	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN 16681)	1544-1571	1858-1885	2908-2935	2912-3016	3117-3147				
PVLA DEN17	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 3 (STRAIN 16681-PDK53)	1544-1571	1858-1885	2483-2519	2908-2935	2982-3016	3117-3147			
PVLA DEN18	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 4 (STRAIN JAMAICA)	1544-1571	1858-1885	2908-2935	3117-3147	3346-3373				
PVLA DEN19	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN PR13951)	1544-1571	1858-1885	2908-2935	2979-3013	3114-3144	3343-3370			
PVLA DEN20	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 3 (STRAIN TONGA 1974)	1134-1161	1448-1475							
PVLA DEN21	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 4	812-864	1542-1569	1857-1884	2404-2521	2980-3014	3345-3372			
PVLA DEN22	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 3	2835-2910	2977-3011	3342-3369						
PVLA DEN23	DNA POLYMERASE	DUCK HEPATITIS B VIRUS (BROWN SHANGHAI DUCK ISOLATE S3)	5-39								
PVLA DEN24	DNA POLYMERASE	DUCK HEPATITIS B VIRUS (SHANGHAI DUCK ISOLATE S3)	5-39								
PVLA DEN25	DNA POLYMERASE	DUCK HEPATITIS B VIRUS (WHITE SHANGHAI DUCK ISOLATE S3)	5-39								
PVLA DEN26	DNA POLYMERASE	EPSTEIN-BARR VIRUS (STRAIN B95-4)	145-172	1215-1242	1344-1371	1876-1903					
PVLA DEN27	LARGE TEGUMENT PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-4)	115-142	313-340	542-569						
PVLA DEN28	VIRION PROTEIN BB95-1	EPSTEIN-BARR VIRUS (STRAIN B95-4)	15-42								
PVLA DEN29	HYPOTHETICAL PROTEIN BB95-1	EPSTEIN-BARR VIRUS (STRAIN B95-4)	185-211	987-814							
PVLA DEN30	PROB DNA REPLICATION PROTEIN BSLF1	EPSTEIN-BARR VIRUS (STRAIN B95-4)	409-436								
PVLA DEN31	HYPOTHETICAL PROTEIN BICR1	EPSTEIN-BARR VIRUS (STRAIN B95-4)	107-144	168-196							
PVLA DEN32	HYPOTHETICAL PROTEIN BDLF4	EPSTEIN-BARR VIRUS (STRAIN B95-4)	847-874								
PVLA DEN33	MAJOR CAPSID PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-4)	68-102								
PVLA DEN34	PROBABLE MEMBRANE GLYCOPROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-4)	95-122	631-658							
PVLA DEN35	GLYCOPROTEIN GP110 PRECURSOR	EPSTEIN-BARR VIRUS (STRAIN B95-4)	349-376	619-648							
PVLA DEN36	GLYCOPROTEIN GP45 PRECURSOR	EPSTEIN-BARR VIRUS (STRAIN B95-4)	104-149								
PVLA DEN37	PROBABLE MEMBRANE ANTIGEN GP45	EPSTEIN-BARR VIRUS (STRAIN B95-4)									

PCGENE	10711214	All Virus (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
GENE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
VP40 EBV	CAPSID PROTEIN P40	EPSTEIN-BARR VIRUS (STRAIN 195-8)	400-470								
PKR2 EBV	PROBABLE DNA PACKAGING PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 195-8)	314-290								
PKR3 EBV	HYPOTHEICAL BKRF1 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 195-8)	90-121								
PKR4 EBV	HYPOTHEICAL BKRF4 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 195-8)	19-53								
PKR5 EBV	HYPOTHEICAL BKRF1 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 195-8)	27-54								
PKR6 EBV	HYPOTHEICAL BKRF2 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 195-8)	132-179								
PKR7 EBV	BZLF1 TRANS-ACTIVATOR PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 195-8)	191-220								
PKR8 EBV	MAJOR DNA-BINDING PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 195-8)	977-1004								
PKR9 EBV	EARLY ANTIGEN PROTEIN R	EPSTEIN-BARR VIRUS (STRAIN 195-8)	55-82								
PKR10 EBV	LATENT MEMBRANE PROTEIN 1	EPSTEIN-BARR VIRUS (STRAIN 195-8)	148-175								
PKR11 EBV	GENE TERMINAL PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 195-8)	294-321								
PKR12 EBV	LATENT MEMBRANE PROTEIN 1	EPSTEIN-BARR VIRUS (STRAIN 195-8)	148-175								
PKR13 EBV	LATENT MEMBRANE PROTEIN 1	EPSTEIN-BARR VIRUS (STRAIN 195-8)	148-175								
PKR14 EBV	MAJOR ENVELOPE GLYCOPROTEIN 300	EQUINE HERPESVIRUS TYPE 1	145-175								
PKR15 EBV	GLYCOPROTEIN C PRECURSOR	EQUINE HERPESVIRUS TYPE 1	124-151								
PKR16 EBV	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (ISOLATE HV521A)	403-470								
PKR17 EBV	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD1)	403-470								
PKR18 EBV	ALPHA TRANS-IND FACTOR 42 KD PRO	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	294-321								
PKR19 EBV	PROBABLE HELICASE	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	255-289								
PKR20 EBV	RIBONUC-DIPHOSPH REDUCT LARGE CHA	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	184-211								
PKR21 EBV	LARGE TEGUMENT PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	75-102								
PKR22 EBV	HYPOTHEICAL GENE 54 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	239-256								
PKR23 EBV	HYPOTHEICAL GENE 41 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	600-667								
PKR24 EBV	GENE 40 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	247-286								
PKR25 EBV	GENE 21 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	44-71								
PKR26 EBV	DNA REPLICATION PROTEIN UL52	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	715-749								
PKR27 EBV	GENE 3 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	193-220								
PKR28 EBV	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	146-176								
PKR29 EBV	GLYCOPROTEIN G PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	403-470								
PKR30 EBV	PROB INTEGRAL MEMBRANE PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	147-174								
PKR31 EBV	CAPSID PROTEIN VP26	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	36-63								
PKR32 EBV	GENE 3 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	146-176								
PKR33 EBV	CELL FUSION PROTEIN PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN KENTUCKY A)	403-470								
PKR34 EBV	97 KD ALPHA TRANS-INDUCING PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAINS AD4P and KY A)	312-339								
PKR35 EBV	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 4	190-217								
PKR36 EBV	GLYCOPROTEIN G PRECURSOR	EQUINE HERPESVIRUS TYPE 4	486-513								
PKR37 EBV	DEOXY 5'-TRIPHOSPH NUCLEOTIDYLASE	EQUINE HERPESVIRUS TYPE 4 (STRAIN 1942)	271-298								
PKR38 EBV	PROBABLE E3 PROTEIN	EUROPEAN ELK PAPILLOMAVIRUS	90-117								
PKR39 EBV	POL FIVE	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE PETALUNA)	120-150								
PKR40 EBV	POL FIVE	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE PETALUNA)	650-680								
PKR41 EBV	POL FIVE	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE PETALUNA)	442-473								
PKR42 EBV	POL FIVE	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE SAN DIEGO)	639-668								
PKR43 EBV	POL FIVE	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE TMD)	640-679								
PKR44 EBV	POL FIVE	FELINE LEUKEMIA PROVIRUS (CLONE CFE-6)	509-538								
PKR45 EBV	MYC TRANSFORMING PROTEIN	FELINE LEUKEMIA PROVIRUS FT	391-420								
PKR46 EBV	MYC TRANSFORMING PROTEIN	FELINE LEUKEMIA VIRUS	191-220								
PKR47 EBV	MYC TRANSFORMING PROTEIN	FELINE LEUKEMIA VIRUS (STRAIN AG1ASGOW-1)	490-519								
PKR48 EBV	MYC TRANSFORMING PROTEIN	FELINE LEUKEMIA VIRUS (STRAIN LAMBDA-01)	510-539								
PKR49 EBV	MYC TRANSFORMING PROTEIN	FELINE LEUKEMIA VIRUS (STRAIN SARNA)	487-516								
PKR50 EBV	MYC TRANSFORMING PROTEIN	FRIEND MURINE LEUKEMIA VIRUS (ISOLATE 57)	523-557								
PKR51 EBV	MYC TRANSFORMING PROTEIN	FRIEND MURINE LEUKEMIA VIRUS (ISOLATE F829)	523-557								
PKR52 EBV	MYC TRANSFORMING PROTEIN	FRIEND MURINE LEUKEMIA VIRUS (ISOLATE PVC-211)	523-557								
PKR53 EBV	MYC TRANSFORMING PROTEIN	GIBBON APE LEUKEMIA VIRUS	176-203								
PKR54 EBV	MYC TRANSFORMING PROTEIN	GIBBON APE LEUKEMIA VIRUS	196-443								
PKR55 EBV	MYC TRANSFORMING PROTEIN	GIBBON APE LEUKEMIA VIRUS	535-582								
PKR56 EBV	MYC TRANSFORMING PROTEIN	GROUND SQUIRREL HEPATITIS VIRUS	271-335								





PCGENE	10717184	All Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PCGENE	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PPOL_HSV5A	DNA POLYMERASE	HERPESVIRUS SAIMIRI (STRAIN 11)	621-632								
PDU1_HSV5A	DEOXYU-5'-TRIPHOSPH NUCOTIDYLASE	HERPESVIRUS SAIMIRI (STRAIN 11)	179-213								
PHL1_HSV5A	PROBABLE HELICASE	HERPESVIRUS SAIMIRI (STRAIN 11)	418-449								
PIC1_HSV5A	PROBABLE PROC & TRANSPORT PRO	HERPESVIRUS SAIMIRI (STRAIN 11)	58-83	482-532							
PIE4_HSV5A	IMMEDIATE-EARLY PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	48-78								
PKTH_HSV5A	THYMIDINE KINASE	HERPESVIRUS SAIMIRI (STRAIN 11)	340-386								
PR1_HSV5A	RIBONUC-DIPHOSPH REDUCT LARGE CHA	HERPESVIRUS SAIMIRI (STRAIN 11)	324-351								
PTG1_HSV5A	PROBABLE LARGE TEGUMENT PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	534-607	672-700	777-814	846-898	949-986	990-1017	1467-1497	2102-2113	
PTYS_HSV5A	THYMIDYLATE SYNTHASE	HERPESVIRUS SAIMIRI (STRAIN 11)	120-147								
PUL6_HSV5A	VIRION GENE 43 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	15-42	302-358	368-402						
PUL3_HSV5A	VIRION GENE 19 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	34-61	204-231	367-389						
PUL4_HSV5A	GENE 67 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	208-235								
PUL7_HSV5A	GENE 63 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	31-65	685-737							
PUL3_HSV5A	PROB DNA REP GENE 34 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	100-157								
PUL3_HSV5A	HYPOTHETICAL GENE 33 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	9-36								
PUL3_HSV5A	HYPOTHETICAL GENE 24 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	582-609								
PUL9_HSV5A	HYPOTHETICAL GENE 31 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	92-122								
PUNG_HSV5A	URACIL-DNA GLYCOSYLASE	HERPESVIRUS SAIMIRI (STRAIN 11)	135-176								
PVCA_HSV5A	MAJOR CAPSID PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	769-799								
PVGA_HSV5A	HYPOTHETICAL GENE 43 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	138-165								
PVG4_HSV5A	HYPOTHETICAL GENE 41 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	360-394								
PVG3_HSV5A	HYPOTHETICAL GENE 32 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	47-74								
PVGL_HSV5A	GLYCOPROTEIN H PRECURSOR	HERPESVIRUS SAIMIRI (STRAIN 11)	388-413								
VNXP_HSV5A	INTEGRAL MEMBRANE PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	80-107								
VP22_HSV5A	PROBABLE CAPSID PROTEIN VP22	HERPESVIRUS SAIMIRI (STRAIN 11)	2-29								
VP26_HSV5A	CAPSID PROTEIN VP26	HERPESVIRUS SAIMIRI (STRAIN 11)	48-75								
VP40_HSV5A	CAPSID PROTEIN P40	HERPESVIRUS SAIMIRI (STRAIN 11)	205-232	344-372							
VP73_HSV5A	PROBABLE MEMBRANE ANTIGEN 73	HERPESVIRUS SAIMIRI (STRAIN 11)	181-208	929-977							
PDB1_HSV5A	MAJOR DNA-BINDING PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	333-368	512-539							
PCG2_HSV5A	CYCLIN HOMOLOG	HERPESVIRUS SAIMIRI (STRAIN 11)	127-154								
PDH1_HSV5C	HYPOTH 24.1 KD IN DHFR 3 REGION	HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 48)	161-188								
PDH4_HSV5C	HYPOTH 9.9 KD IN DHFR 3 REGION	HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 48)	52-82								
PERV_MLV50	ENV POLYPROTEIN	HOMULY MORINE LEUKEMIA VIRUS	51-83								
PDOL_HCMVA	DNA POLYMERASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	510-540								
PIC18_HCMVA	PROB PROC & TRANSPORT PRO UL36	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	733-760								
PIC03_HCMVA	HYPOTHETICAL PROTEIN IRL3	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	294-324								
PIC17_HCMVA	HYPOTHETICAL PROTEIN IRL12	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	32-49								
PIC17_HCMVA	HYPOTHETICAL PROTEIN IRL13	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	74-161								
PTG1_HCMVA	PROBABLE LARGE TEGUMENT PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	31-82								
PUL1_HCMVA	RIBONUC-DIPHOSPH REDUCT LARGE CHA	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	623-649								
PUL08_HCMVA	HYPOTHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	1231-1281	2202-2229							
PUL13_HCMVA	HYPOTHETICAL PROTEIN UL13	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	6-47								
PUL10_HCMVA	HYPOTHETICAL PROTEIN UL16	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	347-374								
PUL20_HCMVA	HYPOTH PRO UL20 PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	81-112								
PUL31_HCMVA	HYPOTHETICAL PROTEIN UL31	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	14-61								
PUL33_HCMVA	HYPOTHETICAL PROTEIN UL33	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	623-649								
PUL47_HCMVA	PROTEIN UL47	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	114-148	448-483	763-790	802-833					
PUL50_HCMVA	PROTEIN UL50	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	159-186								
PUL59_HCMVA	HYPOTHETICAL PROTEIN UL59	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	74-101								
PUL70_HCMVA	PROB DNA REP PROTEIN UL70	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	65-92								
PUL73_HCMVA	UL73 GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	5-73								
PUL74_HCMVA	HYPOTHETICAL PROTEIN UL74	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	45-79								
PUL91_HCMVA	PROTEIN UL91	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	26-53	314-381							
PUL93_HCMVA	HYPOTHETICAL PROTEIN UL93	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	37-71								
PUL44_HCMVA	VIRION PROTEIN UL104	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	4-31	461-477							
PUL89_HCMVA	HYPOTHETICAL PROTEIN UL119	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	33-78								

FCGGENE	10711784	All Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PUL.D1	HCXVA	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	90-124									
PUS99	HCXVA	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	70-47									
PUS14	HCXVA	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	277-308									
PUS18	HCXVA	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	191-218									
PVGLB	HCXVA	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	35-88	397-424	400-467	451-478						
PVGLH	HCXVA	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	107-136	270-297								
PVGLI	HCXVA	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	47-111									
PVTEK	HCXVA	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	417-431									
PVDBI	HCXVA	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	437-464									
PVDBK	HCXVA	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	194-221									
PVGLB	HCXVA	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	50-88	397-424	413-461	452-479						
PVGLH	HCXVA	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	106-135									
PENV	HV1A2	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ARV2/SF2 ISOLATE)	544-592	610-682	790-835							
PGAG	HV1A2	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ARV2/SF2 ISOLATE)	97-118									
POL	HV1A2	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ARV2/SF2 ISOLATE)	218-245	620-661								
PVPU	HV1A2	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ARV2/SF2 ISOLATE)	3-31									
PENV	HV1B1	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 AND RHX3 ISOLATES)	5-48									
PPOL	HV1B1	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	545-594	631-683	791-818							
PENV	HV1B1	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	230-237	637-673								
PPOL	HV1B5	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	230-237	637-673								
PENV	HV1B8	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	540-589	626-678	786-813							
PVPU	HV1B8	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	21-48									
PENV	HV1B8	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	267-294	331-365	367-390	678-679	787-813					
PVPU	HV1B8	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	22-49									
PENV	HV1B8	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	530-599	636-688	796-833							
PPOL	HV1B8	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	230-237	637-673								
PENV	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	5-48									
PVPU	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	397-424	357-406	647-693	1007-1035						
PENV	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	3-30									
PPOL	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	235-296	386-413	343-391	628-680						
PENV	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	81-119									
PPOL	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	217-244	624-660								
PENV	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	6-33									
PPOL	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	545-594	631-683	791-818							
PENV	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	218-245	620-661	921-931							
PPOL	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	5-48									
PENV	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	545-594	631-683	791-818							
PPOL	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	350-377	356-405	642-694	1002-1029						
PENV	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	91-118									
PPOL	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	2-29									
PENV	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	336-363	627-675	783-811							
PPOL	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	222-249	624-665								
PENV	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	22-49									
PPOL	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	547-595	633-707	794-826							
PENV	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	217-244	476-510	619-660							
PPOL	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	5-32									
PENV	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	543-592	629-681	789-816							
PPOL	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	343-370	367-395	632-684	791-819						
PENV	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	82-118									
PPOL	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	231-248	621-664								
PENV	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	249-290	336-383	621-673	783-813						
PPOL	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	81-119									
PENV	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	217-244	624-660								
PPOL	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	6-33									
PENV	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	218-245	622-661								
PPOL	HV1C4	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	544-593	630-674	789-820							

PCGENE	10717144	All Virus (no bacteriophage)									
FILE NAME	PROTEIN	VIRUS									
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (OVI ISOLATE)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (PV21 ISOLATE)	218-245	620-661							
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (PV21 ISOLATE)	545-594	631-683							
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (PV21 ISOLATE)	210-237	637-673							
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (PV21 ISOLATE)	5-48								
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (PV21 ISOLATE)	280-307	534-562	640-692	800-832					
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RE/HAT ISOLATE)	217-244	619-660							
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RE/HAT ISOLATE)	62-89								
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (SC ISOLATE)	318-365	545-593							
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (SF162 ISOLATE)	313-363	536-585	622-674	782-809					
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (SF162 ISOLATE)	22-49								
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (SF162 ISOLATE)	541-589	637-679	787-815						
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (STRAIN KD-1-OP22)	274-301	555-596	637-677	776-824					
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (STRAIN UGANDAN/1 ISOLATE)	217-244	513-540	619-660						
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (WMJ1 ISOLATE)	318-365	545-593	631-683	791-818					
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (WMJ1 ISOLATE)	314-361	536-584	622-674	782-809					
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	286-307	571-601	634-678	797-828					
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	255-296	542-591	628-680	790-820					
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	217-244	619-660							
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	251-292								
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	256-297	545-593	630-682	792-822					
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	18-174								
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	545-594	627-666	791-823						
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	61-88	532-591	621-648	653-697					
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	18-115								
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	491-522								
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	534-593	623-650	655-699						
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	471-562								
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	61-88	532-591	655-699	644-688					
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	18-115								
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	509-600								
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	491-568								
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	60-87	574-551	556-583	613-640	641-693				
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	471-562								
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	61-88	534-551	556-583	613-640	663-689				
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	18-115								
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	471-529								
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	58-85	533-592	632-698						
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	472-563								
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	552-584	614-673							
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	473-562								
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	442-476	537-554	559-586	648-692					
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	88-115								
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	491-582								
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	442-476	537-554	559-586	648-692					
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	81-108								
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	30-60								
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	157-184	334-361							
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	61-105	312-342							
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	66-93								
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	60-87								
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	310-340								
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	59-86								
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	75-102								
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	183-210								
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	159-186								
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	407-445								
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z244 ISOLATE)	21-48								

PCGENE	10711744	All Viruses (no bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
FILE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PVE2 HPV2A	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 2A	158-191									
PVE4 HPV31	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 31	75-102									
PVE6 HPV31	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 31	69-96									
PVE1 HPV33	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 33	180-207									
PVE2 HPV33	PROBABLE L1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 33	304-331									
VL1 HPV33	PROBABLE L1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 33	19-46									
PVE2 HPV33	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 33	158-192	327-334								
PVE3 HPV33	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 33	27-34									
PVE1 HPV39	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 39	103-130									
PVE2 HPV39	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 39	7-34	323-337								
PVE6 HPV39	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 39	71-102									
PVE1 HPV41	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	51-89									
PVE4 HPV41	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	83-97									
PVE6 HPV41	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	119-146									
VL1 HPV41	PROBABLE L1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	345-372									
VL2 HPV41	PROBABLE L2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	415-442									
PVE1 HPV42	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 42	25-59									
PVE6 HPV42	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 42	75-102									
PVE1 HPV47	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	146-173									
PVE3 HPV47	E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	17-51	148-175	276-303							
PVE2 HPV50	PROBABLE E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 5	17-51									
PVE4 HPV50	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 5	202-229									
PVE2 HPV51	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 51	137-184									
PVE6 HPV51	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 51	72-99									
VL1 HPV51	PROBABLE L1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 51	19-46									
PVE1 HPV57	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 57	21-48									
PVE2 HPV57	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 57	166-193									
PVE3 HPV58	E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 58	2-36	309-336								
VL1 HPV58	PROBABLE L1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 58	45-72									
PVE2 HPV58	PROBABLE E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 58	17-51									
PVE3 HPV58	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 58	202-229									
PVE4 HPV58	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 58	11-41									
PVE5A HPV68	PROBABLE E5A PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 68	30-60									
PVE5A HPV6C	PROBABLE E5A PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 6C	30-60									
VL1 HPV6A	PROBABLE L1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 8	354-392									
PVE6 HPV6E	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE ME180	71-102									
PRCP1 P111D	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C13)	84-111	234-261	373-416							
PRCP2 P111C	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C13)	377-404	455-482								
PRCP3 P111C	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C13)	84-111	234-261	373-416							
PVGLF P111C	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C13)	147-174	210-266								
PRCP1 P111E	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C1-1/83)	84-111	244-271	373-416							
PVNSC P111U	NONSTRUCTURAL PROTEIN C	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C1-1/83)	41-75									
PRCP1 P111D	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C1-5/73)	84-111	232-262	373-416							
PRCP2 P111H	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN WASHINGTON/1957)	79-110	366-393								
PRCP3 P111H	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN WASHINGTON/1957)	377-404	444-488								
PRCP1 P11H	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 2 VIRUS	167-194	232-236								
PVGLF P11H	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 2 VIRUS	90-117	141-175	218-266	483-528						
PVGLF P11H	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN GREER)	90-117	141-175	218-266	483-528						
PRCP1 P11H	RNA POLYMERASE BETA SUBUNIT	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSHIBA)	322-349	1564-1598	1687-1721	1901-1946						
PRCP2 P11H	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSHIBA)	167-194	232-236								
PVGLF P11H	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSHIBA)	90-117	141-175	218-266	483-528						
PRCP1 P11T	MATRIX PROTEIN	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN TOSHIBA)	96-123									
PRCP2 P11T	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN TOSHIBA)	27-61									
PRCP3 P11H	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NIH 47185)	376-403									
PRCP4 P11H	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NIH 47185)	27-61									
PRCP1 P11H	RNA POLYMERASE BETA SUBUNIT	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NIH 47185)	52-86	136-163	604-638	1081-1133	1994-2036	2115-2142				
PRCP2 P11H	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NIH 47185)	114-144	269-299								

















PCGENE	10717184	All Viruses (see bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PENY MLVX1	ENV POLYPROTEIN	KIRSTEN MURINE LEUKEMIA VIRUS	40-81								
PENY MLVX2	GLYCOPROTEIN B PRECURSOR	MAKER'S DISEASE HERPESVIRUS (STRAIN RH-10)	93-120	332-379							
PENY MLVX3	ENV POLYPROTEIN	MINK CELL FOCUS-FORMING MURINE LEUKEMIA VIRUS	471-512								
PENY MLVX4	ENV POLYPROTEIN	MOLONEY MURINE LEUKEMIA VIRUS (ISOLATE CL-3)	488-515								
PENY MLVX5	ENV POLYPROTEIN	MOLONEY MURINE LEUKEMIA VIRUS	502-543								
PENY MLVX6	MAJOR DNA-BINDING PROTEIN	MURINE CYTOMEGALOVIRUS (STRAIN SMITH)	584-618								
PENY MLVX7	PROB PRO C & TRANSPORT PRO	MURINE CYTOMEGALOVIRUS (STRAIN SMITH)	661-691								
PENY MLVX8	GLYCOPROTEIN B PRECURSOR	MURINE CYTOMEGALOVIRUS (STRAIN SMITH)	381-408	441-475							
PENY MLVX9	IMMEDIATE-EARLY PROTEIN I	MURINE CYTOMEGALOVIRUS (STRAIN SMITH)	261-288								
PENY MLVX10	E2 PROTEIN	PYGMY CHIMPANZEE PAPILLONAVIRUS TYPE I	267-294	327-361							
PENY MLVX11	PROBABLE E3 PROTEIN	PYGMY CHIMPANZEE PAPILLONAVIRUS TYPE I	35-62								
PENY MLVX12	ENV POLYPROTEIN	RADIATION MURINE LEUKEMIA VIRUS	497-538								
PENY MLVX13	ENV POLYPROTEIN	RADIATION MURINE LEUKEMIA VIRUS	716-743	805-832							
PENY MLVX14	ENV POLYPROTEIN	RADIATION MURINE LEUKEMIA VIRUS (STRAIN KAPLAN)	497-538								
PENY MLVX15	POL POLYPROTEIN	RADIATION MURINE LEUKEMIA VIRUS (STRAIN KAPLAN)	101-128	190-217							
PENY MLVX16	MAJOR DNA-BINDING PROTEIN	SIMIAN CYTOMEGALOVIRUS (STRAIN COLBURN)	435-462	532-559							
PENY MLVX17	GENOME POLYPROTEIN	SIMIAN HEPATITIS A VIRUS (STRAIN AGM-27)	207-241	1025-1052							
PENY MLVX18	ENV POLYPROTEIN	SIMIAN HEPATITIS A VIRUS (STRAIN CY-145)	203-237								
PENY MLVX19	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGN155 ISOLATE)	269-310	561-588	592-619	652-679	697-724				
PENY MLVX20	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGN155 ISOLATE)	431-458	547-574	637-671						
PENY MLVX21	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGN266 ISOLATE)	45-72								
PENY MLVX22	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGN266 ISOLATE)	270-301	566-593	597-624	658-685	703-730				
PENY MLVX23	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGN266 ISOLATE)	416-463	482-516	642-669						
PENY MLVX24	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGN313 ISOLATE)	71-91								
PENY MLVX25	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (F216353H14 ISOLATE)	281-308	553-612	642-669	691-718					
PENY MLVX26	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (F216353H14 ISOLATE)	88-115								
PENY MLVX27	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (F216353H14 ISOLATE)	496-523								
PENY MLVX28	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE AGM7/CLONE GRI-1)	252-291	1136-122	1548-603	634-708					
PENY MLVX29	GAO POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE AGM7/CLONE GRI-1)	431-507								
PENY MLVX30	NEGATIVE FACTOR	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE AGM7/CLONE GRI-1)	76-137								
PENY MLVX31	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE AGM7/CLONE GRI-1)	478-515								
PENY MLVX32	VIRION INFECTIVITY FACTOR	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE AGM7/CLONE GRI-1)	2-26								
PENY MLVX33	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE GRI1)	8-35	158-185	559-650	784-816					
PENY MLVX34	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE GRI1)	222-254	636-670							
PENY MLVX35	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (KAW ISOLATE)	553-608								
PENY MLVX36	GAO POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (KAW ISOLATE)	88-115								
PENY MLVX37	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (KAW ISOLATE)	533-560								
PENY MLVX38	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	349-608								
PENY MLVX39	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	120-150	550-609	671-715						
PENY MLVX40	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	533-560								
PENY MLVX41	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	156-215	277-289							
PENY MLVX42	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	286-313	554-593	646-722						
PENY MLVX43	GAO POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	88-115								
PENY MLVX44	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	499-526								
PENY MLVX45	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	88-115								
PENY MLVX46	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (TYO-1 ISOLATE)	2-30	264-294	590-617	651-678					
PENY MLVX47	REV PROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (TYO-1 ISOLATE)	657-691								
PENY MLVX48	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (TYO-1 ISOLATE)	41-68								
PENY MLVX49	POL POLYPROTEIN	SIMIAN MASON-PFIZER VIRUS	422-470								
PENY MLVX50	GAO POLYPROTEIN	SIMIAN MASON-PFIZER VIRUS	374-612	670-697							
PENY MLVX51	ALKALINE EXONUCLEASE	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	322-260								
PENY MLVX52	PROBABLE HELICASE	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	109-159								
PENY MLVX53	RBONUCLEOPHOSPH REDUCT LARGE CHA	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	490-517	701-728							
PENY MLVX54	LARGE TEGUMENT PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	119-146								
PENY MLVX55	HYPOTHETICAL GENE 46 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	1121-1158	1579-1609							
PENY MLVX56	GENE 11 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	64-101								
PENY MLVX57			380-407								

FCGID	10111814	All Viruses (no bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	VIRUS	117-119								
PULJ4 VZVD	YINON GENE 24 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)									
PULJ7 VZVD	GENE 21 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	107-114	485-512	719-746	976-1003					
PUL41 VZVD	HOST SHUTOFF VIRION PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	305-364								
PUL41 VZVD	GENE 15 MEMBRANE PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	176-156	312-349							
PUL33 VZVD	PROB DNA REP GENE 6 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	301-337								
PVGLC VZVD	GLYCOPROTEIN GPV	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	295-322								
PV740 VZVD	CAPSID PROTEIN P40	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	174-208	495-522							
PV740 VZVD	PROBABLE DNA PACKAGING PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	394-421								
PVGLC VZVS	GLYCOPROTEIN GPV	VARICELLA-ZOSTER VIRUS (STRAIN SCOTT)	285-326								
PDOL WHV1	DNA POLYMERASE	WOODCHUCK HEPATITIS VIRUS 1	290-311								
PDOL WHV39	DNA POLYMERASE	WOODCHUCK HEPATITIS VIRUS 39	212-242								
PDOL WHV7	DNA POLYMERASE	WOODCHUCK HEPATITIS VIRUS 7	211-241	290-331							
PDOL WHV8	DNA POLYMERASE	WOODCHUCK HEPATITIS VIRUS 8	212-242	285-330							
PDOL WHV81	DNA POLYMERASE	WOODCHUCK HEPATITIS VIRUS 8	212-242	290-331							

TABLE VIII

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL PROCARYOTIC PROTEINS

PCGENE	10711714	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	ORGANISM	81-110	240-298	335-382	638-672	746-738	1168-1202			
P120K_RICRI	120 KD SURFACE-EXPOSED PROTEIN	RICKETTSIA RICKETTSII									
P17K_RICRY	17 KD ANTIGEN PRECURSOR	RICKETTSIA TYPHI	67-94								
P190K_RICRI	190 KD ANTIGEN PRECURSOR (CELL SURFACE)	RICKETTSIA RICKETTSII	241-268	460-487	607-634	734-781	829-836	904-931	1220-1234	1344-1371	1723-1730
P72KD_DESMO	72.6 KD PROTEIN	DESULFOCOCCUS MOBILIS	2065-2096	2131-2168							
P40KD_VIBAN	40 KD PROTEIN PRECURSOR	VIBRIO ANGUILLARUM	35-52	59-89	120-147						
P60MD_ECOLI	60 KD INNER-MEMBRANE PROTEIN	ESCHERICHIA COLI	511-538								
P60IM_PROMI	60 KD INNER-MEMBRANE PROTEIN	PROTEUS MIRABILIS	14-41								
P63KD_ZYMO	63 KD PROTEIN	ZYMONOMAS MOBILIS	95-122	44-524							
P6PGD_BACSU	PROB 6-PHOSPHOGLUCONATE DEHYDROGENASE	BACILLUS SUBTILIS	24-51	218-246							
P6PGD_ECOLI	6-PHOSPHOGLUCONATE DEHYDROGENASE	ESCHERICHIA COLI	205-232								
P6PGD_SALTY	6-PHOSPHOGLUCONATE DEHYDROGENASE	SALMONELLA TYPHIMURIUM	205-232								
P6ACA_STAAL	6'-AMINOGLYCOSIDE N-ACETYLTRANSFERASE	STAPHYLOCOCCUS AUREUS	450-477								
P6AT1_BAGSP	ASPARTATE AMINOTRANSFERASE	BACILLUS SP	146-173	183-212							
P6AT1_ECOLI	ASPARTATE AMINOTRANSFERASE	ESCHERICHIA COLI	351-378								
P6BC_ECOLI	ABC PROTEIN	ESCHERICHIA COLI	176-203								
P6BIC_LACLA	ABORTIVE PHAGE RESISTANCE PROTEIN ABIC	LACTOCOCCUS LACTIS	85-126	170-204	209-223						
P6ACCR_AGRTU	TRANSCRIPTIONAL REPRESSOR ACCR	AGROBACTERIUM TUMEFACIENS	127-154								
P6ACEA_ECOLI	ISOCITRATE LYASE	ESCHERICHIA COLI	398-432								
P6ACON_BACSU	ACONITATE HYDRATASE	BACILLUS SUBTILIS	48-75								
P6ACOR_ALCEU	ACONITATE HYDRATASE	ESCHERICHIA COLI	41-68	613-640							
P6ACP_ECOLI	ACETONIN CATABOLISM REG PRO	ALCALIGENES EUTROPHUS	85-112								
P6ACRA_ECOLI	ACRYL CARRIER PROTEIN	ESCHERICHIA COLI	4-31								
P6ACRB_ECOLI	ACRYLAVIN RESISTANCE PROTEIN A PRECURSOR	ESCHERICHIA COLI	320-357								
P6ACRF_ECOLI	ACRYLAVIN RESISTANCE PROTEIN B	ESCHERICHIA COLI	320-357								
P6ACT1_STRCO	PUTATIVE KETOACYL REDUCTASE	STREPTOMYCES COELICOLOR	512-530	726-753							
P6ACTA_LISMO	ACTIN-ASSEMBLY INDUCING PROTEIN PRECURSOR	LISTERIA MONOCYTOGENES	337-384	576-601							
P6ACVS_NOCLO	ACTV SYNTHETASE	NOCAOIA LACTANDURANS	3179-3163								
P6ADAX_BACSU	METHYLTRANSFERASE	BACILLUS SUBTILIS	136-170								
P6ADDA_BACSU	ATP-DEPENDENT NUCLEASE SUBUNIT A	BACILLUS SUBTILIS	398-425	454-481	532-556	1005-1032					
P6ADDB_BACSU	ATP-DEPENDENT NUCLEASE SUBUNIT B	BACILLUS SUBTILIS	337-384	870-903	943-977						
P6ADHI_CLOAB	NADPH-DEPENDENT BUTANOL DEHYDROGENASE	CLOSTRIDIUM ACETUBUTYLICUM	284-311								
P6ADHB_CLOAB	NADH-DEPENDENT BUTANOL DEHYDROGENASE A	CLOSTRIDIUM ACETUBUTYLICUM	298-325								
P6ADHC_CLOAB	NADH-DEPENDENT BUTANOL DEHYDROGENASE B	CLOSTRIDIUM ACETUBUTYLICUM	298-325								
P6ADHE_ECOLI	ALCOHOL DEHYDROGENASE	ESCHERICHIA COLI	651-680	775-806							
P6ADY_ECOLI	PUTATIVE REGULATORY PROTEIN ADYI	ESCHERICHIA COLI	271-298								
P6ADY_MYCOE	140 KD ADHESIN PRECURSOR	MYCOPLASMA GENITALIUM	45-72								
P6ADPT_MYCPN	ADHESIN P1 PRECURSOR	MYCOPLASMA PNEUMONIAE	90-131	697-724	923-950	990-1017	1169-1199	1387-1414			
P6ADT_RICPR	ADP-ATP CARRIER PROTEIN	RICKETTSIA PROVAZEKII	376-367								
P6AERA_AERHY	AEROXYLASE PRECURSOR	AEROMONAS HYDROPHILA	278-305								
P6AOL_STRAUJ	ALPHA-GALACTOSIDASE	STREPTOCOCCUS MUTANS	419-483	597-633							
P6AGAR_PSEAT	BETA-AARASE PRECURSOR	PSEUDOMONAS ATLANTICA	26-53								
P6AGR_STAAL	ACCESSORY GENE REGULATORY PROTEIN	STAPHYLOCOCCUS AUREUS	129-159	165-192							
P6AL_YEREN	ATTACH INVAS LOCUS PROTEIN PRECURSOR	YERSINIA ENTEROCOLITICA	19-46								
P6AKH_ECOLI	ASPARTOKINASE I	ESCHERICHIA COLI	3-30	468-493	503-530						
P6AKH_ECOLI	ASPARTOKINASE II	ESCHERICHIA COLI	51-78	608-635							
P6AK3_BACSU	ASPARTATE KINASE II ALPHA AND BETA SUBUNITS	BACILLUS SUBTILIS	268-312								
P6AKAB_CORG	ASPARTATE KINASE ALPHA AND BETA SUBUNITS	CORYNEBACTERIUM GLUTAMICUM	5-32								
P6ALF_ECOLI	FRUCTOSE-BISPHOSPHATE ALDOLASE	ESCHERICHIA COLI	286-316								
P6ALGB_PSEAE	ALGNATE BIOSYN TRANS REG PROTEIN ALGB	PSEUDOMONAS AERUGINOSA	160-194								
P6ALGE_PSEAE	ALGNATE PRODUCTION PROTEIN ALGE PRECURSOR	PSEUDOMONAS AERUGINOSA	149-176								
P6ALGP_PSEAE	TRANSCRIPTIONAL REGULATORY PROTEIN ALGP	PSEUDOMONAS AERUGINOSA	81-115								
P6ALKE_PSEOL	ALKANE-1 MONOOXYGENASE	PSEUDOMONAS OLEOVORANS	115-142								
P6ALKT_PSEOL	KUBREDOXIN-NADH REDUCTASE	PSEUDOMONAS OLEOVORANS	138-172	338-365							
P6ALD3_ECOLI	ALANINE RACEMASE, CATABOLIC PRECURSOR	ESCHERICHIA COLI	9-16								

PCGENE	10117144	Proteolytic Sequences	AMPA.1	AMPA.2	AMPA.3	AMPA.4	AMPA.5	AMPA.6	AMPA.7	AMPA.8	AMPA.9
FILENAME	PROTEIN	ORGANISMI									
PALR_BACST	ALANINE RACEMASE	BACILLUS STEAROTHERMOPHILUS	126-151								
PALSR_BACSU	ALS OPERON REGULATORY PROTEIN	BACILLUS SUBTILIS	119-146								
PALYS_BACSP	AUTOLYSIN PRECURSOR	BACILLUS SP	151-187								
PALYS_BACSU	AUTOLYSIN PRECURSOR	BACILLUS SUBTILIS	147-191								
PALYS_STA0U	AUTOLYSIN	STAPHYLOCOCCUS AUREUS	244-271								
PAMIA_STRPN	AMIA PROTEIN PRECURSOR	STREPTOCOCCUS PNEUMONIAE	221-264	146-473							
PAMD_PSECL	AMIDASE	PSEUDOMONAS CILICORAPIUS	72-99								
PAMIE_STRPN	OLIGOPETIDE TRANSPORT PROTEIN AMIE	STREPTOCOCCUS PNEUMONIAE	187-214								
PAMPA_ECOLI	AMINOPEPTIDASE A1	ESCHERICHIA COLI	111-138	199-226							
PAMPC_SERMA	BETA-LACTAMASE PRECURSOR	SERRAIA MARCESCENS	231-258								
PAMPL_RICPR	CYTOSOL AMINOPEPTIDASE	RICKETTSIA PROWAZEKII	3-47	72-99							
PAMPN_ECOLI	AMINOPEPTIDASE N	ESCHERICHIA COLI	655-682								
PAMPP_ECOLI	X-PRO AMINOPEPTIDASE	ESCHERICHIA COLI	110-137								
PAMPT_THBAO	AMINOPEPTIDASE T	THERMUS AQUATICUS	281-308								
PAMV1_DICTH	ALPHA-AMYLASE 1	DICTYOGLOMUS THERMOPHILUM	307-534								
PAMV2_DICTH	ALPHA-AMYLASE 2	DICTYOGLOMUS THERMOPHILUM	151-178	307-534							
PAMV3_DICTH	CYTOSOL AMYLASE	SALMONELLA TYPHIMURUM	70-104								
PAMV4_DICTH	ALPHA-AMYLASE 3	DICTYOGLOMUS THERMOPHILUM	280-307								
PAMV5_DICTH	ALPHA-AMYLASE 4	BACILLUS CIRCULANS	61-88								
PAMV6_DICTH	BETA-AMYLASE PRECURSOR	BACILLUS CIRCULANS	61-88								
PAMV7_DICTH	BETA-AMYLASE	BACILLUS POLYMYXA	60-87	266-293	1143-1184						
PAMV8_DICTH	BETA-AMYLASE	CLOSTRIDIUM THERMOSULFUROGENES	269-296	178-405	459-486						
PAMV9_DICTH	GLUCOAMYLASE PRECURSOR	CLOSTRIDIUM SP	103-148	480-510							
PAMV10_DICTH	MALTOGENIC ALPHA-AMYLASE PRECURSOR	BACILLUS STEAROTHERMOPHILUS	426-453								
PAMV11_DICTH	RAW-STARCH-DIGESTING AMYLASE	BACILLUS SP	210-237	435-465	615-642						
PAMV12_DICTH	ALPHA-AMYLASE PRECURSOR	AEROMONAS HYDROPHILA	415-433								
PAMV13_DICTH	ALPHA-AMYLASE PRECURSOR	ALTEROMONAS HALOPLANKTIS	166-193								
PAMV14_DICTH	ALPHA-AMYLASE PRECURSOR	BACILLUS AMYLOLIQUEFACIENS	102-136								
PAMV15_DICTH	ALPHA-AMYLASE PRECURSOR	BACILLUS CIRCULANS	212-239	437-474							
PAMV16_DICTH	ALPHA-AMYLASE PRECURSOR	BACILLUS MEGATERIUM	61-88	441-482							
PAMV17_DICTH	ALPHA-AMYLASE PRECURSOR	BACILLUS SUBTILIS	165-203	281-308							
PAMV18_DICTH	ALPHA-AMYLASE PRECURSOR	BUTYRIVIBRIO FIBRISOLVENS	372-418	546-571	579-606	793-822					
PAMV19_DICTH	PUTATIVE ALPHA-AMYLASE	CLOSTRIDIUM ACETOBYTILICUM	283-310								
PAMV20_DICTH	ALPHA-AMYLASE PRECURSOR	CLOSTRIDIUM THERMOSULFUROGENES	431-468	612-642							
PAMV21_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	173-200								
PAMV22_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV23_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV24_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV25_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV26_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV27_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV28_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV29_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV30_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV31_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV32_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV33_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV34_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV35_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV36_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV37_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV38_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV39_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV40_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV41_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV42_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV43_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV44_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV45_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV46_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV47_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV48_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV49_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV50_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV51_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV52_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV53_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV54_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV55_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV56_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV57_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV58_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV59_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV60_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV61_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV62_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV63_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV64_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV65_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV66_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV67_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV68_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV69_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV70_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV71_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV72_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV73_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV74_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV75_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV76_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV77_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV78_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV79_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV80_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV81_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV82_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV83_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV84_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV85_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV86_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV87_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV88_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV89_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV90_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV91_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV92_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV93_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV94_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV95_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV96_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV97_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV98_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV99_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV100_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								

PGENE	1071714	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
FILENAME	PROTEIN	ORGANISM	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PAPK1 ECOLI	SHIKIMATE KINASE I	ESCHERICHIA COLI	84-118								
PAPM1 STRYP	IGA RECEPTOR PRECURSOR	STREPTOCOCCUS PYOGENES	12-46	127-137	266-324						
PAPP1 ECOLI	ADP PROTEIN	ESCHERICHIA COLI	201-282								
PASB1 ECOLI	ARSENICAL PUMP-DRIVING ATPASE	ESCHERICHIA COLI	201-238								
PASB2 ECOLI	ARSENICAL PUMP MEMBRANE PROTEIN	ESCHERICHIA COLI	291-318								
PASB3 STAAU	ARSENICAL PUMP MEMBRANE PROTEIN	STAPHYLOCOCCUS AUREUS	27-71	295-322							
PASB4 STAAU	ARSENICAL PUMP MEMBRANE PROTEIN	STAPHYLOCOCCUS AUREUS	27-71	295-322							
PASB5 STAAU	ARSENICAL RESIST OPERON REPRESSOR PROTEIN	STAPHYLOCOCCUS AUREUS	56-93								
PART1 ECOLI	ARTA PROTEIN	ESCHERICHIA COLI	3-30								
PART2 ECOLI	TRANSPORT SYSTEM PROTEIN ART1	ESCHERICHIA COLI	105-132	213-240							
PART3 ECOLI	TRANSPORT SYSTEM PROTEIN ART2	ESCHERICHIA COLI	176-266								
PASAT1 ENTITA	AGGREGATION SUBSTANCE PRECURSOR	ENTEROCOCCUS FAECALIS	193-234	478-505	799-826	859-906					
PASNA1 ECOLI	ASPARTATE-AMMONIA LIGASE	ESCHERICHIA COLI	127-158								
PASNB1 ECOLI	ASPARAGINE SYNTHETASE II	ESCHERICHIA COLI	436-477								
PASNC1 ECOLI	REGULATORY PROTEIN ASNC	ESCHERICHIA COLI	116-141								
PASPA1 DACSU	ASPARTATE AMMONIA-LYASE	BACILLUS SUBTILIS	7-34								
PASPA2 ECOLI	ASPARTATE AMMONIA-LYASE	ESCHERICHIA COLI	204-236								
PASPA3 SERMA	ASPARTATE AMMONIA-LYASE	SERRATIA MARCESCENS	204-231								
PASPA4 BACLI	L-ASPARAGINASE	BACILLUS LICHENIFORMIS	233-288								
PASPO1 ERWCH	L-ASPARAGINASE PRECURSOR	ERWINIA CHRYSAENTHEMI	188-218								
PASPO2 ACIGL	GLUTAMINASE-ASPARAGINASE	ACINETOBACTER GLUTAMINIFICANS	46-80								
PASPY1 ECOLI	ARGININOSUCCINATE SYNTHASE	ESCHERICHIA COLI	334-381								
PASPY2 METBA	ARGININOSUCCINATE SYNTHASE	METHANOSARCINA BARKEI	287-314								
PATPA1 STAAU	POTENTIAL ATP-BINDING PROTEIN	STAPHYLOCOCCUS AUREUS	201-245								
PATPA2 ENTITA	POTASSIUMCOPPER-TRANSPORTING ATPASE A	ENTEROCOCCUS FAECALIS	41-68	201-245							
PATPA3 ENTITA	POTASSIUMCOPPER-TRANSPORTING ATPASE B	ENTEROCOCCUS FAECALIS	41-80	247-374							
PATPB1 SALTU	MGE(2) TRANSPORT ATPASE P-TYPE	SALMONELLA TYPHIMURUM	280-310	450-477							
PATPB2 SYN76	ATP SYNTHASE A CHAIN	SYNECHOCOCCUS SP	501-530								
PATPB3 VIBAL	ATP SYNTHASE A CHAIN	VIBRIO ALGINOLYTICUS	233-260								
PATPA4 ANASP	ATP SYNTHASE ALPHA CHAIN	ANABAENA SP	11-38	96-130							
PATPA5 BACME	ATP SYNTHASE ALPHA CHAIN	BACILLUS MEGATERIUM	4-36	453-480							
PATPA6 ECOLI	ATP SYNTHASE ALPHA CHAIN	ESCHERICHIA COLI	486-513								
PATPA7 ENTITA	ATP SYNTHASE ALPHA CHAIN	ENTEROCOCCUS FAECALIS	4-36	484-518							
PATPA8 MYCGA	ATP SYNTHASE ALPHA CHAIN	MYCOPLASMA GALLISEPTICUM	362-409								
PATPA9 PROMO	ATP SYNTHASE ALPHA CHAIN	PROFIBRILLUM MODESTUM	6-36								
PATPA10 RHORU	ATP SYNTHASE ALPHA CHAIN	RHODOPIRILLUM RUBRUM	165-200	459-486							
PATPA11 SULAC	ATPASE ALPHA CHAIN	SULFOLOBUS ACIDOCALDARIUS	318-345	562-589							
PATPA12 SYN71	ATP SYNTHASE ALPHA CHAIN	SYNECHOCOCCUS SP	7-44								
PATPA13 SYN73	ATP SYNTHASE ALPHA CHAIN	SYNECHOCOCCUS SP	8-45	362-389							
PATPA14 THEP3	ATP SYNTHASE ALPHA CHAIN	SYNECHOCYSTIS SP	8-37	454-500							
PATPA15 VIBAL	ATP SYNTHASE ALPHA CHAIN	THERMOPHILIC BACTERIUM PS-1	9-36								
PATPB1 ANASP	ATP SYNTHASE BETA CHAIN	VIBRIO ALGINOLYTICUS	444-513								
PATPB2 BACFI	ATP SYNTHASE BETA CHAIN	ANABAENA SP	280-307	370-397							
PATPB3 MYCGA	ATP SYNTHASE BETA CHAIN	BACILLUS FIRMIUS	163-190	358-385							
PATPB4 RHORU	ATP SYNTHASE BETA CHAIN	MYCOPLASMA GALLISEPTICUM	375-402								
PATPB5 SULAC	ATPASE BETA CHAIN	RHODOPIRILLUM RUBRUM	339-386								
PATPB6 SYN71	ATP SYNTHASE BETA CHAIN	SULFOLOBUS ACIDOCALDARIUS	164-191								
PATPB7 SYN76	ATP SYNTHASE BETA CHAIN	SYNECHOCOCCUS SP	381-408								
PATPB8 SYN73	ATP SYNTHASE BETA CHAIN	SYNECHOCOCCUS SP	291-318	381-408							
PATPB9 BACFI	ATP SYNTHASE BETA CHAIN	ANABAENA SP	309-339	143-170							
PATPD1 ENTITA	ATP SYNTHASE DELTA CHAIN	BACILLUS MEGATERIUM	63-90	133-160							
PATPD2 PROMO	ATP SYNTHASE DELTA CHAIN	ENTEROCOCCUS FAECALIS	14-41								
PATPD3 RHORU	ATP SYNTHASE DELTA CHAIN	PROFIBRILLUM MODESTUM	79-116	118-149							
PATPD4 RHORU	ATP SYNTHASE DELTA CHAIN	RHODOPIRILLUM RUBRUM	125-152								
PATPD5 RHORU	ATP SYNTHASE DELTA CHAIN	RHODOPIRILLUM RUBRUM	119-146								





PCGENE	1071714	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9	AREA.10
PIE NARJE	PROTEIN	ORGANISM	824-551									
PBOAL CLOAB	BETA-GALACTOSIDASE	CLOSTRIDIUM ACETORUTYLICUM	161-191									
PBOAL CLOTB	BETA-GALACTOSIDASE	CLOSTRIDIUM THERMOSULFURIGENES	245-272									
PBOAL KLEPN	BETA-GALACTOSIDASE	KLEBSIELLA PNEUMONIAE	105-132									
PBOAL LACDE	BETA-GALACTOSIDASE	LACTOBACILLUS DELBRUECKII	188-215									
PBOAL STRTR	BETA-GALACTOSIDASE	STREPTOCOCCUS THERMOPHILUS	59-86	179-206								
PBOAL SULSO	BETA-GALACTOSIDASE	SULFOLOBUS SOLFATARICUS	179-156									
PBOAL LEULA	BETA-GALACTOSIDASE	LEUCONOSTOC LACTIS	352-380	418-445								
PBOAL SULSO	BETA-GALACTOSIDASE	SULFOLOBUS SOLFATARICUS	259-286	375-409	534-581	631-665						
PBOAL CLOTM	BETA-GALACTOSIDASE A	CLOSTRIDIUM THERMOCILLUM	464-494	536-563								
PBOAL CLOTM	THERMOSTABLE BETA-GLUCOSIDASE B	CLOSTRIDIUM THERMOCILLUM	421-448									
PBOAL ECOLI	BETA-GLUCURONIDASE	ESCHERICHIA COLI	85-112	435-462	692-719	738-765						
PBOAL AGASP	BETA-GLUCOSIDASE	AGROBACTERIUM SP	60-87									
PBOAL BUTFI	BETA-GLUCOSIDASE A	BUTYRIVIBRIO TIBRIOLVENS	163-197									
PBOAL STAAU	POTENTIAL DNA-INVERTASE BINJ	STAPHYLOCOCCUS AUREUS	163-190									
PBOAL STAAU	TRANSPOSON TNS51 RESOLVASE	STAPHYLOCOCCUS AUREUS	163-190									
PBOAL STAAU	DNA-INVERTASE BINR	STAPHYLOCOCCUS AUREUS	31-60									
PBOAL BACSH	AMINO-TRANSFERASE	BACILLUS SPIAERICUS	145-172									
PBOAL BACSH	BIOTIN SYNTHETASE	BACILLUS SPIAERICUS	130-157									
PBOAL ECOLI	BIOTIN SYNTHETASE	ESCHERICHIA COLI	144-171									
PBOAL BACSH	DETHIOTIN SYNTHASE	BACILLUS SPIAERICUS	91-118	275-305								
PBOAL BACCE	BETA-LACTAMASE PRECURSOR, TYPE I	BACILLUS CEREUS	152-179	204-231								
PBOAL HAENI	BETA-LACTAMASE ROB-1 PRECURSOR	HAEMOPHILUS INFLUENZAE	18-67	201-228								
PBOAL BACCE	BETA-LACTAMASE PRECURSOR, TYPE II	BACILLUS CEREUS	18-67	201-228								
PBOAL BACCP	BETA-LACTAMASE PRECURSOR, TYPE II	BACILLUS SP	33-83	93-129								
PBOAL BACCE	BETA-LACTAMASE PRECURSOR, TYPE III	BACILLUS CEREUS	19-50									
PBOAL PSEAE	BETA-LACTAMASE PSE-4 PRECURSOR	PSEUDOMONAS AERUGINOSA	20-56	200-227								
PBOAL BACCE	BETA-LACTAMASE PRECURSOR, TYPE II	BACILLUS CEREUS	22-49									
PBOAL BACFR	BETA-LACTAMASE PRECURSOR, TYPE II	BACTEROIDES FRAGILIS	93-120	276-303								
PBOAL BACCE	BETA-LACTAMASE PRECURSOR, TYPE I	BACILLUS CEREUS	47-74	86-115								
PBOAL BACLI	BETA-LACTAMASE PRECURSOR	BACILLUS LICHENIFORMIS	191-221									
PBOAL PROMJ	BETA-LACTAMASE PRECURSOR	PROTEUS MIRABILIS	4-38	240-267								
PBOAL PROVO	BETA-LACTAMASE	PROTEUS VULGARIS	43-70									
PBOAL STRAL	BETA-LACTAMASE PRECURSOR	STREPTOMYCES ALBUS G	121-148									
PBOAL KLEPN	BETA-LACTAMASE PRECURSOR	KLEBSIELLA PNEUMONIAE	19-74	99-126								
PBOAL STAAU	PENICILLINASE PREPRESSOR	STAPHYLOCOCCUS AUREUS	118-166	235-262								
PBOAL ECOLI	BETA-LACTAMASE PRECURSOR	ESCHERICHIA COLI	155-196									
PBOAL ECOLI	BETA-LACTAMASE PSE-2 PRECURSOR	ESCHERICHIA COLI	87-114	122-161	234-261	281-312	503-539					
PBOAL BACLI	REGULATORY PROTEIN BLAR1	BACILLUS LICHENIFORMIS	312-346									
PBOAL STAAU	REGULATORY PROTEIN BLAR1	STAPHYLOCOCCUS AUREUS	277-304									
PBOAL TREPA	BASIC MEMBRANE PROTEIN PRECURSOR	TREPONEMA PALLIDUM	36-63									
PBOAL BACSU	MULTIDRUG RESISTANCE PROTEIN	BACILLUS SUBTILIS	119-153									
PBOAL PSEPU	BENZENE 1,2-DIOXYGENASE ALPHA SUBUNIT	PSEUDOMONAS PUTIDA	179-213									
PBOAL PSEPU	BENZENE 1,2-DIOXYGENASE BETA SUBUNIT	PSEUDOMONAS PUTIDA	157-217	242-290	311-355	391-425	543-573					
PBOAL DESAM	BP52 PROTEIN	DESULFURELOBUS AMBIVALENS	260-287	313-340								
PBOAL PSEAE	CARRIER PROTEIN	PSEUDOMONAS AERUGINOSA	254-281									
PBOAL PSEAE	TRANSPORT PROTEIN BRAE	PSEUDOMONAS AERUGINOSA	7-34									
PBOAL PSEAE	BRAG PROTEIN	PSEUDOMONAS AERUGINOSA	439-466									
PBOAL ECOLI	VITAMIN B12 RECEPTOR PRECURSOR	ESCHERICHIA COLI	6-33									
PBOAL ECOLI	VITAMIN B12 TRANSPORT PERIPLASMIC PROTEIN	ESCHERICHIA COLI	174-205									
PBOAL BORPE	TRANSCRIPTION REGULATOR BVGA	BORDETTELLA PERTUSSIS	116-143									
PBOAL BORPE	PERIPLASMIC PROTEIN BVGB PRECURSOR	BORDETTELLA PERTUSSIS	39-66	202-229								
PBOAL BORPE	SENSOR PROTEIN BVGC	BORDETTELLA PERTUSSIS	113-143	241-268	501-531							
PBOAL BORER	VITALENCE BVGS PROTEIN PRECURSOR	BORDETTELLA BRONCHISEPTICA	313-340									
PBOAL CLOBO	BOTULINUM NEUROTOXIN TYPE A PRECURSOR	CLOSTRIDIUM BOTULINUM	666-693	720-762	802-832	853-890	1004-1031	1058-1089				
PBOAL CLOBO	BOTULINUM NEUROTOXIN TYPE B PRECURSOR	CLOSTRIDIUM BOTULINUM										

PGCENE	1071784	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
FILENAME	PROTEIN	ORGANISM	86-113	314-341	710-773	798-825	830-892				
PBXCI_CLOBO	CLOSTRIDIUM NEUROTOXIN TYPE C1 PRECURSOR	CLOSTRIDIUM BOTULINUM	86-113	314-341	710-773	798-825	830-892				
PBXDO_CLOBO	CLOSTRIDIUM NEUROTOXIN TYPE D PRECURSOR	CLOSTRIDIUM BOTULINUM	471-500	526-576	721-770	804-831	847-892	906-963	1060-1087		
PBXE_CLOBO	CLOSTRIDIUM NEUROTOXIN TYPE E PRECURSOR	CLOSTRIDIUM BOTULINUM	234-291	350-381	704-733	773-811	890-917	992-1019	1113-1149		
PBXF_CLOBO	CLOSTRIDIUM NEUROTOXIN TYPE F PRECURSOR	CLOSTRIDIUM BOTULINUM	234-291	350-381	704-733	773-811	890-917	992-1019	1113-1149		
PCASO_MICAE	CYTCHROME C550	MICROCYSTIS AERUGINOSA	3-70	733-772	892-919	1013-1040	1093-1122	1183-1210			
PCADA_BACFI	PROBABLE CADMIUM-TRANSPORTING ATPASE	BACILLUS FIRMIUS	30-37	100-131	163-192	276-306	333-367				
PCADA_STAAU	PROBABLE CADMIUM-TRANSPORTING ATPASE	STAPHYLOCOCCUS AUREUS	282-309	316-370							
PCADC_ECOLI	TRANSCRIPTIONAL ACTIVATOR CADC	ESCHERICHIA COLI	54-85	412-443							
PCAFI_YERPE	F1 CAPSULE ANCHORING PROTEIN PRECURSOR	YERSINIA PESTIS	201-240	416-437	510-537	619-646					
PCAPB_BACAN	CAPP PROTEIN	BACILLUS ANTHRACIS	108-118								
PCAPP_ANANI	PHOSPHOENOLPYRUVATE CARBOXYLASE	ANACYSTIS NIDULANS	36-70								
PCAPP_ANASP	PHOSPHOENOLPYRUVATE CARBOXYLASE	ANABAENA SP	98-123	137-184	687-728						
PCAPP_CORGL	PHOSPHOENOLPYRUVATE CARBOXYLASE	CORYNEBACTERIUM GLUTAMICUM	15-42								
PCAPP_ECOLI	PHOSPHOENOLPYRUVATE CARBOXYLASE	ESCHERICHIA COLI	35-62								
PCARA_BACSU	CARBAMOYL-PHOSPHATE SYNTHASE	BACILLUS SUBTILIS	274-319								
PCARB_BACSU	CARBAMOYL-PHOSPHATE SYNTHASE	BACILLUS SUBTILIS	790-831								
PCARB_ECOLI	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAI	ESCHERICHIA COLI	434-481								
PCAT2_STAAU	CHLORAMPHENICOL ACETYLTRANSFERASE	STAPHYLOCOCCUS AUREUS	7-34	87-114							
PCAT3_STAAU	CHLORAMPHENICOL ACETYLTRANSFERASE	STAPHYLOCOCCUS AUREUS	7-34	87-114							
PCATA_AGICA	CATECHOL 1,2-DIOXYGENASE	ACINETOBACTER CALCOACETICUS	31-63								
PCATA_BACST	PEROXIDASE / CATALASE	BACILLUS STEAROTHERMOPHILUS	440-470								
PCATA_ECOLI	CATALASE HPI	ESCHERICHIA COLI	570-606								
PCATA_MICLU	CATALASE	MICROCOCCUS LUTEUS	433-480								
PCATA_SALTY	CATALASE HPI	SALMONELLA TYPHIMURUM	515-542	380-607							
PCATE_ECOLI	CATALASE HPI	ESCHERICHIA COLI	175-202								
PCAT_CAMGO	CHLORAMPHENICOL ACETYLTRANSFERASE	CAMPYLOBACTER COLI	84-111								
PCAT_CLOBU	CHLORAMPHENICOL ACETYLTRANSFERASE	CLOSTRIDIUM BUTYRICUM	88-115								
PCAT_ECOLI	CHLORAMPHENICOL ACETYLTRANSFERASE	ESCHERICHIA COLI	92-119								
PCAT_PROMI	CHLORAMPHENICOL ACETYLTRANSFERASE	PROTEUS MIRABILIS	92-119								
PCAT_STAM	CHLORAMPHENICOL ACETYLTRANSFERASE	STAPHYLOCOCCUS INTERMEDIUS	7-34	87-114							
PCAT_STAO	CHLORAMPHENICOL ACETYLTRANSFERASE	STREPTOCOCCUS AGALACTICAE	7-34	87-114							
PCBIHE_COXBU	CBHE PROTEIN	COXIELLA BURNETII	300-236								
PCBFT_THEYU	CARBOXYPEPTIDASE T PRECURSOR	THERMOACTINOMYCES VULGARIS	48-75								
PCCA_ECOLI	TRNA NUCLEOTIDYLTRANSFERASE	ESCHERICHIA COLI	376-403								
PCCHAK_STN97	COI CONC MECH PROTEIN CCNOK	SYNECHOCOCCUS SP	29-36								
PCCHM_STN97	COI CONC MECH PROTEIN CCNOK	SYNECHOCOCCUS SP	212-236	331-372	445-486						
PCDAS_THIEE	CYCLOMALTODEXTRINASE	THERMOANEROBACTER ETIANOLICUS	305-332								
PDD01_BACMA	CYCLOMALTODEXTRIN PRECURSOR	BACILLUS MACERANS	439-466	610-643							
PDD02_BACMA	CYCLOMALTODEXTRIN PRECURSOR	BACILLUS MACERANS	210-231	416-466	615-642						
PDD03_BACCI	CYCLOMALTODEXTRIN PRECURSOR	BACILLUS CIRCULANS	217-244	442-472	594-631						
PDD04_BACCI	CYCLOMALTODEXTRIN PRECURSOR	BACILLUS CIRCULANS	217-244	442-472	594-631						
PDD05_BACOH	CYCLOMALTODEXTRIN PRECURSOR	BACILLUS LICHENIFORMIS	217-244	442-472	594-631						
PDD06_BACOH	CYCLOMALTODEXTRIN PRECURSOR	BACILLUS LICHENIFORMIS	430-471								
PDD07_BAC50	CYCLOMALTODEXTRIN PRECURSOR	BACILLUS SP	210-237	433-462	615-642						
PDD08_BAC51	CYCLOMALTODEXTRIN PRECURSOR	BACILLUS SP	409-471								
PDD09_BAC51	CYCLOMALTODEXTRIN PRECURSOR	BACILLUS SP	210-237	433-462	614-641						
PDD10_BAC51	CYCLOMALTODEXTRIN PRECURSOR	BACILLUS SP	210-237	433-462	615-642						
PDD11_BAC51	CYCLOMALTODEXTRIN PRECURSOR	BACILLUS SP	217-244	442-472	594-631						
PDD12_BAC51	CYCLOMALTODEXTRIN PRECURSOR	BACILLUS SP	516-646								
PDD13_BAC51	CYCLOMALTODEXTRIN PRECURSOR	BACILLUS STEAROTHERMOPHILUS	212-239								
PDD14_KLEPN	CYCLOMALTODEXTRIN PRECURSOR	KLEBSIELLA PNEUMONIAE	44-71	283-326							
PCEA1_ECOLI	COLICIN E1 PROTEIN	ESCHERICHIA COLI	44-71	283-326							
PCEA2_ECOLI	COLICIN E2	SHIGELLA SONNEI	44-71	283-326	413-440						
PCEA3_ECOLI	COLICIN E3	ESCHERICHIA COLI	314-368								
PCEA4_ECOLI	COLICIN E4	ESCHERICHIA COLI	314-368								
PCEA5_ECOLI	COLICIN E5	ESCHERICHIA COLI	314-368								
PCEA6_ECOLI	COLICIN E6	ESCHERICHIA COLI	314-368								
PCEA7_ECOLI	COLICIN B	ESCHERICHIA COLI	283-341								

PCGENE	10117104	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
FILENAME	PROLIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PCB01 ECOLI	COLICIN D	ESCHERICHIA COLI	244-311									
PCB02 ECOLI	COLICIN M	ESCHERICHIA COLI	178-227									
PCB03 ECOLI	COLICIN N	ESCHERICHIA COLI	119-146									
PCB04 ECOLI	COLICIN A	CITROBACTER FREUNDII	228-258									
PCB05 ECOLI	ISOPENICILLIN N EPIMERASE	STREPTOMYCES CLAVULIGERUS	170-197									
PCB06 ECOLI	COLICIN IA PROTEIN	ESCHERICHIA COLI	68-93									
PCB07 ECOLI	COLICIN IB PROTEIN	ESCHERICHIA COLI	68-93									
PCB08 ECOLI	UTP URIDYL TRANSFERASE	ACETOBACTER XYLINUM	59-89									
PCB09 ECOLI	PROTEIN CELA	ESCHERICHIA COLI	76-103									
PCB10 ECOLI	CFAT FIMBRIAL SUBUNIT A PRECURSOR	ESCHERICHIA COLI	27-38									
PCB11 ECOLI	CFAT FIMBRIAL SUBUNIT C PRECURSOR	ESCHERICHIA COLI	138-187									
PCB12 ECOLI	CFAT FIMBRIAL SUBUNIT D	ESCHERICHIA COLI	133-160									
PCB13 ECOLI	CFAT FIMBRIAL SUBUNIT E	ESCHERICHIA COLI	180-207									
PCB14 ACTPS	10 KD CHAPERONIN	ACTYTHOSIPHON PISONI SYMBIOTIC BACTERIU	57-93									
PCB15 BACSU	10 KD CHAPERONIN	BACILLUS SUBTILIS	66-93									
PCB16 CHLTR	10 KD CHAPERONIN	CHLAMYDIA TRACHOMATIS	64-91									
PCB17 ECOLI	10 KD CHAPERONIN	ESCHERICHIA COLI	57-84									
PCB18 HAEDU	10 KD CHAPERONIN	HAEMOPHILUS DUCREYI	68-93									
PCB19 LEGMI	10 KD CHAPERONIN	LEGIONELLA MICHIGANENSIS	57-84									
PCB20 RICTS	10 KD CHAPERONIN	RICKETTSIA TSUTSUGAMUSHI	65-92									
PCB21 THEP3	10 KD CHAPERONIN	THERMOPHILIC BACTERIU PS-3	66-93									
PCB22 ACTPS	60 KD CHAPERONIN	ACTYTHOSIPHON PISONI SYMBIOTIC BACTERIU	341-382									
PCB23 AORTU	60 KD CHAPERONIN	AGROBACTERIUM TUMEFACIENS	117-163									
PCB24 AMOPS	60 KD CHAPERONIN	AMOEBA PROTEUS SYMBIOTIC BACTERIU	299-333									
PCB25 BACSU	60 KD CHAPERONIN	BACILLUS SUBTILIS	298-332									
PCB26 BORBU	60 KD CHAPERONIN	BORRELIA BURGDORFERI	125-163									
PCB27 BRUAB	60 KD CHAPERONIN	BRUCELLA ABORTUS	117-144									
PCB28 CHLPN	60 KD CHAPERONIN	CHLAMYDIA PNEUMONIAE	4-31									
PCB29 CHLTR	60 KD CHAPERONIN	CHLAMYDIA TRACHOMATIS	4-31									
PCB30 CHRV1	60 KD CHAPERONIN	CHROMATIUM VINOSUM	300-327									
PCB31 CLOAB	60 KD CHAPERONIN	CLOSTRIDIUM ACETOBUTYLICUM	218-322									
PCB32 CLOPE	60 KD CHAPERONIN	CLOSTRIDIUM PERFRINGENS	337-368									
PCB33 COXBU	60 KD CHAPERONIN	COXIELLA BURNETII	300-327									
PCB34 HAEDU	60 KD CHAPERONIN	HAEMOPHILUS DUCREYI	339-366									
PCB35 LEGMI	60 KD CHAPERONIN	LEGIONELLA MICHIGANENSIS	299-333									
PCB36 LEGPN	60 KD CHAPERONIN	LEGIONELLA PNEUMOPHILA	298-332									
PCB37 MYCLE	60 KD CHAPERONIN	MYCOBACTERIUM LEPTAE	123-132									
PCB38 MYCTU	60 KD CHAPERONIN	MYCOBACTERIUM TUBERCULOSIS & BOVIS	123-132									
PCB39 PSEAE	60 KD CHAPERONIN	PSEUDOMONAS AERUGINOSA	339-366									
PCB40 RHUV	60 KD CHAPERONIN	RHIZOBIUM LEGUMINOSARUM	117-163									
PCB41 RICTS	60 KD CHAPERONIN	RICKETTSIA TSUTSUGAMUSHI	103-130									
PCB42 STNPT	60 KD CHAPERONIN	SYNECHOCOCCLUS SP	308-333									
PCB43 STNPT	60 KD CHAPERONIN	SYNECHOCYSTIS SP	338-363									
PCB44 THEP3	60 KD CHAPERONIN	THERMOPHILIC BACTERIU PS-3	337-364									
PCB45 STRAL	60 KD CHAPERONIN 2	STREPTOMYCES ALBUS G	116-148									
PCB46 VIBHA	N-F-DIACETYL CHITINBIASE PRECURSOR	VIBRIO HARVEYI	21-48									
PCB47 BACSU	CHEMOTAXIS PROTEIN CHEA	BACILLUS SUBTILIS	373-400									
PCB48 ECOLI	CHEMOTAXIS PROTEIN CHEA	ESCHERICHIA COLI	256-286									
PCB49 SALTY	CHEMOTAXIS PROTEIN CHEA	SALMONELLA TYPHIMURIUM	162-197									
PCB50 BACSU	CHEMOTAXIS PROTEIN METHYLTRANSFERASE	BACILLUS SUBTILIS	124-151									
PCB51 ECOLI	PURINE-BINDING CHEMOTAXIS PROTEIN	ESCHERICHIA COLI	88-115									
PCB52 SALTY	PURINE-BINDING CHEMOTAXIS PROTEIN	SALMONELLA TYPHIMURIUM	88-115									
PCB53 ECOLI	CHEMOTAXIS PROTEIN CHEY	ESCHERICHIA COLI	22-49									
PCB54 SALTY	CHEMOTAXIS PROTEIN CHEY	SALMONELLA TYPHIMURIUM	22-49									
PCB55 BACCI	CHITINASE A1 PRECURSOR	BACILLUS CIRCULANS	491-518									
PCB56 ALTSO	CHITINASE A PRECURSOR	ALTERNONAS SP	345-372									
PCB57 SERMA	CHITINASE A PRECURSOR	SERRATIA MARCESCENS	346-373									

PCGENE	10117144	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
ULK1NAMK	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PC1HD BACCI	CHITINASE D PRECURSOR	BACILLUS CIRCULANS	102-161	189-216							
PC1HT SACER	CHITINASE	SACCHAROPOLYSPORA ERYTHRAEA	92-119								
PC1HT STRPL	CHITINASE	STREPTONYCES PULICATUS	250-284								
PC1MD BACSU	CHORISMATE MUTASE	BACILLUS SUBTILIS	3-17								
PC1OD BREST	CHOLESTEROL OXIDASE PRECURSOR	BREVIBACTERIUM STEROLICUM	263-290								
PC1TA VIBCH	CHOLESTEROL OXIDASE PRECURSOR	VIBRIO CHOLERAE	79-106								
PC1VA AGRTU	BETA(1->2)GLUCAN EXPORT PROTEIN	AGROBACTERIUM TUMEFACIENS	4-31	181-208							
PC1VE AGRTU	RECEPTOR PROTEIN CHVE PRECURSOR	AGROBACTERIUM TUMEFACIENS	403-462								
PC1RI CITFR	CITROLYSIN PROTEIN I	CITROBACTER FREUNDII	146-173								
PC1RA ECOLI	COLICIN I RECEPTOR PRECURSOR	ESCHERICHIA COLI	378-405								
PC1SA BACSU	PUTATIVE DNA RECOMBINASE	BACILLUS SUBTILIS	143-170								
PC1SY ACIAN	CITRATE SYNTHASE	ACINETOBACTER ANITRATUM	24-51								
PC1SY BACCO	CITRATE SYNTHASE	BACILLUS COAGULANS	154-181								
PC1TA SALTY	CITRATE-PROTON SYMPORT	SALMONELLA TYPHIMURIUM	194-221								
PC1TN KLEPN	CITRATE-SODIUM SYMPORT	KLEBSIELLA PNEUMONIAE	194-221								
PC1TN SALDU	CITRATE-SODIUM SYMPORT	SALMONELLA DUBLIN	13-36								
PC1TN SALPU	CITRATE-SODIUM SYMPORT	SALMONELLA PULLORUM	13-36								
PC1CA PSEPU	CHLOROCATECHOL 1,2-DIOXYGENASE	PSEUDOMONAS PUTIDA	13-167								
PC1DI ECOLI	CHAIN LENGTH DETERMINANT PROTEIN	ESCHERICHIA COLI	178-212	250-277							
PC1D2 ECOLI	CHAIN LENGTH DETERMINANT PROTEIN	ESCHERICHIA COLI	96-127	151-212							
PC1D3 ECOLI	CHAIN LENGTH DETERMINANT PROTEIN	SALMONELLA TYPHIMURIUM	30-58	497-524							
PC1OS CLOHI	ALPHA-CLOSTRUPAIN PRECURSOR	CLOSTRIDIUM HISTOLYTICUM	653-693								
PC1PA ECOLI	ATP-BINDING SUBUNIT CLPA	ESCHERICHIA COLI	419-466								
PC1PA RHOBL	CLPA HOMOLOG PROTEIN	RHODOSPIRILLUM RUBRUM	116-137	442-476	558-595						
PC1PB BACNO	CLPB HOMOLOG PROTEIN	BACTEROIDES NODOSUS	444-489	563-590							
PC1PB ECOLI	CLPB PROTEIN	ESCHERICHIA COLI	215-242	312-359							
PC1PX AZOVI	CLPX HOMOLOG PROTEIN	AZOTOBACTER VINELANDII	353-383								
PC1PX ECOLI	ATP-BINDING SUBUNIT CLPX	ESCHERICHIA COLI	50-77								
PC1N8 ECOLI	2,3-CYCLO-L-ALC-2-PHOSPHODIESTERASE PRECURSOR	ESCHERICHIA COLI	102-129								
PC1DA ECOLI	CYTOSINE DEAMINASE	ESCHERICHIA COLI	108-135	186-213							
PC1M1 BACSU	A COMPETENCE PROTEIN I	BACILLUS SUBTILIS	154-239								
PC1M0 BACSU	COMPETENCE REGULATORY PROTEIN	BACILLUS SUBTILIS	2-53								
PC1P4 STAAU	COP-4 PROTEIN	STAPHYLOCOCCUS AUREUS	140-167								
PC1P8 PSESM	COPPER RESISTANCE PROTEIN B PRECURSOR	PSEUDOMONAS SYRINGAE	134-161								
PC1P4 ECOLI	MAGNESIUM/COBALT TRANSPORT PROTEIN CORA	ESCHERICHIA COLI	134-161								
PC1P4 SALTY	MAGNESIUM/COBALT TRANSPORT PROTEIN CORA	SALMONELLA TYPHIMURIUM	42-92								
PC1TE BACSU	SPORE COAT PROTEIN E	BACILLUS SUBTILIS	380-407								
PC1X1 BRAJA	CYTCHROME C OXIDASE POLYPEPTIDE I	BRADYRHIZOBIUM JAPONICUM	383-410								
PC1X1 PARDE	CYTCHROME C OXIDASE POLYPEPTIDE I	PARACOCCLUS DENTRIFICANS	396-423								
PC1X1 RHOSH	CYTCHROME C OXIDASE POLYPEPTIDE I	RHODOBACTER SPHAEROIDES	36-63								
PC1X1 BACFI	OXIDASE ASSEMBLY FACTOR	BACILLUS FIRMIUS	49-76								
PC1X1 BACSU	OXIDASE ASSEMBLY FACTOR	BACILLUS SUBTILIS	72-99	165-209							
PC1P8 NEIGO	CRYPTIC PLASMID PROTEIN B	NEISSERIA GONORRHOEA	309-336								
PC1SB ECOLI	MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE	ESCHERICHIA COLI	311-338								
PC1SB SALTY	MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE	SALMONELLA TYPHIMURIUM	254-281								
PC1XA ECOLI	SENSOR PROTEIN CPXA	ESCHERICHIA COLI	157-184								
PC1X0 STRSQ	CYTCHROME P450 10C1	STREPTOMYCES SP	233-260								
PC1PX SACER	6-DEOXYERYTHRONOLIDE B (DEB) HYDROXYLASE	SACCHAROPOLYSPORA ERYTHRAEA	240-283								
PC1X0 BACSU	CYTCHROME P450 109	BACILLUS SUBTILIS	98-125								
PC1X0 ANASP	PROBABLE CYTOCHROME P450	ANABENA SP	153-187								
PC1R7 BACTI	27 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	153-187								
PC1R7 BACTM	27 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	153-187								
PC1R4 BACSH	19 KD INSECTICIDAL TOXIN	BACILLUS SPHAEERICUS	276-308								
PC1R3 BACSH	19 KD INSECTICIDAL TOXIN	BACILLUS SPHAEERICUS	276-308								
PC1R3 BACSH	41.9 KD INSECTICIDAL TOXIN	BACILLUS SPHAEERICUS	207-234	429-463							
PC1R0 BACTD	70 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	57-84	125-159	427-464						
PC1R0 BACTO	73 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS									

PCGENK	1071284	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
FILENAME	PROTEIN	ORGANISM	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
PCRD_BACTI	70 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	899-226	244-271	421-433					
PCRTI_BACTI	70 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	91-133	191-218	332-615					
PCRT2_BACTI	72 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	74-111	381-414						
PCRT3_BACTI	70 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	91-133	191-218	332-393					
PCRT7_BACTI	77 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	308-335	302-329						
PCREC_ECOLI	SENSOR PROTEIN CREC	ESCHERICHIA COLI	102-130							
PCRED_ECOLI	INNER MEMBRANE PROTEIN CREC	ESCHERICHIA COLI	94-121							
PCRP_ECOLI	CATABOLITE GENE ACTIVATOR	ESCHERICHIA COLI &	26-53	127-134						
PCRP_SALTY	CATABOLITE GENE ACTIVATOR	SHIGELLA FLEXNERI	26-53	127-134						
PCRTI_ERWHE	PHYTOENE DEHYDROGENASE	SALMONELLA TYPHIMURUM	26-53	127-134						
PCRTI_RHOCA	PHYTOENE DEHYDROGENASE	KLEBSIELLA AEROGES	231-238							
PCRTI_RHOCA	CRY7 PROTEIN	ERWINIA HERBICOLA	389-416							
PCRY5_BACTI	132 KD CRYSTAL PROTEIN	RHODOBACTER CAPSULATUS	133-160	314-361	431-438					
PCRY5_BACTI	130 KD CRYSTAL PROTEIN	DACILLUS THURINGIENSIS	721-755	875-902						
PCRY5_BACTI	130 KD CRYSTAL PROTEIN	DACILLUS THURINGIENSIS	710-771	865-892	1031-1080					
PCRY5_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	710-771	865-892						
PCRY5_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	218-252	701-728	775-802					
PCRY5_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	737-771	865-892	1031-1080					
PCRY5_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	710-771	865-892						
PCRYT_BACTI	134 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	745-779	899-926	1031-1080					
PCRYT_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	217-231	354-384	701-728	775-802				
PCRYT_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	737-771	865-892						
PCRYU_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	710-771	865-892						
PCRYU_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	710-771	865-892						
PCRYV_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	710-771	865-892						
PCRYV_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	710-771	865-892						
PCRYV_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	710-771	865-892						
PCRYW_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	710-771	865-892						
PCRYW_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	710-771	865-892						
PCRYX_BACTI	139 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	92-119	227-254	605-632	783-817	937-964			
PC311_ECOLI	C53 PILI SYNTHESIS 63 KD PROTEIN	ESCHERICHIA COLI	42-69	226-253	290-317	344-378				
PC311_ECOLI	C53 PILI SYNTHESIS 48 KD PROTEIN	ESCHERICHIA COLI	90-117	154-181	208-242					
PC314_ECOLI	C53 PILI SYNTHESIS 33 KD PROTEIN	ESCHERICHIA COLI	20-47	74-108						
PC314_ECOLI	CELL SURFACE GLYCOPROTEIN PRECURSOR	HALOBACTERIUM HALOBUR	256-283	384-611						
PC314_ECOLI	CELL SURFACE GLYCOPROTEIN PRECURSOR	HALOBACTERIUM VOLCANI	143-170	217-271						
PC314_ECOLI	CELL SURFACE GLYCOPROTEIN PRECURSOR	METHANOTHEANUS FERVIDUS	59-107							
PC314_ECOLI	CELL SURFACE GLYCOPROTEIN PRECURSOR	METHANOTHEANUS SOCIABILIS	59-107							
PC314_ECOLI	CELL SURFACE GLYCOPROTEIN PRECURSOR	ESCHERICHIA COLI	25-36							
PC314_ECOLI	COA-TRANSFERASE SUBUNIT A	CLOSTRIDIUM ACETOBUTYLICUM	118-143							
PC314_ECOLI	COA-TRANSFERASE SUBUNIT B	CLOSTRIDIUM ACETOBUTYLICUM	174-208							
PC314_ECOLI	INNER MEMBRANE PROTEIN CTRB	NEISSERIA MENINGITIDIS	132-193							
PC314_ECOLI	CYTOTOXIN PRECURSOR	PSLEUDOMONAS AERUGINOSA	78-113	124-151	160-194	217-231				
PC314_ECOLI	COLICIN V SECRETION PROTEIN CVAA	ESCHERICHIA COLI	104-138	161-219						
PC314_ECOLI	COLICIN V SECRETION PROTEIN CVAB	ESCHERICHIA COLI	151-178							
PC314_ECOLI	MIDDLE CELL WALL PROTEIN PRECURSOR	BACILLUS BREVIS	197-224	411-418	1010-1044					
PC314_ECOLI	OUTER CELL WALL PROTEIN PRECURSOR	BACILLUS BREVIS	178-216	360-387	947-988					
PC314_ECOLI	ADENYLATE CYCLASE PRECURSOR	BORDETELLA PERTUSSIS	48-75	617-659	962-996					
PC314_ECOLI	ADENYLATE CYCLASE	YERSINIA INTERMEDIA	343-387	591-630						
PC314_ECOLI	CYAD PROTEIN	BORDETELLA PERTUSSIS	541-568							
PC314_ECOLI	CYAD PROTEIN	BORDETELLA PERTUSSIS	178-212							
PC314_ECOLI	CYAD PROTEIN	BORDETELLA PERTUSSIS	313-340							
PC314_ECOLI	CYTOCHROME B	RHODOBACTER CAPSULATUS	38-63							
PC314_ECOLI	TRANSFERRIN PROTEIN CYDD	ESCHERICHIA COLI	3-30	382-409						
PC314_ECOLI	APOCYTOCHROME F PRECURSOR	NOSTOC SP	209-243							

PCGENE	10711714	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PCYMO ACISF	CYCLOHEXANONE MONOOXYGENASE	ACINETOBACTER SP	419-471								
PCYNT SYN7	CARBONIC ANHYDRASE	SYNECHOCOCCUS SP	170-200								
PCYNX ECOLI	CYNX PROTEIN	ESCHERICHIA COLI	51-80								
PCYOB ECOLI	CYTOCHROME O UBIQUINOL OXIDASE SUBUNIT 1	ESCHERICHIA COLI	31-58								
PCYTH SYN7	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE	SYNECHOCOCCUS SP	107-141								
PCYSA ECOLI	SULFATE PERMEASE A PROTEIN	ESCHERICHIA COLI	164-191								
PCYSB ECOLI	CYS REGULATOR TRANSCRIPTIONAL ACTIVATOR	ESCHERICHIA COLI	3-30								
PCYSB SALTY	CYS REGULATOR TRANSCRIPTIONAL ACTIVATOR	SALMONELLA TYPHIMURUM	3-30								
PCYSE ECOLI	SERINE ACETYLTRANSFERASE	ESCHERICHIA COLI	164-191								
PCYSE ECOLI	SERINE ACETYLTRANSFERASE	SALMONELLA TYPHIMURUM	164-191								
PCYSO ECOLI	SIROHEM SYNTHASE	ESCHERICHIA COLI	405-432								
PCYSO SALTY	SIROHEM SYNTHASE	SALMONELLA TYPHIMURUM	405-432								
PCYSN ECOLI	SULFATE ADENYLATE TRANSFERASE SUBUNIT 1	ESCHERICHIA COLI	64-91								
PCYSW ECOLI	SULFATE PERMEASE W PROTEIN	ESCHERICHIA COLI	201-228								
PCYSW SYN7	SULFATE PERMEASE W PROTEIN	SYNECHOCOCCUS SP	211-228								
PCZCB ALCEU	CATION EFFLUX SYSTEM PROTEIN CZCB	ALCALIGENES EUTROPIUS	241-268	283-320	364-391						
PCZCD ALCEU	CATION EFFLUX SYSTEM PROTEIN CZCD	ALCALIGENES EUTROPIUS	139-169								
PDACB BACSU	PENICILLIN-BINDING PROTEIN 5* PRECURSOR	BACILLUS SUBTILIS	86-107								
PDADA ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	127-154								
PDAGA ALTHA	NA(+)-LINKED D-ALANINE GLYCINE PERMEASE	ALTEROMONAS HALOPLANKTIS	372-373								
PDAMX ECOLI	DAMX PROTEIN	ESCHERICHIA COLI	68-93	349-380							
PDAPA ECOLI	DIIHYDRODIPICOLINATE SYNTHASE	ESCHERICHIA COLI	27-54	157-184							
PDATI BACSU	DNA-PROTEIN-CYS-STEINE METHYLTRANSFERASE	BACILLUS SUBTILIS	13-47								
PDDBH ECOLI	DNA-BINDING PROTEIN HU-ALPHA	ESCHERICHIA COLI	12-59								
PDDBH CLOFA	DNA-BINDING PROTEIN HU	CLOSTRIDIUM PASTEURIANUM	12-59								
PDCCM ECOLI	DECARBOXYLASE PROENZYME	ESCHERICHIA COLI	146-173								
PDCCA CORGL	DIAMINOPIMELATE DECARBOXYLASE	CORYNEBACTERIUM GLUTINICUM	134-161								
PDCCA PSEAE	DIAMINOPIMELATE DECARBOXYLASE	PSLEUDOMONAS AERUGINOSA	53-84								
PDCEB ECOLI	GLUTAMATE DECARBOXYLASE BETA	ESCHERICHIA COLI	4-31								
PDCHS ENTAE	HISTIDINE DECARBOXYLASE	ENTEROBACTER AEROGENES	111-138								
PDCHS KLEPL	HISTIDINE DECARBOXYLASE	KLEBSIELLA PLANTIGOLA	111-138								
PDCHS MORMO	HISTIDINE DECARBOXYLASE	MORGANELLA MORGANII	111-138								
PDCHD BACSU	DIPETIDE TRANSPORT PROTEIN DCIAD	BACILLUS SUBTILIS	188-222								
PDCLY HAFAL	LYSINE DECARBOXYLASE	HAFNIA ALVEI	305-332								
PDCCA KLEPN	OXALOACETATE DECARBOXYLASE ALPHA CHAIN	KLEBSIELLA PNEUMONIAE	261-288	342-369							
PDCCA SALTY	OXALOACETATE DECARBOXYLASE ALPHA CHAIN	SALMONELLA TYPHIMURUM	261-288	342-369							
PDCCB SALTY	OXALOACETATE DECARBOXYLASE BETA CHAIN	SALMONELLA TYPHIMURUM	261-288	342-369							
PDCTB RHILE	TRANSPORT SENSOR PROTEIN DCTB	RHIZOBIUM LEGUMINOSARUM	372-411								
PDCTB RHIME	TRANSPORT SENSOR PROTEIN DCTB	RHIZOBIUM NELLOTTI	372-411								
PDEAD ECOLI	ATP-DEPENDENT RNA HELICASE DEAD	ESCHERICHIA COLI	511-538								
PDEAD KLEPN	ATP-DEPENDENT RNA HELICASE DEAD	KLEBSIELLA PNEUMONIAE	267-294	519-546							
PDEDA ECOLI	DEDA PROTEIN	ESCHERICHIA COLI	106-133								
PDEGS BACSU	SENSOR PROTEIN DEGS	BACILLUS SUBTILIS	31-70	75-159	292-327						
PDEHI MORSP	HALOACETATE DEHALOGENASE H-2	MORAXELLA SP	114-141								
PDEOC ECOLI	DEOXYRIBOSE-PHOSPHATE ALDOLASE	ESCHERICHIA COLI	134-161								
PDEHAL PSEOL	ALDHEDYDE DEHYDROGENASE	PSLEUDOMONAS OLEOVORANS	6-33								
PDHAS BACSU	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE	BACILLUS SUBTILIS	150-184								
PDHAS CORGL	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE	CORYNEBACTERIUM GLUTINICUM	43-70	312-339							
PDHAS ECOLI	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE	ESCHERICHIA COLI	229-256								
PDHAS VBCH	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE	VIBRIO CHOLERAE	109-136								
PDHAS BACSH	ALANINE DEHYDROGENASE	BACILLUS SPHAERICUS	149-176								
PDHAS BACST	ALANINE DEHYDROGENASE	BACILLUS STEAROTHERIOPHILUS	94-121								
PDEH3 CLODI	NAD-SPECIFIC GLUTAMATE DEHYDROGENASE	CLOSTRIDIUM DIFFICILE	116-143								
PDEH3 PEPAS	D-SPECIFIC GLUTAMATE DEHYDROGENASE	PEPTOSTREPTOCOCCUS ASACCIIAROLYTICUS	247-274	345-380							
PDEH3 SULSO	GLUTAMATE DEHYDROGENASE	SULFOLOBUS SOLFATARICUS	2-36								
PDEH3 CORGL	NADP-SPECIFIC GLUTAMATE DEHYDROGENASE	CORYNEBACTERIUM GLUTINICUM	184-215	229-256							
PDEHA ACICA	GLUCOSE DEHYDROGENASE-A	ACINETOBACTER CALCOACETICUS	10-59	190-217							



PCGENE	1071711.4	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
BLKMANE	PROTEIN	ORGANISMI	27-57								
PDHGB	BACHE	BACILLUS MEGATERIUM									
PDHGC	GLUCOSE DEHYDROGENASE	ESCHERICHIA COLI	416-463								
PDHGL	GLUCOSE DEHYDROGENASE	STREPTOMYCES VIOLACEORUBER	168-195								
PDHGL	GLUCOSE DEHYDROGENASE	BACILLUS STEAROTHERMOPHILUS	192-219								
PDHGL	GLUCOSE DEHYDROGENASE	AGROBACTERIUM TUMEFACIENS	317-344								
PDHGL	GLUCOSE DEHYDROGENASE	METHYLOBACTERIUM EXTOQUEUS	131-187	190-224							
PDHGL	GLUCOSE DEHYDROGENASE	METHYLOBACTERIUM ORGANOPHILUM	153-187	190-224							
PDHGL	GLUCOSE DEHYDROGENASE	PARACOCUS DENTRIFICANS	195-222								
PDHGL	GLUCOSE DEHYDROGENASE	BACILLUS SP	284-314								
PDHGL	GLUCOSE DEHYDROGENASE	ESCHERICHIA COLI	180-214								
PDHGL	GLUCOSE DEHYDROGENASE	BACILLUS SUBTILIS	73-107	406-433							
PDHGL	GLUCOSE DEHYDROGENASE	CORYNEBACTERIUM GLUTINICUM	105-132								
PDHGL	GLUCOSE DEHYDROGENASE	BACILLUS SPHAERICUS	212-239								
PDHGL	GLUCOSE DEHYDROGENASE	ESCHERICHIA COLI	482-512								
PDHGL	GLUCOSE DEHYDROGENASE	ANABAEUM CYLINDRICA	86-113	130-168							
PDHGL	GLUCOSE DEHYDROGENASE	SYNECHOCOCCUS SP	133-160								
PDHGL	GLUCOSE DEHYDROGENASE	METHYLOTROPHUS METHYLOPHILUS	439-466								
PDHGL	GLUCOSE DEHYDROGENASE	ESCHERICHIA COLI	584-611								
PDHGL	GLUCOSE DEHYDROGENASE	BACILLUS SUBTILIS	54-82	114-141							
PDHGL	GLUCOSE DEHYDROGENASE	PSEUDOMONAS PUTIDA	93-120								
PDHGL	GLUCOSE DEHYDROGENASE	AZOTOBACTER VINELANDII	18-45	224-276							
PDHGL	GLUCOSE DEHYDROGENASE	BACILLUS STEAROTHERMOPHILUS	82-124								
PDHGL	GLUCOSE DEHYDROGENASE	BACILLUS SUBTILIS	82-109								
PDHGL	GLUCOSE DEHYDROGENASE	ESCHERICHIA COLI	108-135								
PDHGL	GLUCOSE DEHYDROGENASE	PSEUDOMONAS FLUORESCENS	124-151	223-275							
PDHGL	GLUCOSE DEHYDROGENASE	PSEUDOMONAS PUTIDA	63-90								
PDHGL	GLUCOSE DEHYDROGENASE	BACILLUS SUBTILIS	497-524	548-581							
PDHGL	GLUCOSE DEHYDROGENASE	BACILLUS SUBTILIS	456-483								
PDHGL	GLUCOSE DEHYDROGENASE	BACILLUS SUBTILIS	116-180								
PDHGL	GLUCOSE DEHYDROGENASE	BORRELLIA BURGDORFERI	182-216	248-275	341-387	416-463					
PDHGL	GLUCOSE DEHYDROGENASE	BUCHNERA APHIDICOLA	73-100	111-138	353-380						
PDHGL	GLUCOSE DEHYDROGENASE	ESCHERICHIA COLI	366-400								
PDHGL	GLUCOSE DEHYDROGENASE	MICROCOCCUS LUTEUS	383-413								
PDHGL	GLUCOSE DEHYDROGENASE	MYCOPLASMA CAPRICOLUM	8-36	73-112	274-310	330-389					
PDHGL	GLUCOSE DEHYDROGENASE	PROTEUS MIRABILIS	365-399								
PDHGL	GLUCOSE DEHYDROGENASE	PSEUDOMONAS PUTIDA	398-439								
PDHGL	GLUCOSE DEHYDROGENASE	SPYROPLASMA CITRI	43-72	76-110	145-180						
PDHGL	GLUCOSE DEHYDROGENASE	CHLAMYDIA TRACHOMATIS	312-351								
PDHGL	GLUCOSE DEHYDROGENASE	ESCHERICHIA COLI	82-109								
PDHGL	GLUCOSE DEHYDROGENASE	SALMONELLA TYPHIMURUM	146-190								
PDHGL	GLUCOSE DEHYDROGENASE	ESCHERICHIA COLI	497-524	548-581							
PDHGL	GLUCOSE DEHYDROGENASE	BORRELLIA BURGDORFERI	512-594								
PDHGL	GLUCOSE DEHYDROGENASE	BRUCELLA OVIS	248-275	512-546							
PDHGL	GLUCOSE DEHYDROGENASE	CAULOBACTER CRESCENTUS	561-588								
PDHGL	GLUCOSE DEHYDROGENASE	CLOSTRIDIUM ACETOBUTYLICUM	496-526								
PDHGL	GLUCOSE DEHYDROGENASE	CLOSTRIDIUM PERFRINGENS	496-526								
PDHGL	GLUCOSE DEHYDROGENASE	METHANOSARCINA NAZEI	523-550								
PDHGL	GLUCOSE DEHYDROGENASE	MYCOBACTERIUM TUBERCULOSIS	502-529								
PDHGL	GLUCOSE DEHYDROGENASE	STREPTOMYCES COELICOLOR	43-72	533-572							
PDHGL	GLUCOSE DEHYDROGENASE	ESCHERICHIA COLI	114-141								
PDHGL	GLUCOSE DEHYDROGENASE	ZYMOGENON MOBILIS	658-712								
PDHGL	GLUCOSE DEHYDROGENASE	STREPTOMYCES PEUCETIUS	74-51								
PDHGL	GLUCOSE DEHYDROGENASE	STREPTOMYCES PEUCETIUS	104-172								
PDHGL	GLUCOSE DEHYDROGENASE	BACILLUS SUBTILIS	58-83	417-444	1382-1416						
PDHGL	GLUCOSE DEHYDROGENASE	ESCHERICHIA COLI	72-104								
PDHGL	GLUCOSE DEHYDROGENASE	SACCHAROPOLYSPORA ERYTHRAEA	230-257								



PGCENE	1071/1714	Polysaccharide Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PDPA1_SALTY	DNA POLYMERASE III, ALPHA CHAIN	SALMONELLA TYPHIMURUM	77-104								
PDPA2_BACSU	DNA POLYMERASE III, BETA CHAIN	BACILLUS SUBTILIS	212-319								
PDPA3_BORBU	DNA POLYMERASE III, BETA CHAIN	BORRELIA BURGDORFERI	266-113								
PDPA4_BUCAP	DNA POLYMERASE III, BETA CHAIN	BUCINERA APHIDIOLA	11-62	108-359							
PDPA5_MICLU	DNA POLYMERASE III, BETA CHAIN	MICROCOCCUS LUTEUS	191-318								
PDPA6_MYCCA	DNA POLYMERASE III, BETA CHAIN	MYCOPLASMA CAPRICOLUM	36-70								
PDPA7_PSEFU	DNA POLYMERASE III, BETA CHAIN	PSEUDOMONAS PUTIDA	10-60								
PDPA8_SPICI	DNA POLYMERASE III, BETA CHAIN	SPIROPLASMA CITRI	78-112	129-177	273-310						
PDPA9_BACSU	DNA POLYMERASE III, SUBUNIT GAMMA AND TAU	BACILLUS SUBTILIS	211-272								
PDPA10_ECOLI	DNA PRIMASE TRAC-3	ESCHERICHIA COLI	691-743								
PDPA11_ECOLI	DNA PRIMASE TRAC-4	ESCHERICHIA COLI	401-448								
PDPA12_STRPN	DPND PROTEIN	STREPTOCOCCUS PNEUMONIAE	29-170								
PDPA13_BAGCA	DNA POLYMERASE I	BACILLUS CALDOTENAX	208-235								
PDPA14_STRPN	DNA POLYMERASE I	STREPTOCOCCUS PNEUMONIAE	198-235	398-425	571-598	643-672					
PDPA15_THEAO	DNA POLYMERASE I	THERMUS AQUATICUS	196-223	602-629							
PDPA16_THEFL	DNA POLYMERASE II	THERMUS AQUATICUS	397-628								
PDPA17_ECOLI	DNA POLYMERASE II	ESCHERICHIA COLI	569-596								
PDPA18_PYRFU	DNA POLYMERASE	PYROCOCCUS FURIOSUS	746-773								
PDPA19_SULSO	DNA POLYMERASE	SULFOLOBUS SOLFATARICUS	379-406	416-463	635-659	747-774					
PDPA20_THELI	DNA POLYMERASE	THERMOCOCCUS LITORALIS	312-370	551-389	892-926	1004-1031	1153-1194				
PDPA21_LACLA	DIPETIDYL PEPTIDASE IV	LACTOCOCCUS LACTIS	716-753								
PDPA22_LACLC	DIPETIDYL PEPTIDASE IV	LACTOCOCCUS LACTIS	716-753								
PDPA23_ECOLI	DNA PROTECTION DURING STARVATION PROTEIN	ESCHERICHIA COLI	4-43								
PDPA24_STRFQ	DEOXYRIBONUCLEASE PRECURSOR	STREPTOCOCCUS EQUITIMILIS	33-60	291-318							
PDPA25_STRFE	DAUNORUBICIN RESISTANCE ATP-BINDING PROTEIN	STREPTOMYCES PEUCETIUS	286-313								
PDPA26_STAAL	DIPHOSPHOLATE REDUCTASE TYPE I	STAPHYLOCOCCUS AUREUS	63-89								
PDPA27_BACCI	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A1 PREC	BACILLUS CIRCULANS	134-161	305-339	424-451						
PDPA28_ECOLI	ATTACHING AND EFFACING PROTEIN	ESCHERICHIA COLI	66-100	158-185	535-552	691-725	802-836	871-903			
PDPA29_ECOLI	EBG OPERON REPRESSOR PROTEIN	ESCHERICHIA COLI	151-178								
PDPA30_STAAL	ETHIDIUM BROMIDE RESISTANCE PROTEIN	STAPHYLOCOCCUS AUREUS	68-98								
PDPA31_RHOCA	ENOYL COA HYDRATASE HOMOLOG	RHODOBACTER CAPSULATUS	232-249								
PDPA32_ECOLI	CHAPERONE PROTEIN ECPD PRECURSOR	ESCHERICHIA COLI	20-47								
PDPA33_ZYMOO	PHOSPHOGLUCONATE DEHYDRATASE	ZYMONONAS MOBILIS	12-39								
PDPA34_STAAL	EPIDERMAL CELL DIFF INH PRECURSOR	STAPHYLOCOCCUS AUREUS	52-79	119-146							
PDPA35_DESMO	ELONGATION FACTOR 2	DESULFOCOCCUS MOBILIS	427-461								
PDPA36_HALOR	ELONGATION FACTOR 2	HALOBACTERIUM HALOBILUM	186-213								
PDPA37_HALHA	ELONGATION FACTOR 2	METHANOCOCCUS VANNIELII	409-436								
PDPA38_METVA	ELONGATION FACTOR 2	SULFOLOBUS ACIDOCALDARIUS	36-63	145-180							
PDPA39_SULAC	ELONGATION FACTOR 2	THERMOPHILASMA ACIDOPHILUM	13-40	46-76	220-247						
PDPA40_THEAC	ELONGATION FACTOR 2	ANACYSTIS NIDULANS	332-359								
PDPA41_ANANI	ELONGATION FACTOR 2	ESCHERICHIA COLI	332-359								
PDPA42_ECOLI	ELONGATION FACTOR 2	ESCHERICHIA COLI	332-359								
PDPA43_MYCLE	ELONGATION FACTOR 2	MYCOBACTERIUM LEPRAE	211-259	330-357							
PDPA44_ECOLI	ELONGATION FACTOR 2	SALMONELLA TYPHIMURUM	234-261								
PDPA45_SPLA	ELONGATION FACTOR 2	SPIRULINA PLATENSIS	334-374	481-511							
PDPA46_SVNYO	ELONGATION FACTOR 2	SYNECHOCYSTIS SP	14-41								
PDPA47_STRRA	ELONGATION FACTOR TU1	STREPTOMYCES KANAMICINUS	221-258								
PDPA48_STRRA	ELONGATION FACTOR TU2	STREPTOMYCES KANAMICINUS	221-258								
PDPA49_STRRA	ELONGATION FACTOR TU3	STREPTOMYCES KANAMICINUS	228-255								
PDPA50_ECOLI	ELONGATION FACTOR EX-13	ESCHERICHIA COLI	101-135								
PDPA51_SPICI	ELONGATION FACTOR EX-13	SPIROPLASMA CITRI	27-54	134-161							
PDPA52_BACFR	ELONGATION FACTOR TU	BACTEROIDES FRAGILIS	18-45	229-256							
PDPA53_BACSU	ELONGATION FACTOR TU	BACILLUS SUBTILIS	11-45	210-357							
PDPA54_BURCH	ELONGATION FACTOR TU	BURKHOLDERIA CEPACIA	26-51								
PDPA55_CULTR	ELONGATION FACTOR TU	CHILANTHIA TRACHOMATIS	218-245								
PDPA56_DEISP	ELONGATION FACTOR TU	DEINONEMA SP	230-257								
PDPA57_FLESI	ELONGATION FACTOR TU	FLEXISTIPES SINUSARABICI	221-248								
PDPA58_HALHA	ELONGATION FACTOR TU	HALOARCTIA MARISMORTUI	4-31								



PCGENE	1071714	Prokaryotic Sequences	AUEA1	AUEA2	AUEA3	AUEA4	AUEA5	AUEA6	AUEA7	AUEA8	AUEA9
KLE.NANP	PROTIN	URICANIN	22-56								
PEMB STAAU	POSSIBLE PROTEIN PEMB	STAPHYLOCOCCUS AUREUS									
PEFN STNP2	FERRIC DOXIN-NADP REDUCTASE	SYNECHOCOCCUS SP	4-31								
PEPC ECOLI	FERRIC ENTEROACTIN TRANSPORT PROTEIN PEPC	ESCHERICHIA COLI	176-203								
PEPE ECOLI	FERRIC ENTEROACTIN TRANSPORT PROTEIN PEPE	ESCHERICHIA COLI	182-214	281-308							
PEPO ECOLI	FERRIC ENTEROACTIN TRANSPORT PROTEIN PEPO	ESCHERICHIA COLI	128-155								
PEPX ANASP	FERRIC DOXIN, HETEROCYST	ANABAEANA SP	2-29								
PEFX ANASP	FERRIC DOXIN-LIKE PROTEIN IN NIP REGION	ANABAEANA SP	67-94								
PHAB BORPE	FILAMENTOUS HEMAGGLUTININ	BORDETELLA PERTUSSIS	1128-1158	1359-1386	2063-2114	2841-2868	1051-1085	3167-3194			
PHAC BORPE	HAEMOLYSIN-LIKE PROTEIN PHAC PRECURSOR	BORDETELLA PERTUSSIS	342-369								
PHLA ECOLI	FORMATE HYDROGENYLASE TRANSACTIVATOR	ESCHERICHIA COLI	36-63	350-384	401-428						
PHUA ECOLI	FERRIC CHROMO-IRON RECEPTOR PRECURSOR	ESCHERICHIA COLI	458-485								
PHUB ECOLI	PROTEIN PHUB PRECURSOR	ESCHERICHIA COLI	227-254								
PHUE ECOLI	OUTER-MEMBRANE RECEPTOR	ESCHERICHIA COLI	587-614								
PHIB SPICI	FIBRIL PROTEIN	SPIROPLASMA CITRI	161-195	376-367							
PFIC ECOLI	CELL FILAMENTATION PROTEIN FIC	ESCHERICHIA COLI	151-178								
PFIC SALTY	CELL FILAMENTATION PROTEIN FIC	SALMONELLA TYPHIMURIUM	151-178								
PFMC BORPE	OUTER MEMBRANE PROTEIN FMC PRECURSOR	BORDETELLA PERTUSSIS	208-235	540-567	618-645						
PFMC ECOLI	CHAPERONE PROTEIN FMC PRECURSOR	ESCHERICHIA COLI	51-78								
PFMD ECOLI	FIND PROTEIN PRECURSOR	ESCHERICHIA COLI	222-253	458-485	534-561	563-590					
PFME ECOLI	TYPE I FIMBRINAE REGULATORY PROTEIN FIME	ESCHERICHIA COLI	163-192								
PFMY SALTY	FIMBRINAE Y PROTEIN	SALMONELLA TYPHIMURIUM	49-76								
PFMZ ECOLI	FIMBRINAE Z PROTEIN	ESCHERICHIA COLI	42-69	162-192	196-230						
PFNZ SALTY	FIMBRINAE Z PROTEIN	SALMONELLA TYPHIMURIUM	175-209								
PFNQ ECOLI	FIMBRIAL Y PROTEIN	ESCHERICHIA COLI	143-172								
PFRA RICKI	FIRA PROTEIN	RICKETTSIA RICKETTSII	162-189								
PFIX AZOCA	FIXC PROTEIN	AZORHIZOBIIUM CAULINODANS	139-156								
PFIX AZOCA	SENSOR PROTEIN FIXL	AZORHIZOBIIUM CAULINODANS	247-274								
PFIX BRUA	SENSOR PROTEIN FIXL	BRADYRHIZOBIIUM JAPONICUM	27-54	253-280							
PLA1 BORBU	FLAGELLAR FILAMENT 41 KD CORE PROTEIN	BORRELIA BURGDORFERI	8-35	271-298							
PLA1 HALHA	FLAGELLIN A1 PRECURSOR	HALOBACTERIUM HALOBIIUM	61-92	157-184							
PLA1 METVO	FLAGELLIN B1 PRECURSOR	METHANOCOCCUS VOLTAE	38-71	133-160							
PLA2 METVO	FLAGELLIN B1 PRECURSOR	METHANOCOCCUS VOLTAE	28-66								
PLA3 HALHA	FLAGELLIN B1 PRECURSOR	HALOBACTERIUM HALOBIIUM	36-63								
PLA3 METVO	FLAGELLIN B1 PRECURSOR	METHANOCOCCUS VOLTAE	35-76								
PLA4 HALHA	FLAGELLIN B1 PRECURSOR	HALOBACTERIUM HALOBIIUM	36-90	152-184							
PLA5 HALHA	FLAGELLIN B1 PRECURSOR	HALOBACTERIUM HALOBIIUM	36-63	154-181							
PLA6 BACSU	FLAX LOCUS 219 KD PROTEIN	BACILLUS SUBTILIS	73-149	155-186							
PLA6 CAMIE	FLAGELLIN A	CAMPYLOBACTER JEJUNI	15-42	144-191	497-535						
PLA6 CAMIE	FLAGELLIN A	CAMPYLOBACTER JEJUNI	220-266	310-337	500-538						
PLA6 METVO	FLAGELLIN A PRECURSOR	METHANOCOCCUS VOLTAE	28-62								
PLA6 PSEAE	FLAGELLIN	PSEUDOMONAS AERUGINOSA	3-41	51-88	97-124						
PLA6 RHME	FLAGELLIN	RHIZOBIIUM MELIOTI	181-219	228-265	360-391						
PLA6 SP1AU	FLAGELLAR FILAMENT PROTEIN PRECURSOR	SPIROCHAETA AURANTIA	162-189								
PLA6 TREPA	FLAGELLAR FILAMENT PROTEIN PRECURSOR	TREPONEMA HYODYSENTERIAE	55-89	219-285							
PLA6 CAMIE	FLAGELLIN B	CAMPYLOBACTER JEJUNI	243-270	497-535							
PLA6 RHME	FLAGELLIN	RHIZOBIIUM MELIOTI	220-266	310-337	500-538						
PLA6 CLOMP	FLAVODOXIN	GLOSTRIDIUM MP	86-113	177-219	228-255	360-391					
PLA6 CAUCR	REGULATORY PROTEIN FLAY	CAULOBACTER CRESCENTUS	18-52								
PLA6 BACSU	FLAGELLIN	BACILLUS SUBTILIS	291-318	551-578							
PLA6 BACSU	FLAGELLAR BASAL-BODY ROD PROTEIN FLGG	BACILLUS SUBTILIS	102-129	228-255							
PLA6 SALTY	FLAGELLAR HOOK-ASSOCIATED PROTEIN 1	SALMONELLA TYPHIMURIUM	62-89								
PLA6 ECOLI	FLAGELLAR HOOK-ASSOCIATED PROTEIN 1	ESCHERICHIA COLI	12-50	333-360	435-460						
PLA6 ECOLI	FLAGELLAR HOOK-ASSOCIATED PROTEIN 3	SALMONELLA TYPHIMURIUM	61-105	229-266							
PLA6 ECOLI	FLAGELLAR TRANSCRIPTIONAL ACTIVATOR FLHD	ESCHERICHIA COLI	61-105	229-266							
PLA6 PSEAE	FLAGELLAR OPERON RNA POL-SIGMA FACTOR	PSEUDOMONAS AERUGINOSA	6-33								
PLA6 PSEAE	FLAGELLAR OPERON RNA POL-SIGMA FACTOR	PSEUDOMONAS AERUGINOSA	198-232								

PCGENE	1071784	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
ELKNAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PELIC ECOLI	FLAGELLIN	ESCHERICHIA COLI	1-41	186-213	295-379	431-466					
PELIC SALCH	FLAGELLIN	SALMONELLA CHOLERAESUIS	5-41	54-123	136-198						
PELIC SALMU	FLAGELLIN	SALMONELLA MOENCHIEN	5-41	54-88	136-177	232-259	272-299	376-403			
PELIC SALPA	FLAGELLIN	SALMONELLA PARATYPH-A	5-41	54-123	136-184						
PELIC SARU	FLAGELLIN	SALMONELLA RUBISLAW	5-41	54-123	136-186						
PELIC SATY	FLAGELLIN	SALMONELLA TYPHIMURUM	5-41	54-123	136-200						
PELIC SERMA	FLAGELLIN	SERATIA MARCESCENS	5-41	54-123	136-200						
PELIC ECOLI	FLAGELLAR HOOK-ASSOCIATED PROTEIN 2	ESCHERICHIA COLI	32-66	106-133	160-187	216-298	386-445				
PELIC SATY	FLAGELLAR HOOK-ASSOCIATED PROTEIN 2	SALMONELLA TYPHIMURUM	32-66	106-133	235-299	407-438					
PELIC BACSU	FLAG HOOK-BASAL BODY PROTEIN FLIE	BACILLUS SUBTILIS	8-35								
PELIC CAUCR	FLAGELLAR M-RING PROTEIN	BACILLUS SUBTILIS	327-361	391-418							
PELIC CAUCR	FLAGELLAR M-RING PROTEIN	CAULOBACTER CRESCENTUS	24-51	297-324	361-388						
PELIC SATY	FLAGELLAR M-RING PROTEIN	SALMONELLA TYPHIMURUM	484-529								
PELIC BACSU	FLAGELLAR SWITCH PROTEIN FLIO	BACILLUS SUBTILIS	35-62								
PELIC ECOLI	FLAGELLAR SWITCH PROTEIN FLIG	ESCHERICHIA COLI	44-71								
PELIC BACSU	PROBABLE FLIJI PROTEIN	BACILLUS SUBTILIS	19-46	105-132							
PELIC BACSU	PROBABLE FLIJI PROTEIN	BACILLUS SUBTILIS	7-37								
PELIC SATY	FLAGELLAR FLIJI PROTEIN	SALMONELLA TYPHIMURUM	75-118								
PELIC BACSU	PROBABLE FLIK PROTEIN	BACILLUS SUBTILIS	97-104	117-144							
PELIC BACSU	FLIL PROTEIN	BACILLUS SUBTILIS	30-71	78-105	109-136						
PELIC ECOLI	FLIL PROTEIN	ESCHERICHIA COLI	103-132								
PELIC SATY	FLIL PROTEIN	SALMONELLA TYPHIMURUM	103-133								
PELIC BACSU	FLIM PROTEIN	BACILLUS SUBTILIS	148-175								
PELIC ECOLI	FLIM PROTEIN	ESCHERICHIA COLI	251-278								
PELIC CAUCR	FLAGELLAR MOTOR SWITCH PROTEIN	CAULOBACTER CRESCENTUS	56-83								
PELIC ECOLI	FLAGELLAR PROTEIN FLIS	ESCHERICHIA COLI	59-86								
PELIC SATY	FLAGELLAR PROTEIN FLIT	SALMONELLA TYPHIMURUM	9-46	67-106							
PELIC ECOLI	TYPE-1 FIMBRIAL PROTEIN PRECURSOR	PSEUDOMONAS AERUGINOSA	30-67	80-114							
PELIC ECOLI	TYPE-1 FIMBRIAL PROTEIN, A CHAIN PRECURSOR	ESCHERICHIA COLI	5-32								
PELIC ECOLI	TYPE-1 FIMBRIAL PROTEIN, C CHAIN PRECURSOR	ESCHERICHIA COLI	11-38								
PELIC ACTYI	FIMBRIAL SUBUNIT TYPE 1 PRECURSOR	ACTINOMYCES VISCOSUS	248-282	332-379	417-444						
PELIC ECOLI	FIMBRIAL PROTEIN 91P PRECURSOR	ESCHERICHIA COLI	114-141								
PELIC BACNO	FIMBRIAL PROTEIN PRECURSOR	BACTEROIDES NODOSUS	110-137								
PELIC BACNO	FIMBRIAL PROTEIN PRECURSOR	BACTEROIDES NODOSUS	107-134								
PELIC BACNO	FIMBRIAL PROTEIN PRECURSOR	BACTEROIDES NODOSUS	110-137								
PELIC BACNO	FIMBRIAL PROTEIN PRECURSOR	BACTEROIDES NODOSUS	123-150								
PELIC BACNO	FIMBRIAL PROTEIN PRECURSOR	BACTEROIDES NODOSUS	107-141								
PELIC BACNO	FIMBRIAL PROTEIN PRECURSOR	BACTEROIDES NODOSUS	95-122								
PELIC BACNO	FIMBRIAL PROTEIN PRECURSOR	BACTEROIDES NODOSUS	111-145								
PELIC BACNO	FIMBRIAL PROTEIN PRECURSOR	BACTEROIDES NODOSUS	96-123								
PELIC BACNO	FIMBRIAL PROTEIN PRECURSOR	PSEUDOMONAS AERUGINOSA	70-97								
PELIC BACNO	POSSIBLE FIMBRIAL ASSEMBLY PROTEIN FIMD	BACTEROIDES NODOSUS	106-144	335-382							
PELIC BACNO	POSSIBLE FIMBRIAL ASSEMBLY PROTEIN FIMD	BACTEROIDES NODOSUS	106-144	335-382							
PELIC ECOLI	F17 FIMBRIAL PROTEIN PRECURSOR	ESCHERICHIA COLI	97-124								
PELIC NEIGB	FIMBRIAL PROTEIN PRECURSOR	NEISSERIA MENINGITIDIS	70-97								
PELIC MOINO	FIMBRIAL PROTEIN PRECURSOR	NEISSERIA GONORRHOEA	66-97								
PELIC PSEAE	FIMBRIAL PROTEIN PRECURSOR	MORAXELLA NONLUQUEFACIENS	108-146								
PELIC PSEAE	FIMBRIAL PROTEIN PRECURSOR	PSEUDOMONAS AERUGINOSA	30-67	80-114							
PELIC ECOLI	CS1 FIMBRIAL SUBUNIT A PRECURSOR	ESCHERICHIA COLI	60-87	112-139							
PELIC ECOLI	CS1 FIMBRIAL SUBUNIT A PRECURSOR	ESCHERICHIA COLI	60-87	112-139							
PELIC STAUF	FIBRONECTIN-BINDING PROTEIN PRECURSOR	HAEMOPHILUS INFLUENZAE	105-129								
PELIC ECOLI	FOLYGLUTAMATE SYNTHASE	STAPHYLOCOCCUS AUREUS	41-83	188-215	311-365	431-458	517-555	655-686	722-756		
PELIC LACCA	FOLYGLUTAMATE SYNTHASE	ESCHERICHIA COLI	125-159								
PELIC BACFI	FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE	LACTOBACILLUS CASEI	129-156								
PELIC BACFI	FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE	BACILLUS FIRMS	153-180								

PGCENE	1041704.4	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FURNAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PFDA_ECOLI	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT	ESCHERICHIA COLI	395-472								
PFDA_WOLSU	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT	WOLINELLA SUCCINOGENES	8-35	487-514							
PFZE_MYXXA	GLIDING MOTILITY REGULATORY PROTEIN	MYXOCOCCUS XANTHUS	15-42	478-505							
PFTIS_CLOTH	FORMATE--TETRAHYDROFOLATE LIGASE	CLOSTRIDIUM THERMOACETUM	163-190								
PFTT_METH	FORMYLTRANSFERASE	METHANOBACTERIUM THERMAUTOTROPHICUM	9-43								
PFTSA_BACSU	CELL DIVISION PROTEIN FTSB	BACILLUS SUBTILIS	76-110								
PFTSA_ECOLI	CELL DIVISION PROTEIN FTSB	ESCHERICHIA COLI	301-338	375-418							
PFTSL_ECOLI	CELL DIVISION PROTEIN FTSI	ESCHERICHIA COLI	4-31								
PFTSN_ECOLI	CELL DIVISION PROTEIN FTSN	ESCHERICHIA COLI	63-90								
PFTSX_ECOLI	CELL DIVISION PROTEIN FTSX	ESCHERICHIA COLI	151-188								
PFTSY_ECOLI	CELL DIVISION PROTEIN FTSY	ESCHERICHIA COLI	278-305								
PFUCR_ECOLI	L-FUCOSE OPERON ACTIVATOR	ESCHERICHIA COLI	230-260								
PFUMH_BACST	FUMARATE HYDROLYTASE CLASS I AEROBIC	BACILLUS STEAROTHERMOPHILUS	7-45								
PFUMH_BACSU	FUMARATE HYDRATASE	BACILLUS SUBTILIS	290-317								
PFUR_YERPE	FURRIC UPTAKE REGULATION PROTEIN	YERSINIA PESTIS	414-445								
PGIPT_ECOLI	GLYC 3-PHOS DEHYDROGENASE A	ESCHERICHIA COLI	99-130								
PGIPT_ANAVA	GLYC 3-PHOS DEHYDROGENASE 2	ANABAENA VARIABILIS	302-329								
PGIPT_ANAVA	GLYC 3-PHOS DEHYDROGENASE 3	ANABAENA VARIABILIS	87-114								
PGIPT_ECOLI	GLYC 3-PHOS DEHYDROGENASE C	ESCHERICHIA COLI	162-189								
PGIP_BACME	GLYC 3-PHOS DEHYDROGENASE	BACILLUS MEGATERIUM	236-324								
PGIP_DACSU	GLYC 3-PHOS DEHYDROGENASE	BACILLUS SUBTILIS	49-76	237-271							
PGIP_PYRWQ	GLYC 3-PHOS DEHYDROGENASE	PYROCOCUS WOESSEI	49-76								
PGIP_THEMA	GLYC 3-PHOS DEHYDROGENASE	THERMOTOGA MARITIMA	239-286								
PGIPB_BACST	GLUCOSE-6-PHOSPHATE ISOMERASE B	BACILLUS STEAROTHERMOPHILUS	290-328								
PGIPD_ECOLI	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE	ESCHERICHIA COLI	103-143	241-268							
PGIPD_ZYMWQ	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE	ZYMONOMAS MOBILIS	301-378								
PGACA_PSEFL	CYANIDE CONTROL PROTEIN	PSEUDOMONAS FLUORESCENS	165-192								
PGALT_SALTY	GALACTONASE	SALMONELLA TYPHIMURUM	178-205								
PGALT_HAEIN	GAL-1-PHOS URIDYL YLTRANSFERASE	HAEMOPHILUS INFLUENZAE	86-113								
PGALT_LACHE	GAL-1-PHOS URIDYL YLTRANSFERASE	LACTOBACILLUS HELVETICUS	124-158	239-269							
PGALT_SALTY	GALACTOSE OPERON REPRESSOR	SALMONELLA TYPHIMURUM	304-338								
PGALR_HAEIN	GALACTOSE OPERON REPRESSOR	HAEMOPHILUS INFLUENZAE	53-91								
PGALR_PSEFL	DE-D-GALACTOSE 1-DEHYDROGENASE	PSEUDOMONAS FLUORESCENS	182-209								
PGCHE_ECOLI	GTP CYCLOHYDROLASE II	ESCHERICHIA COLI	251-278								
PGCH2_PHOLE	GTP CYCLOHYDROLASE II	PHOTOBACTERIUM LEIOGNATHI	78-105								
PGCH2_ECOLI	GLYCINE CLEAVAGE SYSTEM H PROTEIN	ESCHERICHIA COLI	197-227	246-273							
PGCSP_ECOLI	GLYCINE CLEAVAGE SYSTEM TRANSACTIVATOR	ESCHERICHIA COLI	10-37								
PGCVA_ECOLI	GLYCINE CLEAVAGE SYSTEM TRANSACTIVATOR	ESCHERICHIA COLI	216-246								
PGENK_ECOLI	PROTEIN K	ESCHERICHIA COLI	60-94								
PGER1_BACSU	SPORE GERMINATION PROTEIN I	BACILLUS SUBTILIS	24-51								
PGER3_BACSU	SPORE GERMINATION PROTEIN III PRECURSOR	BACILLUS SUBTILIS	49-83	182-216	350-384						
PGERE_BACSU	GERMINATION PROTEIN GENE	BACILLUS SUBTILIS	293-323								
PGGII_STAHA	ANTIBACTERIAL PROTEIN 2	STAPHYLOCOCCUS HAEMOLYTICUS	13-40								
PGGII_STAHA	ANTIBACTERIAL PROTEIN 3	STAPHYLOCOCCUS HAEMOLYTICUS	6-33								
PGIDA_BACSU	GLUCOSE INHIBITED DIVISION PROTEIN A	BACILLUS SUBTILIS	6-33								
PGIDA_ECOLI	GLUCOSE INHIBITED DIVISION PROTEIN A	ESCHERICHIA COLI	396-423								
PGIDA_PSEPU	GLUCOSE INHIBITED DIVISION PROTEIN A	PSEUDOMONAS PUTIDA	533-568								
PGIDB_BACSU	GLUCOSE INHIBITED DIVISION PROTEIN B	BACILLUS SUBTILIS	539-566								
PGIDB_PSEPU	GLUCOSE INHIBITED DIVISION PROTEIN B	PSEUDOMONAS PUTIDA	34-61								
PGICP_STNY7	GLUCOSE TRANSPORT PROTEIN	SYNECHOCYSTIS SP	25-52								
PGIDA_BACST	GLYCEROL DEHYDROGENASE	BACILLUS STEAROTHERMOPHILUS	288-322								
PGIDA_ECOLI	GLYCEROL SYNTHASE	ESCHERICHIA COLI	20-79								
PGLGC_ECOLI	GLUCOSE-1-PHOSPHATE ADENYL YLTRANSFERASE	ESCHERICHIA COLI	256-283								
PGLOC_SALTY	GLUCOSE-1-PHOSPHATE ADENYL YLTRANSFERASE	SALMONELLA TYPHIMURUM	114-141								
PGLMS_ECOLI	GLUC-6-FRUC-6-PHOSPHOTRANSFERASE	ESCHERICHIA COLI	209-243								
PGLN1_METTL	GLNB-LIKE PROTEIN 1	METHANOCOCCUS THERMOLITHOTROPHICUS	58-85								

PCGENE	107117814	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9	AREA.10	AREA.11	AREA.12
FILENARIE	PROTEIN	ORGANISM												
PLNA ANASP	GLUTAMINE SYNTHETASE	ANADENIA SP	8-42											
PLNA BACSU	GLUTAMINE SYNTHETASE	BACILLUS SUBTILIS	4-31											
PLNA CLOAB	GLUTAMINE SYNTHETASE	CLOSTRIDIUM ACETOBUTYLICUM	413-440											
PLNA ECOLI	GLUTAMINE SYNTHETASE	ESCHERICHIA COLI	144-171											
PLNA METVO	GLUTAMINE SYNTHETASE	METHANOCOCCUS VOLTAE	203-230											
PLNA PROVI	GLUTAMINE SYNTHETASE	PROTEUS VULGARIS	142-169											
PLNA PYREU	GLUTAMINE SYNTHETASE	PYROCOCCUS FURIOSUS	391-421											
PLNA SALTY	GLUTAMINE SYNTHETASE	SALMONELLA TYPHIMURUM	144-171											
PLNA STRCO	GLUTAMINE SYNTHETASE	STREPTOMYCES COELICOLOR	186-211											
PLNI AZOIR	NITROGEN REGULATORY PROTEIN P-II	AZOSYRILLUM BRASILINSE	15-49											
PLNB BIUCA	NITROGEN REGULATORY PROTEIN P-II	RHODOBACTER CAPSULATUS	15-49											
PLNB SYNPE	NITROGEN REGULATORY PROTEIN P-II	SYNECHOCOCCUS SP	52-79											
PLND ECOLI	UDP URIDYL-TRANSFERASE	ESCHERICHIA COLI	120-147	151-178										
PLND SALTY	UDP URIDYL-TRANSFERASE	SALMONELLA TYPHIMURUM	151-178											
PLNE ECOLI	ADENYL-TRANSFERASE	ESCHERICHIA COLI	103-130	431-460	763-790									
PLNH ECOLI	GLUTAMINE-BINDING PROTEIN PRECURSOR	ESCHERICHIA COLI	126-153											
PLNQ BACST	GLUTAMINE PERMEASE OPERON PROTEIN GLNQ	BACILLUS STEAROTHERMOPHILUS	7-34											
PLPD BACSU	AEROBIC GLYC-3-PHOS DEHYDROGENASE	BACILLUS SUBTILIS	194-230											
PLPD ECOLI	AEROBIC GLYC-3-PHOS DEHYDROGENASE	ESCHERICHIA COLI	410-437											
PLPF BACSU	GLYCEROL UPTAKE FACILITATOR PROTEIN	BACILLUS SUBTILIS	233-274											
PLPK BACSU	GLYCEROL KINASE	BACILLUS SUBTILIS	44-93											
PLPK ECOLI	GLYCEROL KINASE	ESCHERICHIA COLI	56-90											
PLPR ECOLI	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR	ESCHERICHIA COLI	5-32											
PLPX ECOLI	GLPX PROTEIN	ESCHERICHIA COLI	297-324											
PLPX SHIFL	GLPX PROTEIN	SHIGELLA FLEXNERI	297-324											
PLXX ECOLI	GLUTAMATE SYNTHASE	ESCHERICHIA COLI	24-51											
PLTB ECOLI	GLUTAMATE SYNTHASE	ESCHERICHIA COLI	482-509											
PLTP ECOLI	PROTON GLUTAMATE SYMPORT PROTEIN	ESCHERICHIA COLI	316-346											
PLVB ECOLI	PHOSPHOTRANSFERASE ENZYME TYPE IIB	ESCHERICHIA COLI	130-157											
PLVA BRAJA	SERINE HYDROXYMETHYLTRANSFERASE	BRADYRHIZOBIUM JAPONICUM	39-60											
PLVA CAMIE	SERINE HYDROXYMETHYLTRANSFERASE	CAMPYLOBACTER JEJUNI	376-401											
PLVA HYPAE	SERINE HYDROXYMETHYLTRANSFERASE	HYPHONICOBACTRIUM METHYLOVORUM	28-53											
POMOT BACSU	COMO OPERON PROTEIN 7	BACILLUS SUBTILIS	37-67	88-122										
POMOT BACSU	GLUCONOKINASE	BACILLUS SUBTILIS	314-271											
POPID CHLTR	VRULENCE PROTEIN PGF1-D	CHLAMYDIA TRACHOMATIS	312-353											
POPID CHLTR	VRULENCE PROTEIN PGF2-D	CHLAMYDIA TRACHOMATIS	97-131											
POPID CHLTR	VRULENCE PROTEIN PGF3-D	CHLAMYDIA TRACHOMATIS	25-52											
POPID CHLTR	VRULENCE PROTEIN PGF4-D	CHLAMYDIA TRACHOMATIS	61-106	193-230										
POPID CHLTR	VRULENCE PROTEIN PGF5-D	CHLAMYDIA TRACHOMATIS	12-60											
POPID CHLTR	VRULENCE PROTEIN PGF6-D	CHLAMYDIA TRACHOMATIS	94-121											
PGREA BICPR	TRANSCRIPTION ELONGATION FACTOR GRE A	RICKETTSIA PROWAZEKII	15-49											
POPE BACSU	GRPE-LIKE PROTEIN	BACILLUS SUBTILIS	27-71											
POPE BORBUB	GRPE-LIKE PROTEIN	BORRELIA BURGDORFERI	2-79											
POPE CLOAB	GRPE-LIKE PROTEIN	CLOSTRIDIUM ACETOBUTYLICUM	12-83											
POPE BACBR	GRAMICIDIN 3 SYNTHETASE	BACILLUS BREVIS	545-572	799-836										
POPE BACBR	GRAMICIDIN 3 SYNTHETASE II	BACILLUS BREVIS	48-75	94-121										
POSHI ECOLI	GLUTAMATE-CYSTEINE LIASE	ESCHERICHIA COLI	239-266	274-301										
PGSHR ECOLI	GLUTATHIONE REDUCTASE	ESCHERICHIA COLI	100-134	270-311										
PGSHR PSEAE	GLUTATHIONE REDUCTASE	PSEUDOMONAS AERUGINOSA	80-114											
PGSIA BACSU	STARVATION-INDUCIBLE PROTEIN A	BACILLUS SUBTILIS	74-101	265-296										
PGSPD ERWCA	PROTEIN D PRECURSOR	ERWINIA CAROTOVORA	238-285	316-343										
PGSPD ERWCH	PROTEIN D PRECURSOR	ERWINIA CHRYSANTHEMI	239-266	274-301										
PGSPD KLEPN	PROTEIN D PRECURSOR	KLEBSIELLA PNEUMONIAE	339-366	351-378	659-686									
PGSPE ERWCA	PROTEIN E	ERWINIA CAROTOVORA	329-367											
PGSPE ERWCH	PROTEIN E	ERWINIA CHRYSANTHEMI	329-367											
PGSPE KLEPN	PROTEIN E	KLEBSIELLA PNEUMONIAE	323-361											
PGSPE PSEAE	PROTEIN E	PSEUDOMONAS AERUGINOSA	122-149	331-369										

PGENE	10117144	Prokaryotic Sequences	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
ELUENIE	PROTEIN	ORGANISMI	18-59								
PGSPF XANCP	PROTEIN F	XANTHONONAS CAMPESTRIS	210-237								
PGSPH PSEAE	PROTEIN H	PSEUDOMONAS AERUGINOSA	18-59								
PGSPH AERHY	PROTEIN I	AEROMONAS HYDROPHILA	22-61								
PGSPH ERWCA	PROTEIN I	ERWINIA CAROTOVORA	35-62								
PGSPF KLEPN	PROTEIN I	KLEBSIELLA PNEUMONIAE	140-167								
PGSPK ERWCA	PROTEIN K	ERWINIA CAROTOVORA	28-55								
PGSPK ERWCH	PROTEIN K	ERWINIA CHRYSAANTHEMI	28-55								
PGSPK KLEPN	PROTEIN K	KLEBSIELLA PNEUMONIAE	72-99								
PGSPK PSEAE	PROTEIN K	PSEUDOMONAS AERUGINOSA	262-289								
PGSPF ERWCH	PROTEIN L	ERWINIA CHRYSAANTHEMI	7-42	246-246							
PGSPF XANCP	PROTEIN L	XANTHONONAS CAMPESTRIS	19-71	397-324							
PGSPM ERWCA	PROTEIN M	ERWINIA CAROTOVORA	108-145								
PGSPD ERWCH	PROTEIN D	ERWINIA CHRYSAANTHEMI	259-302	448-475	346-573	657-684					
POTF1 STRDO	GLUCOSYLTRANSFERASE-I	STREPTOCOCCUS DOWNEI	42-69	177-204	212-239	464-491	1382-1416	1493-1529			
POTF2 STRDO	GLUCOSYLTRANSFERASE-I	STREPTOCOCCUS DOWNEI	171-198	206-231	458-485	1382-1412	1493-1529				
POTF3 STRDO	GLUCOSYLTRANSFERASE-S	STREPTOCOCCUS MUTANS	297-330								
POTF4 STRDO	GLUCOSYLTRANSFERASE-I	STREPTOCOCCUS MUTANS	42-93	110-137	161-188	199-246	313-347	592-627			
POTF5 STRDO	GLUCOSYLTRANSFERASE-SI	STREPTOCOCCUS MUTANS	4-40	110-138	235-262	310-361	614-653				
POTF6 STRDO	GLUCOSYLTRANSFERASE-S	STREPTOCOCCUS DOWNEI	275-316	436-463	1281-1315						
POTM8 METTF	POSSIBLE G-T MISMATCHES REPAIR ENZYME	METHANOBACTERIUM THERMOTOMICICUM	80-107	148-175							
PGUAA BACSU	GMP SYNTHASE	BACILLUS SUBTILIS	314-348	399-436	478-505						
PGUAA ECOLI	GMP SYNTHASE	ESCHERICHIA COLI	105-132								
PGUB BACCI	BETA-GLUCANASE	BACILLUS CIRCULANS	164-191								
PGUB BACLI	BETA-GLUCANASE	BACILLUS LICHENIFORMIS	132-166								
PGUB BACMA	BETA-GLUCANASE	BACILLUS MAGERANS	126-160								
PGUN1 BACSU	ENDOGLUCANASE A	BACILLUS SP	18-49								
PGUN1 BACSU	ENDOGLUCANASE B	BACILLUS SUBTILIS	270-304	376-403							
PGUN1 BUTFI	ENDOGLUCANASE I	BUTYRIVIBRIO FIBRISOLVENS	134-181	432-495							
PGUN1 BACSU	ENDOGLUCANASE E1	BACILLUS SUBTILIS	270-304								
PGUN1 THEFU	ENDOGLUCANASE E1	THERMONONOSPORA FUSCA	201-228								
PGUN2 BACSU	ENDOGLUCANASE C	BACILLUS SUBTILIS	110-137	348-378	518-563						
PGUN2 BACSU	ENDOGLUCANASE C	BACILLUS SUBTILIS	270-304								
PGUN3 BACSU	ENDOGLUCANASE J	FIBROBACTER SUCCINOGENES	542-586								
PGUN3 THEFU	ENDOGLUCANASE E4	THERMONONOSPORA FUSCA	308-342								
PGUN3 THEFU	ENDOGLUCANASE E4	THERMONONOSPORA FUSCA	44-71								
PGUNA BACLA	ENDOGLUCANASE A	BACILLUS LAUTUS	410-437	454-481							
PGUNA CLOTM	ENDOGLUCANASE A	CLOSTRIDIUM THERMOCELLUM	334-384								
PGUNA PSEAL	ENDOGLUCANASE A	PSEUDOMONAS FLUORESCENS	762-789								
PGUNA RUMAL	ENDOGLUCANASE A	RUMINOCOCCUS ALBUS	294-321								
PGUNA RUMFL	CELLULOXYLASE A	RUMINOCOCCUS FLAVEFACIENS	276-303								
PGUNB BACLA	ENDOGLUCANASE B	BACILLUS LAUTUS	375-430								
PGUNB CALSA	ENDOGLUCANASE B	CALDOCELLUM SACCHAROLYTICUM	151-182	444-478							
PGUNB CELFI	ENDOGLUCANASE B	CELLULONONAS FINI	266-293								
PGUNB CLOCL	ENDOGLUCANASE B	CLOSTRIDIUM CELLULOVOXANS	144-171	266-300							
PGUNB CLOTM	ENDOGLUCANASE B	CLOSTRIDIUM THERMOCELLUM	514-541								
PGUNC CELFI	ENDOGLUCANASE C	CELLULONONAS FINI	881-908								
PGUNC PSEAL	ENDOGLUCANASE C	PSEUDOMONAS FLUORESCENS	52-82								
PGUND CLOCE	ENDOGLUCANASE D	CLOSTRIDIUM CELLULOXYLICUM	382-453								
PGUND CLOCL	ENDOGLUCANASE D	CLOSTRIDIUM CELLULOXYLICUM	145-172	271-298							
PGUNE CLOTM	ENDOGLUCANASE E	CLOSTRIDIUM THERMOCELLUM	158-185	207-234	284-311						
PGUNH CLOTM	ENDOGLUCANASE H	CLOSTRIDIUM THERMOCELLUM	46-73	423-452							
PGUNS ERWCA	ENDOGLUCANASE H	ERWINIA CAROTOVORA	20-47	115-149							
PGUNX CLOTM	POTATIVE ENDOGLUCANASE X	CLOSTRIDIUM THERMOCELLUM	105-139								
PGUNZ CLOSR	ENDOGLUCANASE Z	CLOSTRIDIUM STERCORARIUM	296-326	522-549							
PGUN BACPO	ENDOGLUCANASE	BACILLUS POLYMEXA	198-225								
PGUN BACSI	ENDOGLUCANASE	BACILLUS SP	321-348								
PGUN BACSB	ENDOGLUCANASE	BACILLUS SP	198-229	501-538	623-664						



ECGENE	10711784	Polytopic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
CHLORAMPHENICOL ACETYLTRANSFERASE	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PGUTD ECOLI	SORBITOL-4-PHOSPHATE 2-DEHYDROGENASE	ESCHERICHIA COLI	138-163								
PGV1 HALIA	GAS VESICLE PROTEIN, PLASMID	HALOBACTERIUM HALOBIIUM	36-63								
PGV2 HALIA	GAS VESICLE PROTEIN, CHROMOSOMAL	HALOBACTERIUM HALOBIIUM	36-63								
PGV3 APHEL	GAS VESICLE PROTEIN	APHANIZOYENON FLOS-AQUAE	4-31	39-66							
PGV4 FREDI	GAS VESICLE PROTEIN	FREMYELLA DIPLOSPHON	4-31	39-66							
PGV5 HALME	GAS VESICLE PROTEIN	HALOBACTERIUM MEDITERRANEI	37-64								
PGV6 MICBC	GAS VESICLE PROTEIN	MICROCYSTIS SP.	39-66								
PGV7 PSEAN	GAS VESICLE PROTEIN	PSEUDONANADAENA SP.	4-31	39-66							
PGV8 APHEL	GAS VESICLE PROTEIN C	APHANIZOYENON FLOS-AQUAE	8-49								
PGV9 HALIA	GAS VESICLE PROTEIN C	HALOBACTERIUM HALOBIIUM	150-249								
PGV10 HALME	GAS VESICLE PROTEIN C	HALOBACTERIUM MEDITERRANEI	139-169								
PGV11 HALIA	GYPD PROTEIN, PLASMID	HALOBACTERIUM HALOBIIUM	110-147								
PGV12 HALME	GYPD PROTEIN	HALOBACTERIUM MEDITERRANEI	110-147								
PGV13 HALIA	GYPF PROTEIN, PLASMID	HALOBACTERIUM HALOBIIUM	13-47	133-169							
PGV14 HALME	GYPF PROTEIN	HALOBACTERIUM MEDITERRANEI	13-47								
PGV15 HALIA	GYPG PROTEIN	HALOBACTERIUM HALOBIIUM	8-49								
PGV16 HALIA	GYPG PROTEIN, PLASMID	HALOBACTERIUM HALOBIIUM	38-65								
PGV17 HALME	GYPD PROTEIN	HALOBACTERIUM MEDITERRANEI	38-72								
PGV18 HALIA	GYPH PROTEIN	HALOBACTERIUM HALOBIIUM	10-40								
PGV19 HALME	GYPI PROTEIN	HALOBACTERIUM MEDITERRANEI	5-32								
PGV20 HALIA	GYPK PROTEIN	HALOBACTERIUM HALOBIIUM	45-76								
PGV21 HALME	GYPK PROTEIN	HALOBACTERIUM MEDITERRANEI	12-39	42-74							
PGV22 HALIA	GYPL PROTEIN	HALOBACTERIUM HALOBIIUM	11-58	50-77							
PGV23 HALIA	GYPL PROTEIN	HALOBACTERIUM MEDITERRANEI	44-78								
PGV24 HALIA	GYPN PROTEIN	HALOBACTERIUM HALOBIIUM	113-140								
PGV25 HALME	GYPN PROTEIN	HALOBACTERIUM MEDITERRANEI	15-56								
PGV26 HALIA	GYPO PROTEIN	HALOBACTERIUM MEDITERRANEI	49-96	105-132							
PGV27 HALIA	DNA GYRASE SUBUNIT A	BACILLUS SUBTILIS	380-407	429-499							
PGV28 HALIA	DNA GYRASE SUBUNIT A	CAMPYLOBACTER JEJUNI	267-310	381-408	452-479	665-695					
PGV29 HALIA	DNA GYRASE SUBUNIT A	ESCHERICHIA COLI	266-393	449-497							
PGV30 HALIA	DNA GYRASE SUBUNIT A	KLEBSIELLA PNEUMONIAE	266-393	448-496	518-545						
PGV31 HALIA	DNA GYRASE SUBUNIT A	MYCOPLASMA PNEUMONIAE	4-31								
PGV32 HALIA	DNA GYRASE SUBUNIT A	STAPHYLOCOCCUS AUREUS	129-156	346-373	430-479	647-674	812-839				
PGV33 HALIA	DNA GYRASE SUBUNIT B	BACILLUS SUBTILIS	198-239								
PGV34 HALIA	DNA GYRASE SUBUNIT B	BORRELIA BURGDORFERI	154-181								
PGV35 HALIA	DNA GYRASE SUBUNIT B	ESCHERICHIA COLI	616-643								
PGV36 HALIA	DNA GYRASE SUBUNIT B	HALOPHAX SP.	230-237								
PGV37 HALIA	DNA GYRASE SUBUNIT B	MYCOPLASMA PNEUMONIAE	249-283								
PGV38 HALIA	DNA GYRASE SUBUNIT B	NEISSERIA GONORRHOEA	574-558	618-645							
PGV39 HALIA	DNA GYRASE SUBUNIT B	PSEUDOMONAS PUTIDA	122-149	684-711							
PGV40 HALIA	DNA GYRASE SUBUNIT B	SPHILOPLASMA CITRI	40-74	189-238	233-210	341-368	540-579				
PGV41 HALIA	DNA GYRASE SUBUNIT B	STAPHYLOCOCCUS AUREUS	252-279	291-318							
PGV42 HALIA	DNA GYRASE SUBUNIT B	ESCHERICHIA COLI	71-98								
PGV43 HALIA	HELICASE IV	ESCHERICHIA COLI	100-134	559-556							
PGV44 HALIA	HELICASE IV	HAEMOPHILUS INFLUENZAE	58-85								
PGV45 HALIA	GLUTAMYL-TRNA REDUCTASE	CHLORIDIUM VIBRIOFORMES	272-259								
PGV46 HALIA	GLUTAMYL-TRNA REDUCTASE	ESCHERICHIA COLI	289-316								
PGV47 HALIA	3-AMINOLEVULINIC ACID SYNTHASE	RHODOBACTER SPHAEROIDES	71-100								
PGV48 HALIA	GLUTAMYL-TRNA REDUCTASE	SALMONELLA TYPHIMURUM	289-316	344-371							
PGV49 HALIA	GLUTAMYL-TRNA REDUCTASE	SYNECHOCYSTIS SP.	163-190	330-377							
PGV50 HALIA	DELTA-AMINOLEVULINIC ACID DEHYDRATASE	METHANOTHERMUS SOCIABILIS	131-158								
PGV51 HALIA	PUTATIVE UROPORPHYRINOGEN-III SYNTHASE	BACILLUS SUBTILIS	10-37								
PGV52 HALIA	UROPORPHYRINOGEN-III SYNTHASE	ESCHERICHIA COLI	211-238								
PGV53 HALIA	HEMAM PROTEIN	ESCHERICHIA COLI	143-174								
PGV54 HALIA	HEMAM RECEPTOR PRECURSOR	YERSINIA ENTEROCOLITICA	234-261								
PGV55 HALIA	PUTATIVE METHYL-TRANSFERASE	ESCHERICHIA COLI	69-138	1183-219							
PGV56 HALIA	HEMY PROTEIN	BACILLUS SUBTILIS	217-262								



PCGENE	10717144	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PHIEMZ	PROTEIN	ORGANISM	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PHIEMZ	PROTEIN	BACILLUS SUBTILIS	190-226								
PHIETA	ANASP	ANADENA SP	184-211	157-198	157-198						
PHIEXA	STRPN	STREPTOCOCCUS PNEUMONIAE	426-460								
PHIEXB	STRPN	DNA MISMATCH REPAIR PROTEIN HEXB	470-497								
PHIFAB	CAUCR	POS TRANSACTIVATOR PROTEIN HFAB	98-125								
PHIFC	ECOLI	HLFC PROTEIN	113-140								
PHIFLX	ECOLI	GTP-BINDING PROTEIN HFLX	169-196								
PHIFQ	ECOLI	HOST FACTOR-I PROTEIN	24-31								
PHIFC	HAEN	PILIATION PROTEIN HIFC PRECURSOR	350-383	404-431	404-431						
PHIS2	LACLA	PHOSPHORIBOSYL-AMP CYCLOHYDROLASE	126-174								
PHIS4	ECOLI	P-3-A CARBOXYAMIDE RIBOTIDE	125-159								
PHIS4	LACLA	P-3-A CARBOXYAMIDE RIBOTIDE	40-89	181-228							
PHIS4	MEYVA	P-3-A CARBOXYAMIDE RIBOTIDE	115-142								
PHIS4	SALTY	P-3-A CARBOXYAMIDE RIBOTIDE	125-159								
PHIS5	LACLA	AMIDOTRANSFERASE HISH	7-34								
PHIS6	ECOLI	HISF PROTEIN	39-66	142-169							
PHIS6	SALTY	HISF PROTEIN	39-66	142-169							
PHIS7	ECOLI	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE	168-199								
PHIS7	SALTY	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE	161-199								
PHIS8	HALVO	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE	290-317								
PHIS8	LACLA	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE	174-201								
PHIS8	SALTY	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE	161-188								
PHISQ	SALTY	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE	293-320								
PHISX	ECOLI	HISTIDINOL DEHYDROGENASE	8-35								
PHISX	LACLA	HISTIDINOL DEHYDROGENASE	19-46	264-303							
PHISX	MYCSM	HISTIDINOL DEHYDROGENASE	288-329	390-430							
PHISX	SALTY	HISTIDINOL DEHYDROGENASE	393-434								
PHIL4	STAAU	ALPHA-HEMOLYSIN PRECURSOR	69-103								
PHLY1	ECOLI	HEMOLYSIN A, CHROMOSOMAL	5-32	76-103	161-224	234-261	335-380	458-492	534-581	642-728	
PHLY2	ECOLI	HEMOLYSIN SECRETION PROTEIN, CHROMOSOMAL	487-514								
PHLY4	ECOLI	HEMOLYSIN D, CHROMOSOMAL	103-133	176-215	223-331						
PHLYA	ACTPL	HEMOLYSIN	5-39	136-170	184-218	273-300	330-377	459-537	846-924		
PHLYA	ACTSU	HEMOLYSIN	5-39	136-170	184-218	273-300	330-377	459-500	846-924		
PHLYA	ECOLI	HEMOLYSIN A, PLASMID	5-32	76-103	161-263	354-381	432-493	555-582	642-729		
PHLYA	PROMI	HEMOLYSIN PRECURSOR	165-196	290-338	356-400	425-471	498-525	528-576	610-605	705-742	747-774
PHLYA	SERMA	HEMOLYSIN PRECURSOR	789-823	841-868	966-993	1113-1140	1166-1193	1225-1272	1301-1342	1391-1461	1483-1527
PHLYA	ACTPL	HEMOLYSIN C	311-345	477-504	558-585	625-703	718-745	830-864	1081-1108	1151-1202	1249-1286
PHLYA	VIBCH	HEMOLYSIN PRECURSOR	1516-1553								
PHLYB	ACTPL	HAEMOLYSIN SECRETION PROTEIN	335-369	618-665							
PHLYB	ECOLI	HAEMOLYSIN SECRETION PROTEIN, PLASMID	34-61								
PHLYB	PROMI	HAEMOLYSIN ACTIVATOR PROTEIN PRECURSOR	487-514								
PHLYB	PROVU	HAEMOLYSIN SECRETION PROTEIN	16-64	499-547							
PHLYB	SERMA	HAEMOLYSIN ACTIVATOR PROTEIN PRECURSOR	34-68	487-514							
PHLYB	VIBCH	HAEMOLYSIN SECRETION PROTEIN PRECURSOR	110-137								
PHLYC	ACTPL	HEMOLYSIN C	335-398	413-447	458-524						
PHLYD	ACTPL	HEMOLYSIN SECRETION PROTEIN APPD	130-157								
PHLYD	ECOLI	HEMOLYSIN D, PLASMID	191-311								
PHLYD	HAL17	HAEMOLYSIN PRECURSOR	103-133	178-215	223-331						
PHMCD	DESXH	417 K D PROTEIN IN RMC OPERON	484-516								
PHMD	MEYVA	H27-FORMING DEHYDROGENASE	156-186								
PHNS	SERMA	DNA-BINDING PROTEIN H-NS	38-63								
PHOLA	ECOLI	DNA POLYMERASE III DELTA SUBUNIT	35-62								
PHOXA	BIOXA	REG PROTEIN HOXA	94-121	288-322							
PHOXF	MOOPF	HOX F PROTEIN HOXA	113-163	444-471							
PHOXO	ALCEU	HOXO PROTEIN	4-31								
PHOXO	ALCEU	HOXO PROTEIN	76-110								

PCGENE	1071784	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
ELLMANIE	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PI0XX	BRADYRIZORIUM LAPONICUM	BRADYRIZORIUM LAPONICUM	356-381								
PIPI	HEXAGONALLY SURFACE PROTEIN PRECURSOR	DEINOCOCCUS RADIODURANS	483-482								
PIPIR	PHOSPHORIBOSYLTRANSFERASE	LACTOCOCCUS LACTIS	3-39	71-105							
PIHDD	SIGMA FACTOR HSD	STREPTOCOCCUS COELICOLOR	296-323								
PIHBP	REGULATORY PROTEIN HBP	BURKHOLDERIA SOLANACEARUM	171-405								
PIHPS	OUTER MEMBRANE PROTEIN HPS	PSEUDOMONAS SYRINGAE	62-129	310-344							
PIHPS	PROBABLE REGULATORY PROTEIN HPS	PSEUDOMONAS SYRINGAE	24-31								
PIHPS	IN KID HEAT SHOCK PROTEIN	CLOSTRIDIUM ACETOBUTYLICUM	67-108								
PIHPS	HEAT SHOCK 70 KD PROTEIN	HALOARcula MARINORUM	62-576								
PIHPS	HEAT SHOCK 70 KD PROTEIN	MYTUMACTHUM LITHAE	461-485	501-516							
PIHPS	HEAT SHOCK 70 KD PROTEIN	MYCOBACTERIUM PARATUBERCULOSIS	460-487								
PIHPS	HEAT SHOCK PROTEIN C63	ESCHERICHIA COLI	231-248	482-509							
PIHPS	PROTEASE DQ PRECURSOR	ESCHERICHIA COLI	131-400								
PIHPS	HYPER PROTEIN PRECURSOR	ESCHERICHIA COLI	431-484	524-576							
PIHPS	SENSORY RHODOPSIN I TRANSDUCER	HALOBACTERIUM HALOBUTUM	413-471	479-506							
PIHPS	SENSORY RHODOPSIN I TRANSDUCER	HALOBACTERIUM SALINARIUM	114-149	413-471							
PIHPS	HEAT SHOCK 70 KD PROTEIN	BACILLUS SUBTILIS	5-16								
PIHPS	HEAT SHOCK 70 KD PROTEIN	LACTOBACILLUS HELVETICUS	174-212	306-333							
PIHPS	HEAT SHOCK 70 KD PROTEIN	ESCHERICHIA COLI	73-100	106-113							
PIHPS	HEAT SHOCK 70 KD PROTEIN	ESCHERICHIA COLI	251-278								
PIHPS	HEAT SHOCK 70 KD PROTEIN	SALMONELLA TYPHIMURUM	231-278								
PIHPS	HEAT SHOCK 70 KD PROTEIN	ESCHERICHIA COLI	312-319	360-387							
PIHPS	HEAT SHOCK 70 KD PROTEIN	PSEUDOMONAS SP	534-581								
PIHPS	HEAT SHOCK 70 KD PROTEIN	PSEUDOMONAS SP	6-40	96-123							
PIHPS	HEAT SHOCK 70 KD PROTEIN	PSEUDOMONAS SYRINGAE	131-160	297-331							
PIHPS	HEAT SHOCK 70 KD PROTEIN	ESCHERICHIA COLI	24-101								
PIHPS	HEAT SHOCK 70 KD PROTEIN	ERWINIA ANANAS	326-333	422-449	514-561	614-641	662-689	721-748	738-785	854-881	950-977
PIHPS	HEAT SHOCK 70 KD PROTEIN	ERWINIA HERBICOLA	1046-1073								
PIHPS	HEAT SHOCK 70 KD PROTEIN	PSEUDOMONAS FLUORESCENS	310-337	406-433	534-561	646-673	694-721	838-865	886-913	982-1009	
PIHPS	HEAT SHOCK 70 KD PROTEIN	PSEUDOMONAS SYRINGAE	281-308	377-404	425-452	681-708	729-781	795-852			
PIHPS	HEAT SHOCK 70 KD PROTEIN	XANTHOMONAS CAMPESTRIS	584-602	772-847	868-895	909-941					
PIHPS	HEAT SHOCK 70 KD PROTEIN	SHIGELLA FLEXNERI	496-534	555-582	1168-1204	1248-1275					
PIHPS	HEAT SHOCK 70 KD PROTEIN	BACILLUS STEAROTHERMOPHILUS	41-105	438-467							
PIHPS	HEAT SHOCK 70 KD PROTEIN	BACILLUS SUBTILIS	540-567	681-708							
PIHPS	HEAT SHOCK 70 KD PROTEIN	ESCHERICHIA COLI	173-208	394-421							
PIHPS	HEAT SHOCK 70 KD PROTEIN	ESCHERICHIA COLI	686-724	835-862							
PIHPS	HEAT SHOCK 70 KD PROTEIN	ENTEROCOCCUS FACIUM	339-437								
PIHPS	HEAT SHOCK 70 KD PROTEIN	BACILLUS STEAROTHERMOPHILUS	7-34								
PIHPS	HEAT SHOCK 70 KD PROTEIN	ESCHERICHIA COLI	27-34	70-97							
PIHPS	HEAT SHOCK 70 KD PROTEIN	KLEBSIELLA PNEUMONIAE	27-34	70-97							
PIHPS	HEAT SHOCK 70 KD PROTEIN	MYCOPLASMA FERMENTANS	172-211								
PIHPS	HEAT SHOCK 70 KD PROTEIN	PROTEUS VULGARIS	2-29	70-97							
PIHPS	HEAT SHOCK 70 KD PROTEIN	SALMONELLA TYPHIMURUM	27-34	70-97							
PIHPS	HEAT SHOCK 70 KD PROTEIN	SERRATIA MARCESCENS	19-46	70-97							
PIHPS	HEAT SHOCK 70 KD PROTEIN	NEISSERIA GONORRHOEA	245-272	287-314	831-860	1024-1058	1377-1404	1483-1531			
PIHPS	HEAT SHOCK 70 KD PROTEIN	STREPTOCOCCUS SP	46-76	120-150	195-222						
PIHPS	HEAT SHOCK 70 KD PROTEIN	STREPTOCOCCUS SP	46-76	120-150	195-222	270-297					
PIHPS	HEAT SHOCK 70 KD PROTEIN	ESCHERICHIA COLI	47-81	120-147							
PIHPS	HEAT SHOCK 70 KD PROTEIN	SALMONELLA TYPHIMURUM	47-81	120-147							
PIHPS	HEAT SHOCK 70 KD PROTEIN	LACTOCOCCUS LACTIS	20-35								
PIHPS	HEAT SHOCK 70 KD PROTEIN	SALMONELLA TYPHIMURUM	183-212								
PIHPS	HEAT SHOCK 70 KD PROTEIN	ACINETOBACTER CALCOACETICUS	166-193								
PIHPS	HEAT SHOCK 70 KD PROTEIN	BACILLUS SUBTILIS	159-186								
PIHPS	HEAT SHOCK 70 KD PROTEIN	BACILLUS THURINGIENSIS	103-130	324-338							
PIHPS	HEAT SHOCK 70 KD PROTEIN	LISTERIA MONOCYTOGENES	106-143	161-188	196-232						
PIHPS	HEAT SHOCK 70 KD PROTEIN	LISTERIA MONOCYTOGENES	53-94	166-200	381-415						
PIHPS	HEAT SHOCK 70 KD PROTEIN	YERSINIA ENTEROCOLITICA	501-535								



PCUGNE	10317844	Proteome Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PLENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PLEND LACLA	LACTOCOCCIN A SECRETION PROTEIN LGND	LACTOCOCCUS LACTIS	99-126	140-202								
PLCRD YEREN	LOW CALCIUM RESPONSE LOCUS PROTEIN D	YERSINIA ENTEROCOLITICA	122-149	491-518								
PLCRD YERPE	LOW CALCIUM RESPONSE LOCUS PROTEIN D	YERSINIA PESTIS	122-149	491-518								
PLCRV YERPE	VRULENCE-ASSOCIATED V ANTIGEN	YERSINIA PESTIS	22-49	157-184	240-267							
PLCRV YERPS	VRULENCE-ASSOCIATED V ANTIGEN	YERSINIA PSEUDOTUBERCULOSIS	22-49	240-267								
PLCTB BACCA	LCTB PROTEIN	BACILLUS CALDOTTENAX	18-45									
PLCTB BACST	LCTB PROTEIN	BACILLUS STEAROTHERIOPHILUS	14-45									
PLDID LACPL	D-LACTATE DEHYDROGENASE	LACTOBACILLUS PLANTARUM	51-81									
PLDIP BACPS	L-LACTATE DEHYDROGENASE P	BACILLUS PSYCHROSACCCHAROLYTICUS	2-43	241-272	279-306							
PLDIX BACPS	L-LACTATE DEHYDROGENASE X	BACILLUS PSYCHROSACCCHAROLYTICUS	2-43	241-275	279-306							
PLDH BACME	L-LACTATE DEHYDROGENASE	BACILLUS MEGATERIUM	244-274									
PLDH BACST	L-LACTATE DEHYDROGENASE	BACILLUS STEAROTHERIOPHILUS	241-268	279-311								
PLDH BACSU	L-LACTATE DEHYDROGENASE	BACILLUS SUBTILIS	8-42	240-267								
PLDH BIFLO	L-LACTATE DEHYDROGENASE	BIFIDOBACTERIUM LONGUM	22-49									
PLDH LACPL	L-LACTATE DEHYDROGENASE	LACTOBACILLUS PLANTARUM	197-231									
PLDH LISMO	L-LACTATE DEHYDROGENASE	LISTERIA MONOCYTOGENES	42-69									
PLDH MYCHY	L-LACTATE DEHYDROGENASE	MYCOPLASMA HYPONEUMONIAE	276-310									
PLEF BACAN	L-LACTATE DEHYDROGENASE	THERMUS AQUATICUS	3-30									
PLEF BACAN	LETHAL FACTOR PRECURSOR	BACILLUS ANTHRACIS	165-192	204-231	480-514	548-578	619-658	737-764				
PLEP BACFL	LEPA PROTEIN	PSEUDOMONAS FLUORESCENS	23-50									
PLEP BACSU	SIGNAL PEPTIDASE I	BACILLUS SUBTILIS	3-50									
PLEUT ECOLI	2-ISOPROPYLMALATE SYNTHASE	ESCHERICHIA COLI	437-464									
PLEUJ LACLA	2-ISOPROPYLMALATE SYNTHASE	LACTOCOCCUS LACTIS	22-49	379-484								
PLEUJ BACCO	2-ISOPROPYLMALATE DEHYDROGENASE	BACILLUS COAGULANS	311-338									
PLEUJ CLOPA	2-ISOPROPYLMALATE DEHYDROGENASE	CLOSTRIDIUM PASTEURIANUM	185-212									
PLEUJ LACLA	2-ISOPROPYLMALATE DEHYDROGENASE	LACTOCOCCUS LACTIS	163-190									
PLEVR BACSU	TRANSCRIPTIONAL REGULATORY PROTEIN LEVR	BACILLUS SUBTILIS	297-324	676-703	744-774	785-822						
PLEXA ERWCA	LEXA REPRESSOR	ERWINIA CAROTOVORA	146-173									
PLPI MORSP	LIPASE I	MORAXELLA SP	26-53									
PLP2 MORSP	LIPASE 2	MORAXELLA SP	356-383									
PLPB ECOLI	LIPB PROTEIN	ESCHERICHIA COLI	66-93									
PLPB BURCE	LIPASE PRECURSOR	BURKHOLDERIA CEPACIA	176-203									
PLIP PSEFL	LIPASE PRECURSOR	PSEUDOMONAS FLUORESCENS	8-35									
PLIP PSESS	LIPASE PRECURSOR	PSEUDOMONAS SP	176-203									
PLIP STAAU	LIPASE PRECURSOR	STAPHYLOCOCCUS AUREUS	80-146	312-546								
PLIVB SALTY	LEULEVAL/THR-BINDING PROTEIN PRECURSOR	SALMONELLA TYPHIMURUM	193-220									
PLIVG SALTY	LEUCINE-SPECIFIC BINDING PROTEIN PRECURSOR	SALMONELLA TYPHIMURUM	193-222									
PLIVE SALTY	AMINO ACID TRANSPORT PROTEIN LIVE	SALMONELLA TYPHIMURUM	121-148									
PLIVJ ECOLI	AMINO ACID TRANSPORT PROTEIN LIVE	ESCHERICHIA COLI	23-50									
PLIVJ CITR	LEULEVAL-BINDING PROTEIN PRECURSOR	CITROBACTER FREUNDII	193-222									
PLIVJ ECOLI	LEULEVAL-BINDING PROTEIN PRECURSOR	ESCHERICHIA COLI	193-222									
PLIVK ECOLI	LEUCINE-SPECIFIC BINDING PROTEIN PRECURSOR	ESCHERICHIA COLI	193-222									
PLIVM ECOLI	AMINO ACID TRANSPORT PROTEIN LIVM	ESCHERICHIA COLI	121-148									
PLKTA ACTAC	LEUKOTOXIN	ACTINOBACILLUS ACTINOMYCETICOMITANS	113-147	173-213	398-443	451-488	593-620	655-711				
PLKTA PASHA	LEUKOTOXIN	PASTEURELLA HAEMOLYTICA	53-99	179-216	345-372	409-436	435-482	496-530	545-572	811-838	853-926	
PLKTB ACTAC	LEUKOTOXIN SECRETION PROTEIN	ACTINOBACILLUS ACTINOMYCETICOMITANS	487-514									
PLKTB PASHA	LEUKOTOXIN SECRETION PROTEIN	PASTEURELLA HAEMOLYTICA	42-69	78-103								
PLKTC ACTAC	LTC PROTEIN	ACTINOBACILLUS ACTINOMYCETICOMITANS	58-85	116-150								
PLKTC PASHA	LTC PROTEIN	PASTEURELLA HAEMOLYTICA	123-157									
PLKTD AGAC	LKTD PROTEIN	ACTINOBACILLUS ACTINOMYCETICOMITANS	116-164	203-242	278-305	364-391						
PLKTD PASHA	LKTD PROTEIN	PASTEURELLA HAEMOLYTICA	184-219									
PLON ECOLI	ATP-DEPENDENT PROTEASE LA	ESCHERICHIA COLI	121-148									
PLPXA RICR	UDP-N-ACETYLGLUCOSAMINE ACYLTRANSFERASE	RICKETTSIA RICKETTSII	229-256									
PLSPA ECOLI	LIPOPROTEIN SIGNAL PEPTIDASE	ESCHERICHIA COLI	10-37									
PLSPA STAAU	LIPOPROTEIN SIGNAL PEPTIDASE	STAPHYLOCOCCUS AUREUS	134-161									
PLLIK STAAU	LEUKOTOXIN F SUBUNIT PRECURSOR	STAPHYLOCOCCUS AUREUS	161-193									
PLIKS STAAU	LEUKOTOXIN'S SUBUNIT PRECURSOR	STAPHYLOCOCCUS AUREUS	157-207									



PCGENE	10717114	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PNCRU_METFE	METHYL-COENZYMASE M REDUCTASE	METHANOTHIUS FERVIDUS	262-294							
PNCRB_METVO	METHYL-COENZYMASE N REDUCTASE	METHANOCOCCLUS VOLTAE	247-274							
PNCRD_METVO	MCKR PROTEIN	ESCHERICHIA COLI	111-145							
PNCRD_METVO	REDUCTASE OPERON PROTEIN D	METHANOCOCCLUS VOLTAE	34-91							
PNDIH_ECOLI	MALATE DEHYDROGENASE	ESCHERICHIA COLI	127-154							
PNDIH_METFE	MALATE DEHYDROGENASE	METHANOTHIUS FERVIDUS	54-88							
PNDIH_SALTY	MALATE DEHYDROGENASE	SALMONELLA TYPHIMURUM	127-154							
PNDOH_ECOLI	MDL PROTEIN	ESCHERICHIA COLI	464-491	684-711	992-1019					
PNDOH_ECOLI	BIO-SYNTHESIS PROTEIN MDH	ESCHERICHIA COLI	119-132							
PNMCI_STAEP	METHICILLIN RESIS REG PROTEIN MCI	STAPHYLOCOCCUS	88-122							
PNMCR_STAEP	METHICILLIN RESISTANCE MCR1 PROTEIN	EPIDERMIDIS & AUREUS	419-495	546-573						
PNMIB_METCA	METHANE MONOOXYGENASE COMPONENT A	METHYLOCOCCUS CAPSULATUS	214-248							
PNMIB_METTR	METHANE MONOOXYGENASE COMPONENT A	METHYLOCOCCUS TRICHOSPORUM	321-348							
PNMIB_ECOLI	SHCHC SYNTHASE	ESCHERICHIA COLI	333-367							
PNMIB_STRLI	PROBABLE HG TRANSPORT PROTEIN	STREPTOMYCES LIVIDANS	159-186							
PNMIB_BACSR	MERCURIC REDUCTASE	BACILLUS SP	146-180							
PNMIB_STAUI	MERCURIC REDUCTASE	STAPHYLOCOCCUS AUREUS	295-347	352-386						
PNMIB_STAUI	MERCURIC RESISTANCE OPERON REG PROTEIN	STAPHYLOCOCCUS AUREUS	86-113							
PNMIB_ECOLI	CYSTATHIONINE GAMMA-SYNTHASE	ESCHERICHIA COLI	356-383							
PNMIB_ECOLI	CYSTATHIONINE BETA-LYASE	ESCHERICHIA COLI	363-390							
PNMIB_SALTY	CYSTATHIONINE BETA-LYASE	SALMONELLA TYPHIMURUM	2-29							
PNMIB_ECOLI	METHIONINE SYNTHASE	ESCHERICHIA COLI	443-482							
PNMIB_ECOLI	METHIONINE SYNTHASE	ESCHERICHIA COLI	371-398	642-676						
PNMIB_ECOLI	TRANSCRIPTION-REPAIR COUPLING FACTOR	ESCHERICHIA COLI	185-212							
PNMIB_ECOLI	GALACTOSIDE-BINDING PROTEIN	ESCHERICHIA COLI	62-89	312-380						
PNMIB_BACSU	SEPTUM SITE-DETERMINING PROTEIN MNC	BACILLUS SUBTILIS	65-122							
PNMIB_ECOLI	MDK PROTEIN	ESCHERICHIA COLI	102-179							
PNMIB_CHLTR	27 KD MEMBRANE PROTEIN PRECURSOR	CHLAMYDIA TRACHOMATIS	41-75							
PNMIB_LEGMI	OUTER MEMBRANE PROTEIN MIP PRECURSOR	LEGIONELLA MICHAELIS	106-133							
PNMIB_ENTFA	RNA ADENINE N4-METHYLTRANSFERASE	ENTEROCOCCUS FAECALIS	4-81	120-154						
PNMIB_STAUI	RNA ADENINE N4-METHYLTRANSFERASE	STAPHYLOCOCCUS AUREUS	9-47							
PNMIB_ENTFA	RNA ADENINE N4-METHYLTRANSFERASE	ENTEROCOCCUS FAECALIS	4-81	120-154						
PNMIB_BACFR	RNA ADENINE N4-METHYLTRANSFERASE	BACTEROIDES FRAGILIS	16-43							
PNMIB_ECOLI	RNA ADENINE N4-METHYLTRANSFERASE	ESCHERICHIA COLI	4-81	120-154						
PNMIB_STRON	RNA ADENINE N4-METHYLTRANSFERASE	STREPTOCOCCUS PNEUMONIAE	4-81	120-154						
PNMIB_STRON	RNA ADENINE N4-METHYLTRANSFERASE	STREPTOCOCCUS SANGUIS	4-81	120-154						
PNMIB_BACFR	RNA ADENINE N4-METHYLTRANSFERASE	BACTEROIDES FRAGILIS	16-43							
PNMIB_METC	METHANE MONOOXYGENASE REG PROTEIN II	METHYLOCOCCUS CAPSULATUS	34-64							
PNMIB_ECOLI	MOLYBD COFAC BIOSYN PROTEIN B	ESCHERICHIA COLI	49-76							
PNMIB_THIFE	MOBA PROTEIN	THIOBACILLUS FERROOXIDANS	94-121	251-278						
PNMIB_THIFE	MOBA PROTEIN	THIOBACILLUS FERROOXIDANS	20-47							
PNMIB_THIFE	MOBA PROTEIN	THIOBACILLUS FERROOXIDANS	95-132							
PNMIB_ECOLI	MOB PROTEIN	ESCHERICHIA COLI	45-72							
PNMIB_ECOLI	MOLYBDOPTEIN BIOSYNTHESIS MOEA PROTEIN	ESCHERICHIA COLI	243-270							
PNMIB_CLOPA	MOLYBDENUM-PTERIN BINDING PROTEIN I	CLOSTRIDIUM PASTEURIANUM	26-53							
PNMIB_CLOPA	MOLYBDENUM-PTERIN BINDING PROTEIN II	CLOSTRIDIUM PASTEURIANUM	26-64							
PNMIB_PARDE	METHANOL UTIL CONT PROTEIN MOXY	PARACOCCLUS DENITRIFICANS	200-234	307-334						
PNMIB_STAUI	BILIN BIOSYNTHESIS PROTEIN MPEU	SYNECHOCOCCUS SP	2-36	80-107	198-223					
PNMIB_STAUI	BILIN BIOSYNTHESIS PROTEIN MPEV	SYNECHOCOCCUS SP	2-31	175-216						
PNMIB_ECOLI	MPRA PROTEIN	ESCHERICHIA COLI	106-163							
PNMIB_BACSU	PENTAPEPTIDE-TRANSFERASE	BACILLUS SUBTILIS	106-133	247-281						
PNMIB_BACCE	ROD SHAPE-DETERMINING PROTEIN MREB	BACILLUS CEREUS	106-213							
PNMIB_BACSU	ROD SHAPE-DETERMINING PROTEIN MREC	BACILLUS SUBTILIS	65-112							
PNMIB_KLEPN	CHAPERONE PROTEIN MKB3 PRECURSOR	KLEBSIELLA PNEUMONIAE	198-232							
PNMIB_KLEPN	MRKC PROTEIN PRECURSOR	KLEBSIELLA PNEUMONIAE	55-82	451-489	592-622					









PCGENE	10211784	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PNFN BRAJA	BIOSYNTHESIS PROTEIN NFN	BRADYRHIZOBIUM JAPONICUM	219-266						
PNFS ANASP	NIFS PROTEIN	ANABAENA SP	112-119						
PNFS LACDE	NIFS PROTEIN HOMOLOG	LACTOBACILLUS DELBRUECKII	59-86						
PNFT AZOVI	NIFT PROTEIN	AZOTODACTER VINELANDII	6-11						
PNFU ANASL	NFU PROTEIN	ANABAENA SP	7-49						
PNFU ANASP	NFU PROTEIN	ANABAENA SP	148-178						
PNFU KLEPN	NFU PROTEIN	KLEBSIELLA PNEUMONIAE	66-93						
PNKA ECOLI	NICKEL TRANSPORT PROTEIN NIKK PRECURSOR	ESCHERICHIA COLI	172-149	282-309	456-483				
PNKE ECOLI	NICKEL TRANSPORT PROTEIN NIKK	ESCHERICHIA COLI	172-204						
PNKB ECOLI	NITRITE REDUCTASE	ESCHERICHIA COLI	54-81						
PNRC ECOLI	NITRIC PROTEIN	ESCHERICHIA COLI	212-239	345-372					
PNRS PSEST	PSEUDOMONAS CYTOCHROME OXIDASE PRECURSOR	PSEUDOMONAS STUTZERI	303-333						
PNIS LAGLA	117 KD MEMBRANE ASSOCIATED PROTEIN	LACTOCOCCUS LACTIS	202-229	287-312	663-697	886-920			
PNIS LAGLA	NISIN BIOSYNTHESIS PROTEIN NISC	LACTOCOCCUS LACTIS	52-92	140-188					
PNIS LAGLA	NISIN TRANSPORT PROTEIN NIST	LACTOCOCCUS LACTIS	223-237	278-305	426-470				
PNIV CLOPA	HOMOCITRATE SYNTHASE, ALPHA SUBUNIT	CLOSTRIDIUM PASTEURIANUM	100-127	224-268					
PNIV CLOPA	HOMOCITRATE SYNTHASE, OMEGA SUBUNIT	CLOSTRIDIUM PASTEURIANUM	63-94	103-132	213-240	283-310			
PNPC ECOLI	POBIN PROTEIN NMPK PRECURSOR	ESCHERICHIA COLI	22-49	69-96	335-362				
PNDC BRASP	MODULATION PROTEIN C	BRADYRHIZOBIUM SP	3-20						
PNDC RHILQ	MODULATION PROTEIN C	RHIZOBIUM LOTI	286-313						
PNDC RHILQ	MODULATION PROTEIN C	RHIZOBIUM LEGUMINOSARUM	14-48						
PNDF RHILV	MODULATION PROTEIN F	RHIZOBIUM LEGUMINOSARUM	31-58						
PNDF RHIMS	MODULATION PROTEIN F	RHIZOBIUM MELILOTI	39-66						
PNDD RHIME	MODULATION PROTEIN G	RHIZOBIUM MELILOTI	8-35						
PNDD RHIMS	MODULATION PROTEIN G	RHIZOBIUM MELILOTI	8-35						
PNDD RHILV	MODULATION PROTEIN L	RHIZOBIUM LEGUMINOSARUM	26-53						
PNDD AZOBR	MODULATION PROTEIN Q	AZOSPRILLUM BRASILENSE	60-87						
PNDDT RHILT	MODULATION PROTEIN T	RHIZOBIUM LEGUMINOSARUM	104-134	355-382	420-454				
PNDDT RHILV	MODULATION PROTEIN T	RHIZOBIUM LEGUMINOSARUM	364-391	416-443					
PNDDU RHIFA	MODULATION PROTEIN U	RHIZOBIUM FREDII	506-536						
PNDDV BRAJA	MODULATION PROTEIN V	BRADYRHIZOBIUM JAPONICUM	378-419	739-766					
PNDDX RHILV	MODULATION PROTEIN X	RHIZOBIUM LEGUMINOSARUM	232-239						
PNDL RHIFR	MODULATION PROTEIN NOLD	RHIZOBIUM FREDII	131-160						
PNDL RHIME	MODULATION PROTEIN NOLD	RHIZOBIUM MELILOTI	88-115						
PNDS PSEST	NOSD PROTEIN PRECURSOR	PSEUDOMONAS STUTZERI	319-346						
PNDS PSEST	REGULATORY PROTEIN NOSR	PSEUDOMONAS STUTZERI	127-154						
PNDS MEAE	NITROUS-OXIDE REDUCTASE PRECURSOR	PSEUDOMONAS AERUGINOSA	267-294						
PNDS MEAE	NITROUS-OXIDE REDUCTASE PRECURSOR	PSEUDOMONAS STUTZERI	357-391						
PNPAE BACAM	BACILLUS-LYSIN PRECURSOR	BACILLUS ANTHROPUS	113-147	217-244					
PNPAE BACPO	BACILLUS-LYSIN PRECURSOR	BACILLUS POLYMYXA	57-91	187-218					
PNPAE BACPO	BACILLUS-LYSIN PRECURSOR	BACILLUS SUBTILIS	116-146	307-334					
PNPD PARDE	NADH-UBIQUINONE OXIDOREDUCTASE 21 KD CHAIN	PARACOCCLUS DENTRIFICANS	4-45						
PNPD PARDE	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD CHAIN	PARACOCCLUS DENTRIFICANS	125-152						
PNPD ECOLI	ANAER. RHINOUC. TRIPHIUS REDUCTASE	ESCHERICHIA COLI	91-125						
PNPAE ECOLI	CYTOCHROME C33 PRECURSOR	ESCHERICHIA COLI	319-346						
PNRF ECOLI	NRF PROTEIN	ESCHERICHIA COLI	72-111						
PNRL RHORH	ALIPHATIC NITRILASE	RHODOCOCCUS RHODOCITRIOUS	109-136						
PNR LACIA	NISIN-RESISTANCE PROTEIN	LACTOCOCCUS LACTIS	52-79	135-162					
PNR LACIA	ANA-INDUCING PROTEIN VFI	ANABAENA SP	65-92						
PNCA ANASP	GLOBAL NITROGEN REGULATOR	SYNECHOCOCCUS SP	44-91						
PNCA SYN3	GLOBAL NITROGEN REGULATOR	SYNECHOCOCCUS SP	67-94						
PNTRB VIBAL	NITROGEN REGULATION PROTEIN NTRB	VIBRIO ALGINOLYTICUS	194-223						
PNTRC PRUVU	NITROGEN REGULATION PROTEIN NR	PROTEUS VULGARIS	385-412						
PNTRC RHIME	NITROGEN ASSIMILATION REGULATORY PROTEIN	RHIZOBIUM MELILOTI	451-478						
PNJC SYN7	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN	SYNECHOCOCCUS SP	80-107						
PNJC SYN3	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN	SYNECHOCOCCUS SP	27-54						
PNJC SYN7	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN	SYNECHOCOCCUS SP	614-641						



PGCENE	1071784	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
POPAX NEIGO	OPACITY PROTEIN OPAX37	NEISSERIA GONORRHOEAE	71-105								
POPDA ECOLI	OLIGOPEPTIDASE A	ESCHERICHIA COLI	147-174								
POPDA_SALTY	OLIGOPEPTIDASE A	SALMONELLA TYPHIMURUM	147-174								
POIDE_PSEAE	TRANSCRIPTION FACTOR OPDE	PSEUDOMONAS AERUGINOSA	64-91								
POPFA ECOLI	OLIGOPEPTIDE-BINDING PROTEIN PRECURSOR	ESCHERICHIA COLI	402-432								
POPFB_SALTY	OLIGOPEPTIDE PERMEASE PROTEIN OPFB	SALMONELLA TYPHIMURUM	263-299								
POPRI_NEIME	OPACITY-RELATED PROTEIN POPRI	NEISSERIA MENINGITIDIS	108-135								
POPRI_EC	OPACITY-RELATED PROTEIN POPRI	NEISSERIA MENINGITIDIS	94-135								
POSNC ECOLI	OSMOTICALLY INDUCIBLE PROTEIN OSMC	ESCHERICHIA COLI	5-32								
POSRA_BORBU	OUTER SURFACE PROTEIN A PRECURSOR	BORRELLIA BURGDORFERI	63-100	112-139	151-204	223-271					
POTC3_BACSU	ORNITHINE CARBAMOYLTRANSFERASE	BORRELLIA BURGDORFERI	113-239	262-296							
POTCC_PSEAE	ORNITHINE CARBAMOYLTRANSFERASE	BACILLUS SUBTILIS	188-215								
POTCC_PSEPU	ORNITHINE CARBAMOYLTRANSFERASE	PSEUDOMONAS AERUGINOSA	17-44								
POTIB_BACSU	SPORE OUTGROWTH FACTOR B	BACILLUS SUBTILIS	3-33								
POTO_ERWCA	LEADER PEPTIDE SE	ERWINIA CAROTOVORA	223-252								
PP1BK_STRPA	18 KD PROTEIN IN FIMA 3 REGION	STREPTOCOCCUS PARASANGUIS	189-216								
PP1BK_STRPA	18 KD PROTEIN IN SSAB 3 REGION	STREPTOCOCCUS SANGUIS	113-149								
PP1P_LACLC	PLI-TYPE PROTEINASE PRECURSOR	LACTOCOCCUS LACTIS	107-155	904-950	1073-1100	1223-1250	1466-1496	1635-1655			
PP29_MYCHR	PROTEIN P29	MYCOPLASMA HYORHINIS	5-56	101-160	202-246						
PP2P_LACLA	PLI-TYPE PROTEINASE PRECURSOR	LACTOCOCCUS LACTIS	107-155	904-950	1073-1100	1223-1250	1466-1496	1635-1689			
PP2P_LACPA	PLI-TYPE PROTEINASE PRECURSOR	LACTOBACILLUS PARACASEI	107-155	904-941	1073-1100	1223-1250	1466-1496	1635-1655			
PP2J_EC	P20 PROTEIN	ESCHERICHIA COLI	55-82								
PP24_RICRI	PROTEIN P24	RICKETTSIA RICKETTSII	9-47	135-173							
PP27_MYCHR	PROTEIN P27 PRECURSOR	MYCOPLASMA HYORHINIS	38-75								
PP3P_LACLC	PLI-TYPE PROTEINASE PRECURSOR	LACTOCOCCUS LACTIS	107-155	904-950	1073-1100	1223-1250	1466-1496	1635-1655			
PP47K_PSECL	47 KD PROTEIN	PSEUDOMONAS CHLOROPHILIS	288-315								
PP54_ENTFC	P54 PROTEIN PRECURSOR	ENTEROCOCCUS FAECIUM	58-92	141-209							
PP60_LISGR	PROTEIN P60 PRECURSOR	LISTERIA GRAYI	31-61	101-142	300-334	431-458					
PP60_LISIN	PROTEIN P60 PRECURSOR	LISTERIA INNOCUA	67-94	102-143							
PP60_LISIV	PROTEIN P60 PRECURSOR	LISTERIA IVANOVII	101-140	315-359							
PP60_LISUO	PROTEIN P60 PRECURSOR	LISTERIA MONOCYTOGENES	102-144								
PP60_LISWE	PROTEIN P60 PRECURSOR	LISTERIA WELSHIMERI	101-140	370-398	395-432						
PP69_MYCHR	PROTEIN P69	MYCOPLASMA HYORHINIS	113-140	317-361	396-423						
PP69A_BACSU	ADC SYNTHASE	BACILLUS SUBTILIS	264-295	421-464	487-517	544-575					
PP69B_BACSU	4-AMINO-4-DEOXYCHORISMATE LYASE	BACILLUS SUBTILIS	12-41								
PP69C_EC	4-AMINO-4-DEOXYCHORISMATE LYASE	ESCHERICHIA COLI	250-277								
PP69D_EC	4-AMINO-4-DEOXYCHORISMATE LYASE	ESCHERICHIA COLI	140-167								
PP69E_EC	PROTEIN Y	STREPTOMYCES GRISEUS	52-79								
PP69F_EC	PENICILLIN ACYLASE PRECURSOR	ANTHROBACTER VISCOSUS	170-197	333-363	571-606	640-674					
PP69G_EC	PENICILLIN ACYLASE	BACILLUS SPHAERICUS	232-259								
PP69H_EC	PAC PROTEIN PRECURSOR	STREPTOCOCCUS MUTANS	146-276	281-463	538-565	576-630	1035-1102	1159-1186	1381-1434		
PP69I_EC	REGULATORY PROTEIN PA1	BACILLUS SUBTILIS	103-137								
PP69J_EC	REGULATORY PROTEIN PA2	BACILLUS SUBTILIS	145-172								
PP69K_EC	FIMBRIAL PROTEIN PAPE	ESCHERICHIA COLI	42-69	86-123							
PP69L_EC	FIMBRIAL PROTEIN PAPE	ESCHERICHIA COLI	4-31								
PP69M_EC	FIMBRIAL PROTEIN PAPE PRECURSOR	ESCHERICHIA COLI	282-316								
PP69N_EC	PABA PROTEIN	AGROBACTERIUM TUMEFACIENS	60-87								
PP69O_EC	PLASMID PARTITION PAR B PROTEIN	ESCHERICHIA COLI	117-134	249-283							
PP69P_EC	TOPOISOMERASE IV SUBUNIT B	ESCHERICHIA COLI	444-471	526-553							
PP69Q_EC	TOPOISOMERASE IV SUBUNIT B	SALMONELLA TYPHIMURUM	444-471	526-553							
PP69R_EC	PROTECTIVE ANTIGEN PRECURSOR	BACILLUS ANTHRACIS	13-52	123-132	296-335	585-615	650-684				
PP69S_EC	PENICILLIN-BINDING PROTEIN 2	ESCHERICHIA COLI	95-122	178-205	207-241						
PP69T_EC	PENICILLIN-BINDING PROTEIN 2	NEISSERIA GONORRHOEAE	191-220								
PP69U_EC	PENICILLIN-BINDING PROTEIN 2	NEISSERIA MENINGITIDIS	191-220								
PP69V_EC	PENICILLIN-BINDING PROTEIN 2B	STREPTOCOCCUS PNEUMONIAE	144-183	216-243	259-286	605-632					
PP69W_EC	PENICILLIN-BINDING PROTEIN 3 PRECURSOR	ESCHERICHIA COLI	224-251	334-368							

PGCENE	10717144	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
FILENAME	PROTEIN	ORGANISM	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PPBP4_BACSU	PENICILLIN-BINDING PROTEIN 4*	BACILLUS SUBTILIS	374-401								
PPBP4_ECOLI	PENICILLIN-BINDING PROTEIN 4 PRECURSOR	ESCHERICHIA COLI	316-363								
PPBP4_ECOLI	PENICILLIN-BINDING PROTEIN 1A	ESCHERICHIA COLI	145-172								
PPBP4_ECOLI	PENICILLIN-BINDING PROTEIN 1B	ESCHERICHIA COLI	62-96	262-290							
PPBPX_STRPN	PENICILLIN-BINDING PROTEIN 2X	STREPTOCOCCUS PNEUMONIAE	39-116	706-733							
PPBPX_STAAL	PENICILLIN-BINDING PROTEIN	STAPHYLOCOCCUS AUREUS	78-108	176-203	203-224	502-529					
PPCAB_PSEFU	CYCLOISOMERASE	PSEUDOMONAS PUTIDA	115-142	226-253							
PPEL1_ERWCA	PECTATE LYASE III PRECURSOR	ERWINIA CAROTOVORA	110-137								
PPEL2_ERWCA	PECTATE LYASE A PRECURSOR	ERWINIA CAROTOVORA	110-137								
PPEL3_ERWCA	PECTATE LYASE B PRECURSOR	ERWINIA CAROTOVORA	110-137								
PPEL4_ERWCA	PECTATE LYASE C PRECURSOR	ERWINIA CAROTOVORA	110-137								
PPEL5_ERWCH	PECTATE LYASE E PRECURSOR	ERWINIA CHRYSANTHEMI	40-67	209-243							
PPEL6_ERWCA	PERIPLASMIC PECTATE LYASE PRECURSOR	ERWINIA CAROTOVORA	455-482								
PPEL7_ERWCA	PERIPLASMIC PECTATE LYASE PRECURSOR	ERWINIA CAROTOVORA	459-489								
PPEL8_ERWCA	PUTATIVE PECTATE LYASE X PRECURSOR	ERWINIA CAROTOVORA	188-218								
PPELX_ERWCH	EXOPOLYGALACTURONATE LYASE PRECURSOR	ERWINIA CHRYSANTHEMI	466-493								
PPEPD_ECOLI	AMINOACYL-HISTIDINE DIPEPTIDASE	ESCHERICHIA COLI	264-314								
PPEPQ_ECOLI	X-PRO DIPEPTIDASE	ESCHERICHIA COLI	351-378								
PPERT_BORBR	PERTACTIN PRECURSOR	BORDETTELLA BRONCHISEPTICA	617-644								
PPERT_BORPA	PERTACTIN PRECURSOR	BORDETTELLA PARAPERTUSSIS	628-655								
PPERT_BORPE	PERTACTIN PRECURSOR	BORDETTELLA PERTUSSIS	616-643								
PPCK_CORGL	PHOSPHOGLYCERATE KINASE	CORYNEBACTERIUM GLUTINICUM	83-117								
PPCK_ECOLI	PHOSPHOGLYCERATE KINASE	ESCHERICHIA COLI	186-216								
PPCK_METBR	PHOSPHOGLYCERATE KINASE	METHANOBACTERIUM BRYANTII	36-63								
PPCK_THETH	PHOSPHOGLYCERATE KINASE	THERMUS AQUATICUS	222-249								
PPGL1_ERWCA	ENDO-POLYGALACTURONASE PRECURSOR	ERWINIA CAROTOVORA	232-271								
PPGTE_SALTY	OUTER MEMBRANE PROTEASE E PRECURSOR	SALMONELLA TYPHIMURUM	66-93								
PPHA1_FREDI	C-PHYCOCYANIN-1 ALPHA CHAIN	FREMYELLA DIPLOSPHORI	21-48								
PPHA2_FREDI	C-PHYCOCYANIN-2 ALPHA CHAIN	FREMYELLA DIPLOSPHORI	21-48								
PPHA3_FREDI	POLY(1,6-HYDROXYALKANOATE) POLYMERASE I	PSEUDOMONAS OLEOVORANS	264-291								
PPHAB_ANACT	ALLOPHYCOCYANIN BETA CHAIN	ANABAENA CYLINDRICA	7-48								
PPHAB_ANAVA	ALLOPHYCOCYANIN BETA CHAIN	ANABAENA VARIABILIS	14-48								
PPHAB_FREDI	ALLOPHYCOCYANIN BETA CHAIN	FREMYELLA DIPLOSPHORI	8-49								
PPHAB_MASLA	ALLOPHYCOCYANIN BETA CHAIN	MASTIGOCLOADUS LAMINOSUS	14-41								
PPHAB_SYNPA	ALLOPHYCOCYANIN BETA CHAIN	SYNECHOCOCCUS SP	14-41								
PPHAC_SYNPA	ALLOPHYCOCYANIN ALPHA-B CHAIN	SYNECHOCOCCUS SP	33-40								
PPHAG_FREDI	ALLOPHYCOCYANIN GAMMA CHAIN	FREMYELLA DIPLOSPHORI	32-39								
PPHB3_FREDI	C-PHYCOCYANIN-3 BETA CHAIN	FREMYELLA DIPLOSPHORI	29-36								
PPHBD_ALCEU	ACETOACETYL-COA REDUCTASE	ALCALIGENES EUTROPIUS	35-45								
PPHCA_SYNVI	C-PHYCOCYANIN ALPHA CHAIN	SYNECHOCYSTIS SP	21-55								
PPHCB_SYNPA	C-PHYCOCYANIN BETA CHAIN	SYNECHOCOCCUS SP	28-55								
PPHCB_SYNPA	C-PHYCOCYANIN BETA CHAIN	SYNECHOCOCCUS SP	28-55								
PPHCB_SYNPA	C-PHYCOCYANIN BETA CHAIN	SYNECHOCYSTIS SP	21-55								
PPHCB_SYNPA	C-PHYCOCYANIN BETA CHAIN	SYNECHOCYSTIS SP	21-55								
PPHEA_ECOLI	CHORISMATE MUTASE	ESCHERICHIA COLI	10-37								
PPHEA_ERWAB	CHORISMATE MUTASE	ERWINIA HERBICOLA	10-37	159-186	252-286						
PPHEA_FESP	PHENOL 2-MONOOXYGENASE	PSEUDOMONAS SP	171-201	282-314	437-464						
PPHEB_MASLA	PHYCOERYTHROCYANIN BETA CHAIN	MASTIGOCLOADUS LAMINOSUS	21-62								
PPHEB_PESP	CATECHOL 1,2-DIOXYGENASE	PSEUDOMONAS SP	24-51								
PPHEO_SYNPA	LINKER POLYPEPTIDE	SYNECHOCOCCUS SP	158-185								
PPHEP_ECOLI	PHENYLALANINE-SPECIFIC PERMEASE	ESCHERICHIA COLI	384-311								
PPHF1_CLOPA	PERIPLASMIC [FE] HYDROGENASE I	CLOSTRIDIUM PASTEURIANUM	414-471								
PPHL1_BACCE	SPHINGOMYELINASE C PRECURSOR	BACILLUS CEREUS	2-36								
PPHL2_BACCE	SPHINGOMYELINASE C PRECURSOR	BACILLUS CEREUS	2-36								
PPHL3_BACCE	SPHINGOMYELINASE C PRECURSOR	BACILLUS CEREUS	2-36								
PPHLC_BACCE	PHOSPHOLIPASE C PRECURSOR	BACILLUS CEREUS	32-59								
PPHLC_CLOBI	PHOSPHOLIPASE C PRECURSOR	CLOSTRIDIUM BIFERMENTANS	30-77	179-206							
PPHLC_CLOPE	PHOSPHOLIPASE C PRECURSOR	CLOSTRIDIUM PERFRINGENS	210-237	169-198							

EC:ENSE	10717184	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9	AREA.10
FILE NAME	PROTEIN	ORGANISM	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9	AREA.10
PHLC LISMO	PHOSPHOLIPASE C PRECURSOR	LISTERIA MONOCYTOGENES	177-174									
PHLC PSEAE	HEMOLYTIC PHOSPHOLIPASE C PRECURSOR	PSEUDOMONAS AERUGINOSA	685-712									
PHLC STAAU	PHOSPHOLIPASE C PRECURSOR	STAPHYLOCOCCUS AUREUS	6-33									
PHLD BACCE	PHOSPHOLIPASE C PRECURSOR	BACILLUS CEREUS	179-206									
PHLD LEPIN	SPHINGOMYELINASE C PRECURSOR	LEPTOSPIRA INTERROGANS	30-57	394-428								
PHND ECOLI	PHND PROTEIN	ESCHERICHIA COLI	296-326									
PHNK ECOLI	PHNK PROTEIN	ESCHERICHIA COLI	178-205									
PHNM ECOLI	PHNM PROTEIN	ESCHERICHIA COLI	5-35									
PHOB CITFR	OUTER MEMBRANE PORE PROTEIN E PRECURSOR	CITROBACTER FREUNDII	13-40	42-105								
PHOE ECOLI	OUTER MEMBRANE PORE PROTEIN E PRECURSOR	ESCHERICHIA COLI	13-40	64-105	188-195	226-233						
PHOE KLEOX	OUTER MEMBRANE PORE PROTEIN E PRECURSOR	KLEBSIELLA OXYTOCA	13-40	64-91								
PHOE KLEPN	OUTER MEMBRANE PORE PROTEIN E PRECURSOR	KLEBSIELLA PNEUMONIAE	13-40	64-105								
PHOB SALTU	OUTER MEMBRANE PORE PROTEIN E PRECURSOR	SALMONELLA TYPHIMURUM	61-104	370-347								
PHOB BACSU	ALK PHOS SYNTHESIS TRANS REG PROTEIN	BACILLUS SUBTILIS	183-219									
PHOO ECOLI	SENSOR PROTEIN PHOO	ESCHERICHIA COLI	244-278									
PHOO SALTU	VIRULENCE SENSOR PROTEIN PHOO	SALMONELLA TYPHIMURUM	226-260									
PHOB BACSU	ALK PHOS SYNTHESIS SENSOR PROTEIN PHOB	BACILLUS SUBTILIS	89-145	387-415								
PHRA ECOLI	PHOTOREPAIR PROTEIN PHRA	ESCHERICHIA COLI	61-90	207-241								
PHRA SYNPP	R-PHYCOCYANIN II ALPHA CHAIN	SYNECHOCOCCUS SP	20-47									
PHRA SYNPP2	R-PHYCOCYANIN II ALPHA CHAIN	SYNECHOCOCCUS SP	20-47									
PHSO ECOLI	GLYCOCEN PHOSPHORYLASE	ESCHERICHIA COLI	157-184	488-515								
PHSM ECOLI	MALTODEXTRIN PHOSPHORYLASE	ESCHERICHIA COLI	71-108									
PILA NEIGO	PROB SIGNAL RECOGNITION PARTICLE PROTEIN	NEISSERIA GONORRHOEAE	17-68									
PILB PSEAE	FIMBRIAL ASSEMBLY PROTEIN PILB	PSEUDOMONAS AERUGINOSA	16-60									
PILC PSEAE	PILC PROTEIN	PSEUDOMONAS AERUGINOSA	143-170									
PILD NEIGO	LEADER PEPTIDASE	NEISSERIA GONORRHOEAE	110-137									
PILQ PSEAE	FIMBRIAL ASSEMBLY PROTEIN PILQ PRECURSOR	PSEUDOMONAS AERUGINOSA	71-115	639-666								
PILS PSEAE	SENSOR PROTEIN PILS	PSEUDOMONAS AERUGINOSA	9-46									
PILR ECOLI	PI PROTEIN	ESCHERICHIA COLI	156-188									
PIV MORBO	PILIN GENE INVERTING PROTEIN	MORAXELLA BOVIS	42-69	152-182								
PIV MORLA	PILIN GENE INVERTING PROTEIN	MORAXELLA LACUNATA	152-182									
PLC BACCE	PHOSPHODIESTERASE PRECURSOR	BACILLUS CEREUS	217-245									
PLC BACTU	PHOSPHODIESTERASE PRECURSOR	BACILLUS THURINGIENSIS	216-245									
PLC LISMO	PHOSPHODIESTERASE PRECURSOR	LISTERIA MONOCYTOGENES	218-265									
PLSC ECOLI	ACYLTRANSFERASE	ESCHERICHIA COLI	106-133									
PLSX ECOLI	PLSX PROTEIN	ESCHERICHIA COLI	241-270									
PPLYD ERWCA	PECTIN LYASE	ERWINIA CAROTOVORA	27-92									
PNBA ECOLI	PNBA PROTEIN	ESCHERICHIA COLI	9-50									
PNBE ERWCH	PECTINESTERASE PRECURSOR	ERWINIA CHRYSANTHEMI	60-87									
PNBY ECOLI	PHOSPHOGLYCERATE MUTASE	ESCHERICHIA COLI	82-116									
PNBY ZYMM	PHOSPHOGLYCERATE MUTASE	ZYMONOMAS MOBILIS	13-40	80-110								
PNP ECOLI	POLYRIBONUC NUCLEOTIDYL TRANSF	ESCHERICHIA COLI	260-294									
PNIC SALTU	PNIC PROTEIN	SALMONELLA TYPHIMURUM	176-205									
PODX BACSY	PYRUVATE ORTHOPHOSPHATE DIKINASE	BACTEROIDES SYMBIOSUS	51-78									
PORF PSESY	OUTER MEMBRANE PORIN F PRECURSOR	PSEUDOMONAS SYRINGAE	111-138									
PORP PSEAE	PORIN O PRECURSOR	PSEUDOMONAS AERUGINOSA	390-424									
PORP PSEAE	PORIN P PRECURSOR	PSEUDOMONAS AERUGINOSA	139-181	260-287	360-396							
PROD ECOLI	BINDING PROTEIN PRECURSOR	ESCHERICHIA COLI	320-347									
PNITE ECOLI	PUTRISCIN:ORNITHINE ANTIPUTRIN	ESCHERICHIA COLI	91-118									
PROXB ECOLI	PYRUVATE DEHYDROGENASE	ESCHERICHIA COLI	8-38									
PPB1 BACSU	ALKALINE PHOSPHATASE III PRECURSOR	BACILLUS SUBTILIS	109-150	431-460								
PPB4 BACSU	ALKALINE PHOSPHATASE IV PRECURSOR	BACILLUS SUBTILIS	85-123	316-363								
PPB ECOLI	ALKALINE PHOSPHATASE PRECURSOR	ESCHERICHIA COLI	235-262									
PPB ESCFE	ALKALINE PHOSPHATASE PRECURSOR	ESCHERICHIA FERGUSONII	236-263									
PPCE FLAME	PROLYL ENDOPEPTIDASE PRECURSOR	FLAVOBACTERIUM MENINGOSEPTICUM	158-199									
PPCF FLAME	PROLYL ENDOPEPTIDASE PRECURSOR	FLAVOBACTERIUM MENINGOSEPTICUM	158-199									
PPCK ECOLI	PHOSPHOENOLPYRUVATE CARBOXYKINASE	ESCHERICHIA COLI	45-72									

PCGENE	10111714	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
ELLENANR	PROTEIN	ORGANISM	71-107								
PPDA CLOPE	PROTEIN A PRECURSOR	CLOSTRIDIUM PERFRINGENS	49-76								
PPPSA ECOLI	PHOSPHENOLPYRUVATE SYNTHASE	ESCHERICHIA COLI	371-398								
PPQO2 ACICA	COENZYME PQQ SYNTHESIS PROTEIN II	ACINETOBACTER CALCOACETICUS	49-76								
PPRCA ANAYA	CALCIUM DEPENDENT PROTEINASE PRECURSOR	ANABAENA VARIABILIS	371-398								
PPRCA THEAC	PROTEASOME, ALPHA SUBUNIT	THIENOPHOSPHATA ACIDOPHILUM	88-115								
PPRC ECOLI	TAIL-SPECIFIC PROTEINASE PRECURSOR	ESCHERICHIA COLI	158-192								
PPREJ STAAU	PLASMID RECOMBINATION ENZYME	STAPHYLOCOCCUS AUREUS	27-28	152-179	264-147						
PPREJ STAAU	PLASMID RECOMBINATION ENZYME	STAPHYLOCOCCUS AUREUS	48-75	181-208	310-161	366-393					
PPREA LACPL	PLASMID RECOMBINATION ENZYME	LACTOBACILLUS PLANTARUM	37-71	291-318							
PPRE BACLI	REGULATORY PROTEIN	BACILLUS LICHENIFORMIS	2-40								
PPRE BACSF	PLASMID RECOMBINATION ENZYME	BACILLUS SP	181-224	288-345							
PPRE STRAG	PLASMID RECOMBINATION ENZYME	STREPTOCOCCUS AGALACTIAE	385-319	372-339	420-454						
PPRFA LISMO	LISTERIOLYSIN REGULATORY PROTEIN	LISTERIA MONOCYTOGENES	76-110	173-204							
PPRIA ECOLI	PRIMOSOMAL PROTEIN N	ESCHERICHIA COLI	218-245								
PPRIM BACSU	DNA PRIMASE	BACILLUS SUBTILIS	383-433								
PPRIM BUCAP	DNA PRIMASE	BUCHNERA AFRICANICA	11-43	282-319							
PPRIM CLOAB	DNA PRIMASE	CLOSTRIDIUM ACETOBUTYLICUM	87-114								
PPRIM LACLA	DNA PRIMASE	LACTOCOCCUS LACTIS	269-296								
PPRIM RICPR	DNA PRIMASE	RICKETTSIA PROWAZEKII	10-37	245-286	477-504	526-593					
PPRIS DESDE	PRISMALIN PROTEIN	DESULFOVIBRIO DESULFURICANS	30-57								
PPRLB AGHLY	BETA-LYTIC METALLOENDOPEPTIDASE	ACHROMOBACTER LYTIUS	317-344								
PPRLB LYSEN	BETA-LYTIC METALLOENDOPEPTIDASE	LYSOBACTER ENZYMOGENES	121-148								
PPROI LISMO	ZINC METALLOPROTEINASE PRECURSOR	LISTERIA MONOCYTOGENES	111-145	275-316							
PPRO2 LISMO	ZINC METALLOPROTEINASE PRECURSOR	LISTERIA MONOCYTOGENES	111-145								
PPROA SERMA	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE	SEBASTIA MARGESCENS	309-336								
PPROA STAAU	PROTEIN A PRECURSOR	STAPHYLOCOCCUS AUREUS	2-29								
PPROB SERMA	GLUTAMATE KINASE	SERRATIA MARCESCENS	7-34								
PPROB STRAG	PROTEIN B	STREPTOCOCCUS AGALACTIAE	58-85								
PPROC PSEAE	PYRROLINE-5-CARBOXYLATE REDUCTASE	PSEUDOMONAS AERUGINOSA	148-175								
PPROH BACSU	PYRROLINE-5-CARBOXYLATE REDUCTASE HOMOL	BACILLUS SUBTILIS	200-227								
PPROP ECOLI	PROLINBETAINE TRANSPORTER	ESCHERICHIA COLI	460-487								
PPROV ECOLI	PERIPHERAL MEMBRANE PROTEIN PROV	ESCHERICHIA COLI	24-34								
PPROV SALTU	PERIPHERAL MEMBRANE PROTEIN PROV	SALMONELLA TYPHIMURUM	24-34								
PPRBB ECOLI	PRBB PROTEIN	ESCHERICHIA COLI	170-197								
PPRBC ECOLI	ANTICODON NUCLEASE	ESCHERICHIA COLI	282-309								
PPRBD ECOLI	PRBD PROTEIN	ESCHERICHIA COLI	278-305								
PPRSA DACSU	PROTEIN EXPORT PROTEIN PRSA PRECURSOR	BACILLUS SUBTILIS	52-87	95-157							
PPRTA STRGR	PROTEIN A PRECURSOR	STREPTOMYCES GRISEUS	56-110								
PPRTC ERWCH	SECRETED PROTEINASE C PRECURSOR	ERWINIA CHRYSANTHEMI	103-130								
PPRTD ERWCH	COLLAGENASE PRECURSOR	ERWINIA CHRYSANTHEMI	285-312								
PPRTD ERWCH	PROTEASES SECRETION PROTEIN PRTD	ERWINIA CHRYSANTHEMI	378-355								
PPRTE DACNO	EXTRACELLULAR SERINE PROTEINASE PRECURSOR	DACTEROIDES NODORUS	106-133	210-263	146-184						
PPRTE ERWCH	PROTEINASE SECRETION PROTEIN PRTE	ERWINIA CHRYSANTHEMI	108-135	158-192	231-290						
PPRTT ERWCH	PROTEASES SECRETION PROTEIN PRTT	ERWINIA CHRYSANTHEMI	280-310								
PPRTM LACLA	PROTEASE MATURATION PROTEIN PRECURSOR	LACTOCOCCUS LACTIS	76-103	112-139							
PPRTM LACPL	PROTEASE MATURATION PROTEIN PRECURSOR	LACTOCOCCUS LACTIS	76-103	112-139							
PPRTM LACPL	PROTEASE MATURATION PROTEIN PRECURSOR	LACTOCOCCUS LACTIS	76-103	112-139							
PPRTS SERMA	EXTRACELLULAR SERINE PROTEINASE PRECURSOR	SERRATIA MARCESCENS	304-331	376-407	1007-1041						
PPRXT ERWCH	SECRETED PROTEINASE C PRECURSOR	SERRATIA MARCESCENS	304-331	376-407	1007-1041						
PPSAA SYNEN	CHLOROPHYLL A APOPROTEIN A1	ERWINIA CHRYSANTHEMI	314-341								
PPSAA SYNEN	CHLOROPHYLL A APOPROTEIN A1	SYNECHOCOCCUS ELONGATUS NAEGEL	120-147								
PPSAA SYNEN	CHLOROPHYLL A APOPROTEIN A1	SYNECHOCOCCUS SP	109-136	326-356							
PPSAA SYNEN	CHLOROPHYLL A APOPROTEIN A1	SYNECHOCOCCUS VULCANUS	120-147								
PPSAA SYNEN	CHLOROPHYLL A APOPROTEIN A1	SYNECHOCYSTIS SP	44-71	120-147	318-368						
PPSAD YERPE	CYANOPHYLL A APOPROTEIN A1	YERSINIA PESTIS	244-271								
PPSAD SYNEN	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II	SYNECHOCOCCUS SP	11-38								
PPSAE YERPE	PSAE PROTEIN PRECURSOR	YERSINIA PESTIS	66-118								





PCGENE	10717114	Proteolytic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PPYD BACSU	DIHYDROOROTATE DEHYDROGENASE	SALMONELLA TYPHIMURUM	115-142	181-210							
PPYD BACSU	CTP SYNTHASE	BACILLUS SUBTILIS	275-302	372-349							
PPYD BACSU	9.7 KD LINKER POLYPEPTIDE	FREMITELLA DIPLOSPITION	21-48								
PPYD BACSU	QUINONE OXIDOREDUCTASE	ESCHERICHIA COLI	180-215								
PPYD BACSU	QUEUOSINE BIOSYNTHESIS PROTEIN QUESA	ESCHERICHIA COLI	224-261								
PPYD BACSU	14.2 KD PROTEIN IN RUBREDOXIN OPERON	CLOSTRIDIUM PASTEURIANUM	231-50	157-232							
PPYD BACSU	RACC PROTEIN	ESCHERICHIA COLI	5-32								
PPYD BACSU	ASPARTATE RACEMASE	STREPTOCOCCUS THERMOPHILUS	152-189								
PPYD BACSU	PROBABLE AMINO ACID RACEMASE	BACILLUS SUBTILIS	132-162								
PPYD BACSU	ALPHA-GALACTOSIDASE	ESCHERICHIA COLI	86-116								
PPYD BACSU	RAFFINOSE INVERTASE	ESCHERICHIA COLI	348-375								
PPYD BACSU	RIBOSE TRANSPORT SYSTEM COMPONENT	ESCHERICHIA COLI	65-99	195-222							
PPYD BACSU	RIBOKINASE	ESCHERICHIA COLI	200-239								
PPYD BACSU	RIBITOL (RBT) OPERON REPRESSOR	KLISHELLA AEROGINES	6-47								
PPYD BACSU	BIOSYNTHESIS ACTIVATION PROTEIN A	ESCHERICHIA COLI	170-197								
PPYD BACSU	BIOSYNTHESIS ACTIVATION PROTEIN A	ERWINIA AMYLOVORA	92-119	174-201							
PPYD BACSU	BIOSYNTHESIS ACTIVATION PROTEIN A	ERWINIA STEWARTII	174-201								
PPYD BACSU	BIOSYNTHESIS ACTIVATION PROTEIN A	KLISHELLA AEROGINES	168-203								
PPYD BACSU	CAPSULE SYNTHESIS B COMPONENT	ESCHERICHIA COLI	14-41	159-186							
PPYD BACSU	RECA PROTEIN	LEGIONELLA PNEUMOPHILA	262-310								
PPYD BACSU	RECA PROTEIN	ACHILLEPLASMA LAIDLAVII	281-310								
PPYD BACSU	RECA PROTEIN	AGROBACTERIUM TURIDAGIENS	3-30	132-159	281-308						
PPYD BACSU	RECA PROTEIN	ANABAEAE VARIABILIS	372-349								
PPYD BACSU	RECA PROTEIN	AQUIFEX PYROPHILUS	61-90	126-151							
PPYD BACSU	RECA PROTEIN	BACTERIOIDES FRAGILIS	108-135								
PPYD BACSU	RECA PROTEIN	BACILLUS SUBTILIS	262-294								
PPYD BACSU	RECA PROTEIN	BRUCELLA ABORTUS	3-30	132-159	240-307						
PPYD BACSU	RECA PROTEIN	BURKHOLDERIA CEPACIA	75-109								
PPYD BACSU	RECA PROTEIN	ERWINIA CAROTOVORA	284-311								
PPYD BACSU	RECA PROTEIN	LACTOBACILLUS DELBRUECKII	20-47								
PPYD BACSU	RECA PROTEIN	LACTOCOCCUS HELVETICUS	20-47								
PPYD BACSU	RECA PROTEIN	LACTOCOCCUS LACTIS	131-162	232-269	288-315						
PPYD BACSU	RECA PROTEIN	METHYLOHONAS CLARA	266-303								
PPYD BACSU	RECA PROTEIN	METHYLOHONAS CLARA	276-303								
PPYD BACSU	RECA PROTEIN	MYCOPLASMA PULMONIS	30-57								
PPYD BACSU	RECA PROTEIN	MYCOBACTERIUM TUBERCULOSIS	249-276								
PPYD BACSU	RECA PROTEIN	NEISSERIA GONORRHOICAE	261-310								
PPYD BACSU	RECA PROTEIN	PROTEUS MIRABILIS	283-310								
PPYD BACSU	RECA PROTEIN	PSEUDOMONAS AERUGINOSA	282-309								
PPYD BACSU	RECA PROTEIN	RHIZOBIUM LEGUMINOSARUM	3-30	131-158	210-307						
PPYD BACSU	RECA PROTEIN	RHIZOBIUM LEGUMINOSARUM	119-146	268-295							
PPYD BACSU	RECA PROTEIN	RHIZOBIUM MELIOTTI	119-146	268-295							
PPYD BACSU	RECA PROTEIN	RHODOBACTER SPHAEROIDES	119-146								
PPYD BACSU	RECA PROTEIN	STREPTOCOCCUS PNEUMONIAE	134-161	291-317							
PPYD BACSU	RECA PROTEIN	SYNECHOCOCCUS SP	124-151								
PPYD BACSU	RECA PROTEIN	VIBRIO CHOLERAE	290-317								
PPYD BACSU	RECA PROTEIN	BACILLUS SUBTILIS	4-31	178-205							
PPYD BACSU	RECA PROTEIN	ESCHERICHIA COLI	82-109	147-174							
PPYD BACSU	RECA PROTEIN	PROTEUS MIRABILIS	86-113								
PPYD BACSU	RECA PROTEIN	PSEUDOMONAS PUTIDA	84-111								
PPYD BACSU	RECA PROTEIN	SALMONELLA TYPHIMURUM	147-174								
PPYD BACSU	EXONUCLEASE RECI	ESCHERICHIA COLI	52-79								
PPYD BACSU	RECOMBINATION PROTEIN	BACILLUS SUBTILIS	21-48	156-184	192-247	290-316	344-378				
PPYD BACSU	DNA HELICASE RECO	ESCHERICHIA COLI	468-495								
PPYD BACSU	GTP PYROPHOSPHOKINASE	ESCHERICHIA COLI	680-707								
PPYD BACSU	REPLICATION AND MAINTENANCE PROTEIN	BACILLUS SUBTILIS	2-36	81-108							
PPYD BACSU	REPLICATION AND MAINTENANCE PROTEIN	STAPHYLOCOCCUS AUREUS	2-36	81-108							



PCGENE	10717844	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
ELCNAME	PROLIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PREMA STAP	REPLICATION AND MAINTENANCE PROTEIN	STAPHYLOCOCCUS EPIDERMIDIS	2-36	81-108								
PREP1 ECOLI	REPLICATION PROTEIN REPA	ESCHERICHIA COLI	30-77	90-117								
PREPA BACSU	REPA PROTEIN	BACILLUS SUBTILIS	142-173									
PREPA ECOLI	REPA PROTEIN	ESCHERICHIA COLI	91-118	228-235								
PREPA NEIGO	REPLICATION PROTEIN	NEISSERIA GONORRHOEAE	57-84	138-172								
PREPB LACPL	REPLICATION PROTEIN REPB	LACTOBACILLUS PLANTARUM	184-211									
PREPM STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	254-284									
PREPN STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	258-285									
PREPR STRAG	REPR PROTEIN	STREPTOCOCCUS AGALACTIAE	410-467									
PREPS STRY	REPS PROTEIN	STREPTOCOCCUS PYOGENES	423-467									
PREPX STAAU	REP PROTEIN	STAPHYLOCOCCUS AUREUS	111-150	172-210								
PREPY ECOLI	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	288-315									
PREPZ CLOPE	REPLICATION PROTEIN	CLOSTRIDIUM PERFRINGENS	168-195	297-324	341-375							
PREP ECOLI	REP HELICASE	ESCHERICHIA COLI	119-146	205-243								
PREP LACPL	REP PROTEIN	LACTOBACILLUS PLANTARUM	119-199	260-287								
PRESP CLOPE	RESOL VASE	CLOSTRIDIUM PERFRINGENS	68-102	151-185								
PRET1 BACSU	PROBABLE PEPTIDE CHAIN RELEASE FACTOR 1	BACILLUS SUBTILIS	34-68									
PRET2 ECOLI	PEPTIDE CHAIN RELEASE FACTOR 2	ESCHERICHIA COLI	86-113	163-204								
PRET3 SALTY	PEPTIDE CHAIN RELEASE FACTOR 3	SALMONELLA TYPHIMURIUM	86-113	163-204								
PRET ECOLI	PEPTIDE CHAIN RELEASE FACTOR 3	ESCHERICHIA COLI	180-210	403-473								
PRFAB ECOLI	1,6-GALACTOSYLTRANSFERASE	ESCHERICHIA COLI	199-226									
PRFAG ECOLI	BIOSYNTHESIS PROTEIN RFAG	ESCHERICHIA COLI	185-212									
PRFAJ ECOLI	1,2-GLUCOSYLTRANSFERASE	ESCHERICHIA COLI	39-66	233-268								
PRFAJ SALTY	1,2-GLUCOSYLTRANSFERASE	SALMONELLA TYPHIMURIUM	68-95	145-172	236-263							
PRFAK SALTY	1,2-N-ACETYLGLUCOSAMINOTRANSFERASE	SALMONELLA TYPHIMURIUM	333-369									
PRFAL ECOLI	O-ANTIGEN LIGASE	ESCHERICHIA COLI	366-393									
PRFAL SALTY	O-ANTIGEN LIGASE	SALMONELLA TYPHIMURIUM	326-360									
PRFAP ECOLI	BIOSYNTHESIS PROTEIN RFAP	ESCHERICHIA COLI	8-35									
PRFAS ECOLI	BIOSYNTHESIS PROTEIN RFAS	ESCHERICHIA COLI	63-89	184-240								
PRFAZ ECOLI	BIOSYNTHESIS PROTEIN RFAY	ESCHERICHIA COLI	18-45									
PRFAZ ECOLI	BIOSYNTHESIS PROTEIN RFAY	ESCHERICHIA COLI	3-30	85-112								
PRFBB SALTY	DTDP-GLUCOSE 4,6-DEHYDRATASE	SALMONELLA TYPHIMURIUM	320-359									
PRFBM SALTY	MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE	SALMONELLA TYPHIMURIUM	213-361									
PRFBS SALTY	PARATOSE SYNTHASE	SALMONELLA TYPHIMURIUM	22-56	205-232								
PRFEA VIBAN	PRECUSOR FOR YERKIN ANGUINACTIN	VIBRIO ANGUILLARUM	349-376									
PRFPH ECOLI	PEPTIDE CHAIN RELEASE FACTOR HOMOLOG	ESCHERICHIA COLI	83-110									
PRG12 BAGTU	PUTATIVE G12 SITE-SPECIFIC RECOMBINASE	BACILLUS THURINGIENSIS	15-68	190-262	310-383							
PRHAB ECOLI	RHAMNULOXINASE	ESCHERICHIA COLI	175-202									
PRHAB SALTY	RHAMNULOXINASE	SALMONELLA TYPHIMURIUM	175-202									
PRHAR ECOLI	L-RHAMNOSE OPERON TRANSACTIVATOR	ESCHERICHIA COLI	10-41									
PRHAS ECOLI	L-RHAMNOSE OPERON REG PROTEIN RHAS	ESCHERICHIA COLI	152-179									
PRHIR RHILV	RHIR REGULATORY PROTEIN	RHIZOBIUM LEGUMINOSARUM	206-233									
PRHUB ECOLI	RNA HELICASE RHLBANDRA	ESCHERICHIA COLI	118-165									
PRHUB BORBU	TRANS TERM FACTOR RHO	BORDELLIA BURGDORFERI	215-242	327-360								
PRHUP BACSU	PROTEASE PROD REG PROTEIN HPR	BACILLUS SUBTILIS	82-109									
PRHSA ECOLI	RHSA PROTEIN PRECURSOR	ESCHERICHIA COLI	667-694									
PRHSB ECOLI	RHSB PROTEIN PRECURSOR	ESCHERICHIA COLI	667-694									
PRHSC ECOLI	RHSC PROTEIN PRECURSOR	ESCHERICHIA COLI	380-414	667-694	1056-1083							
PRHSD ECOLI	RHSD PROTEIN PRECURSOR	ESCHERICHIA COLI	671-712	1071-1098								
PRHSE ECOLI	RHSE PROTEIN	ESCHERICHIA COLI	345-372									
PRHUL ECOLI	ACETYLTRANSFERASE	ESCHERICHIA COLI	91-127									
PRHUR ECOLI	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE	ESCHERICHIA COLI	167-194									
PRHUR ECOLI	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE	PHOTOBACTERIUM LEIOGNATHII	2-47	131-158								
PRISA PHOLE	RIBOFLAVIN SYNTHASE ALPHA CHAIN	BACILLUS SUBTILIS	8-35									
PRISB BACSU	RIBOFLAVIN SYNTHASE BETA CHAIN	BACILLUS SUBTILIS	14-41									
PRISB PHOLE	RIBOFLAVIN SYNTHASE BETA CHAIN	PHOTOBACTERIUM LEIOGNATHII	14-41									
PRIT0 STRAT	S65 RIBOSOMAL PROTEIN L10	STREPTOCOCCUS ANTITRITICUS	14-72	106-133								
PRIT12 SYNRY	S65 RIBOSOMAL PROTEIN L12	SYNECHOCYSTIS SP	2-34									

FCGENE	10741744	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PR12 THIMA	305 RIBOSOMAL PROTEIN L12	THERMOTOGA NARITIMA	8-35	56-86								
PR14 BACST	305 RIBOSOMAL PROTEIN L14	BACILLUS STEAROTHERMOPHILUS	18-45									
PR14 MICLU	305 RIBOSOMAL PROTEIN L14	MICROCOCCUS LUTEUS	18-45									
PR14 MYCCA	305 RIBOSOMAL PROTEIN L14	MYCOPLASMA CAPRICOLUM	51-92									
PR15 BACLI	305 RIBOSOMAL PROTEIN L15	BACILLUS LICHENIFORMIS	21-48									
PR15 BACST	305 RIBOSOMAL PROTEIN L15	BACILLUS STEAROTHERMOPHILUS	95-114									
PR15 BACSU	305 RIBOSOMAL PROTEIN L15	BACILLUS SUBTILIS	95-122									
PR15 CHLTR	305 RIBOSOMAL PROTEIN L15	CITRAMIDIA TRACHIONATIS	110-144									
PR15 ECOLI	305 RIBOSOMAL PROTEIN L15	ESCHERICHIA COLI	79-113									
PR15 LACLA	305 RIBOSOMAL PROTEIN L15	LACTOCOCCUS LACTIS	8-35									
PR15 NIETVA	305 RIBOSOMAL PROTEIN L15	METHANOCOCCUS VANNIELII	64-102									
PR15 MYCCA	305 RIBOSOMAL PROTEIN L15	MYCOPLASMA CAPRICOLUM	61-135									
PR18 BACST	305 RIBOSOMAL PROTEIN L18	BACILLUS STEAROTHERMOPHILUS	31-58									
PR18 CHLTR	305 RIBOSOMAL PROTEIN L18	CITRAMIDIA TRACHIONATIS	32-86									
PR18 HALMA	305 RIBOSOMAL PROTEIN L18	HALOARCTIA MARISORTUI	40-107									
PR18 MYCCA	305 RIBOSOMAL PROTEIN L18	MYCOPLASMA CAPRICOLUM	61-83									
PR19 ECOLI	305 RIBOSOMAL PROTEIN L19	ESCHERICHIA COLI	25-52									
PR19 HALMA	305 RIBOSOMAL PROTEIN L19	HALOARCTIA MARISORTUI	101-128									
PR19 NIETVA	305 RIBOSOMAL PROTEIN L19	METHANOCOCCUS VANNIELII	45-72									
PR19 PROVU	305 RIBOSOMAL PROTEIN L19	PROTEUS VULGARIS	159-194									
PR17 SULSO	305 RIBOSOMAL PROTEIN L17	SULFOLOBUS SOLFATARICUS	5-32	184-211								
PR20 ECOLI	305 RIBOSOMAL PROTEIN L20	ESCHERICHIA COLI	14-41									
PR20 MYCPE	305 RIBOSOMAL PROTEIN L20	MYCOPLASMA FERNENTANS	14-41									
PR20 MYCST	305 RIBOSOMAL PROTEIN L20	BACILLUS SUBTILIS	4-38									
PR21 BACSU	305 RIBOSOMAL PROTEIN L21	ESCHERICHIA COLI	28-55									
PR22 ECOLI	305 RIBOSOMAL PROTEIN L22	METHANOCOCCUS VANNIELII	30-57									
PR23 NIETVA	305 RIBOSOMAL PROTEIN L23	MYCOPLASMA CAPRICOLUM	32-59									
PR23 MYCCA	305 RIBOSOMAL PROTEIN L23	HALOARCTIA MARISORTUI	48-75									
PR24 HALMA	305 RIBOSOMAL PROTEIN L24	METHANOCOCCUS VANNIELII	61-90									
PR24 NIETVA	305 RIBOSOMAL PROTEIN L24	MICROCOCCUS LUTEUS	36-63									
PR24 CHLTR	305 RIBOSOMAL PROTEIN L24	CITRAMIDIA TRACHIONATIS	19-66									
PR29 ECOLI	305 RIBOSOMAL PROTEIN L29	ESCHERICHIA COLI	36-63									
PR29 MYCST	305 RIBOSOMAL PROTEIN L29	MYCOPLASMA CAPRICOLUM	39-83									
PR29 MYCCA	305 RIBOSOMAL PROTEIN L29	BACILLUS STEAROTHERMOPHILUS	141-168									
PR2 BACST	305 RIBOSOMAL PROTEIN L2	MYCOPLASMA CAPRICOLUM	144-198									
PR2 MYCCA	305 RIBOSOMAL PROTEIN L2	THERMUS AQUATICUS	38-65									
PR2 THETH	305 RIBOSOMAL PROTEIN L2	BACILLUS STEAROTHERMOPHILUS	79-106									
PR2 BACST	305 RIBOSOMAL PROTEIN L2	ESCHERICHIA COLI	19-46									
PR2 ECOLI	305 RIBOSOMAL PROTEIN L2	METHANOCOCCUS VANNIELII	129-159									
PR2 MYCVA	305 RIBOSOMAL PROTEIN L2	BACILLUS STEAROTHERMOPHILUS	47-77									
PR2 ECOLI	305 RIBOSOMAL PROTEIN L2	ESCHERICHIA COLI	122-149									
PR10 HALCU	ACIDIC RIBOSOMAL PROTEIN PO HOMOLOG	HALOBACTERIUM CUTIHUUMI	138-182									
PR10 HALHA	ACIDIC RIBOSOMAL PROTEIN PO HOMOLOG	HALOBACTERIUM HALOBUTUM	138-182									
PR10 HALMA	ACIDIC RIBOSOMAL PROTEIN PO HOMOLOG	HALOARCTIA MARISORTUI	64-91	133-184								
PR10 MYCVA	ACIDIC RIBOSOMAL PROTEIN PO HOMOLOG	METHANOCOCCUS VANNIELII	194-221									
PR1 HALCU	RIBOSOMAL PROTEIN 'A'	HALOPHILIC EUBACTERIUM NRCC 41227	59-86									
PR1 HALHA	305 RIBOSOMAL PROTEIN L20	HALOBACTERIUM HALOBUTUM	2-29									
PR1 HALMA	305 RIBOSOMAL PROTEIN L17	HALOARCTIA MARISORTUI	2-29									
PR1 NIETVA	RIBOSOMAL PROTEIN 'A'	METHANOCOCCUS VANNIELII	2-29									
PR1 MICRU	705 RIBOSOMAL PROTEIN MA	MICROCOCCUS LUTEUS	58-82	90-117								
PR1 SALTY	43 KD RELAXATION PROTEIN	SALMONELLA TYPHIMURUM	226-260									
PR1 STAAU	RLX PROTEIN	STAPHYLOCOCCUS AUREUS	3-30	102-132	177-218	266-300						
PR2 SALTY	32 KD RELAXATION PROTEIN	SALMONELLA TYPHIMURUM	19-53									
PR2 STAAU	RLX PROTEIN	STAPHYLOCOCCUS AUREUS	3-30	102-133	261-295							
PR3 STAAU	RLX PROTEIN	STAPHYLOCOCCUS AUREUS	3-30	146-216								
PRX SULSO	305 RIBOSOMAL PROTEIN LX	SULFOLOBUS SOLFATARICUS	32-62									
PRNIN DIACAM	RIBONUCLEASE PRECURSOR	BACILLUS AMYLOLIQUEFACIENS	33-67	120-156								

PCGENE	10711784	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
ELLENANIE	PROTEIN	ORGANISMI	1037	117-144							
PRNC_ECOLI	RIBONUCLEASE III	ESCHERICHIA COLI	1037	117-144							
PRNE_ECOLI	RIBONUCLEASE E	ESCHERICHIA COLI	413-440	628-662							
PRNP7_BUCSU	RIBONUCLEASE P PROTEIN COMPONENT	BUCHNERA APHIDICOLA	85-114								
PRNPH_BACSU	RIBONUCLEASE PH	BACILLUS SUBTILIS	159-186								
PRNS_ECOLI	REGULATORY PROTEIN RNS	ESCHERICHIA COLI	116-160								
PRN_BACCI	RIBONUCLEASE	BACILLUS CIRCULANS	82-109								
PRN_BACIN	RIBONUCLEASE PRECURSOR	BACILLUS INTERMEDIUS	38-72								
PRP20_BACTK	RNA POLYMERASE SIGMA-28 FACTOR PRECURSOR	BACILLUS THURINGIENSIS	72-107								
PRP22_GITFR	RNA POLYMERASE SIGMA-33 FACTOR	CITROBACTER FREUNDII	30-57								
PRP23_BACTK	RNA POLYMERASE SIGMA-33 FACTOR PRECURSOR	BACILLUS THURINGIENSIS	8-35	61-90							
PRP34_ALCEU	RNA POLYMERASE SIGMA-34 FACTOR	ALCALIGENES EUTROPHIUS	229-266								
PRP34_AZOC	RNA POLYMERASE SIGMA-34 FACTOR	AZORHIZOBIIUM CAULINODANS	174-208								
PRP34_BACSU	RNA POLYMERASE SIGMA-34 FACTOR	BACILLUS SUBTILIS	16-43	97-124	274-308	398-423					
PRP34_BRAJA	RNA POLYMERASE SIGMA-34 FACTOR 1	BRADYRHIZOBIIUM JAPONICUM	97-124								
PRP34_KLEPN	RNA POLYMERASE SIGMA-34 FACTOR	KLEBSIELLA PNEUMONIAE	148-182								
PRP34_RHOCA	RNA POLYMERASE SIGMA-34 FACTOR	RHODOBACTER CAPSULATUS	135-185								
PRP35_BRAJA	RNA POLYMERASE SIGMA-34 FACTOR 2	BRADYRHIZOBIIUM JAPONICUM	145-172								
PRP3M_ALCEU	PROBABLE SIGMA(34) MODULATION PROTEIN	ALCALIGENES EUTROPHIUS	21-51								
PRP3M_ECOLI	PROBABLE SIGMA(34) MODULATION PROTEIN	ESCHERICHIA COLI	21-67								
PRP3M_SALTY	PROBABLE SIGMA(34) MODULATION PROTEIN	SALMONELLA TYPHIMURUM	21-67								
PRP70_BUCAP	RNA POLYMERASE SIGMA-70 FACTOR	BUCHNERA APHIDICOLA	69-96	109-136	172-217	228-255	301-337				
PRP70_CHLTR	RNA POLYMERASE SIGMA-70 FACTOR	CHLAMYDIA TRACHOMATIS	5-32								
PRP70_ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	ESCHERICHIA COLI	327-361								
PRP70_PSEAE	RNA POLYMERASE SIGMA-70 FACTOR	PSEUDOMONAS AERUGINOSA	334-368								
PRP70_RICPR	RNA POLYMERASE SIGMA-70 FACTOR	RICKETTSIA PROVAZEEKII	244-321	348-382							
PRP80_MYXXA	RNA POLYMERASE SIGMA-80 FACTOR	MYXOCOCCUS XANTHIUS	208-235	318-347	359-386						
PRPCE_SYNPF	BILIN BIOSYNTHESIS PROTEIN RPEF	SYNECHOCOCCUS SP	180-207								
PRPDA_BACSU	DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN	BACILLUS SUBTILIS	55-107								
PRPDA_ECOLI	DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN	ESCHERICHIA COLI &	57-105								
PRPDA_HALHA	DNA-DIRECTED RNA POLYMERASE SUBUNIT A	SALMONELLA TYPHIMURUM	861-904								
PRPDA_HALMO	DNA-DIRECTED RNA POLYMERASE SUBUNIT A	HALOBACTERIUM HALOBIIUM	239-270								
PRPDA_METH	DNA-DIRECTED RNA POLYMERASE SUBUNIT A	HALOCOCCUS MORRUIAE	229-270								
PRPDA_SULAC	DNA-DIRECTED RNA POLYMERASE SUBUNIT A	METHANOBACTERIUM THERMAUTOTROPICUM	218-245	486-513	642-669						
PRPDA_THECE	DNA-DIRECTED RNA POLYMERASE SUBUNIT A	SULFOLOBUS ACIDOCALDARIUS	222-256	500-537	691-720						
PRPDB_ECOLI	DNA-DIRECTED RNA POLYMERASE BETA CHAIN	THERMOCOCCUS CELER	238-262								
PRPDB_MYCLE	DNA-DIRECTED RNA POLYMERASE BETA CHAIN	ESCHERICHIA COLI	599-626	1011-1038							
PRPDB_SALTY	DNA-DIRECTED RNA POLYMERASE BETA CHAIN	MYCOBACTERIUM LEPRAE	733-760	1034-1111							
PRPDB_SULAC	DNA-DIRECTED RNA POLYMERASE BETA CHAIN	SALMONELLA TYPHIMURUM	599-626								
PRPDB_THEMA	DNA-DIRECTED RNA POLYMERASE BETA CHAIN	SULFOLOBUS ACIDOCALDARIUS	160-187	958-985	1011-1038						
PRPDC_ANASP	DNA-DIRECTED RNA POLYMERASE GAMMA CHAIN	THERMOTOGA MARITIMA	350-377	255-282	314-361	827-861					
PRPDC_ECOLI	DNA-DIRECTED RNA POLYMERASE BETA CHAIN	ANABAENA SP	152-194								
PRPDC_HALHA	DNA-DIRECTED RNA POLYMERASE SUBUNIT C	ESCHERICHIA COLI	786-813	948-994	1231-1257						
PRPDC_HALMO	DNA-DIRECTED RNA POLYMERASE SUBUNIT C	HALOBACTERIUM HALOBIIUM	175-202								
PRPDC_THALHA	DNA-DIRECTED RNA POLYMERASE SUBUNIT C	HALOCOCCUS MORRUIAE	27-54	117-144	202-234						
PRPDC_MYCLE	DNA-DIRECTED RNA POLYMERASE BETA CHAIN	METHANOBACTERIUM THERMAUTOTROPICUM	58-85	272-302	327-354						
PRPDC_NOSCO	DNA-DIRECTED RNA POLYMERASE GAMMA CHAIN	MYCOBACTERIUM LEPRAE	273-300	860-887	911-938	1131-1158					
PRPDC_SULAC	DNA-DIRECTED RNA POLYMERASE SUBUNIT A*	NOSTOC COMMUNE	150-192								
PRPDC_THECE	DNA-DIRECTED RNA POLYMERASE SUBUNIT A*	SULFOLOBUS ACIDOCALDARIUS	36-63	172-214	224-251						
PRPDD_NOSCO	DNA-DIRECTED RNA POLYMERASE DELTA CHAIN	THERMOCOCCUS CELER	21-58								
PRPDD_ECOLI	DNA-DIRECTED RNA POLYMERASE DELTA CHAIN	NOSTOC COMMUNE	72-116	402-449	539-566						
PRPDD_HALHA	DNA-DIRECTED RNA POLYMERASE SIGMA-E FACTOR	ESCHERICHIA COLI	5-39								
PRPDD_THALHA	DNA-DIRECTED RNA POLYMERASE SUBUNIT B*	ESCHERICHIA COLI	281-308								
PRPSA_AGITU	RNA POLYMERASE SIGMA-A FACTOR	HALOBACTERIUM HALOBIIUM	91-118								
PRPSA_ANASP	RNA POLYMERASE SIGMA-A FACTOR	AGROBACTERIUM TUMEFACIENS	310-347	397-427							
PRPSA_CLOAB	RNA POLYMERASE SIGMA-A FACTOR	ANABAENA SP	71-105								
PRPSA_STRAU	RNA POLYMERASE SIGMA-A FACTOR	CLOSTRIDIUM ACETOBUTYLICUM	2-29								
		STREPTOMYCES AUREOFACIENS	278-305								





PCGENE	10717144	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PSAK	PROTIN	ORGANISMI	30-107	224-231	790-724						
PSAK	BACSU	BACILLUS SUBTILIS									
PSAP	STRATU	STREPTOCOCCUS MUTANS	122-276	281-463	538-565	576-610	1071-1091	1155-1182	1377-1430		
PSAP	BACSU	REGULATORY PROTEIN	4-31	172-199							
PSAP	BACSU	BACILLUS SUBTILIS	55-82	226-267							
PSAP	BACSU	BACILLUS SUBTILIS	12-39								
PSAP	BACSU	BACILLUS SUBTILIS	82-109	153-182							
PSAP	BACSU	BACILLUS SUBTILIS	195-222								
PSAP	BACSU	BACILLUS SUBTILIS	637-664								
PSAP	BACSU	BACILLUS SUBTILIS	278-305								
PSAP	BACSU	BACILLUS SUBTILIS	590-617								
PSAP	BACSU	BACILLUS SUBTILIS	159-186								
PSAP	BACSU	BACILLUS SUBTILIS	301-328								
PSAP	BACSU	BACILLUS SUBTILIS	21-65	107-141	394-428						
PSAP	BACSU	BACILLUS SUBTILIS	151-178	358-385	465-518	579-570	860-904				
PSAP	BACSU	BACILLUS SUBTILIS	32-39								
PSAP	BACSU	BACILLUS SUBTILIS	21-59	101-128							
PSAP	BACSU	BACILLUS SUBTILIS	68-95								
PSAP	BACSU	BACILLUS SUBTILIS	63-104								
PSAP	BACSU	BACILLUS SUBTILIS	61-104								
PSAP	BACSU	BACILLUS SUBTILIS	131-173	178-287	295-483	565-592	676-710	1081-1131			
PSAP	BACSU	BACILLUS SUBTILIS	125-152								
PSAP	BACSU	BACILLUS SUBTILIS	66-93								
PSAP	BACSU	BACILLUS SUBTILIS	90-119	172-199	280-311						
PSAP	BACSU	BACILLUS SUBTILIS	90-117	264-291							
PSAP	BACSU	BACILLUS SUBTILIS	47-74								
PSAP	BACSU	BACILLUS SUBTILIS	36-63								
PSAP	BACSU	BACILLUS SUBTILIS	183-210								
PSAP	BACSU	BACILLUS SUBTILIS	209-236	281-308							
PSAP	BACSU	BACILLUS SUBTILIS	209-236								
PSAP	BACSU	BACILLUS SUBTILIS	209-236								
PSAP	BACSU	BACILLUS SUBTILIS	435-462	572-583	605-639						
PSAP	BACSU	BACILLUS SUBTILIS	40-67	89-116	121-148	554-597					
PSAP	BACSU	BACILLUS SUBTILIS	37-74								
PSAP	BACSU	BACILLUS SUBTILIS	61-94								
PSAP	BACSU	BACILLUS SUBTILIS	64-91								
PSAP	BACSU	BACILLUS SUBTILIS	191-222								
PSAP	BACSU	BACILLUS SUBTILIS	91-118								
PSAP	BACSU	BACILLUS SUBTILIS	36-63	250-277							
PSAP	BACSU	BACILLUS SUBTILIS	197-224								
PSAP	BACSU	BACILLUS SUBTILIS	86-117								
PSAP	BACSU	BACILLUS SUBTILIS	197-224								
PSAP	BACSU	BACILLUS SUBTILIS	197-224								
PSAP	BACSU	BACILLUS SUBTILIS	55-108	613-654	741-768						
PSAP	BACSU	BACILLUS SUBTILIS	62-89								
PSAP	BACSU	BACILLUS SUBTILIS	449-476								
PSAP	BACSU	BACILLUS SUBTILIS	112-139								
PSAP	BACSU	BACILLUS SUBTILIS	357-387	725-752	790-821						
PSAP	BACSU	BACILLUS SUBTILIS	310-357								
PSAP	BACSU	BACILLUS SUBTILIS	49-76	351-386							
PSAP	BACSU	BACILLUS SUBTILIS	405-432								
PSAP	BACSU	BACILLUS SUBTILIS	7-34								
PSAP	BACSU	BACILLUS SUBTILIS	340-367	407-441							
PSAP	BACSU	BACILLUS SUBTILIS	546-573	607-634	744-771						
PSAP	BACSU	BACILLUS SUBTILIS	344-381	487-514							
PSAP	BACSU	BACILLUS SUBTILIS	378-403								
PSAP	BACSU	BACILLUS SUBTILIS	1010-1037								

PCGENE	10717814	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PSY1_ECOLI	LYSYL-TRNA SYNTHETASE	ESCHERICHIA COLI	201-310								
PSY2_ECOLI	LYSYL-TRNA SYNTHETASE, HEAT INDUCIBLE	ESCHERICHIA COLI	43-72	283-310							
PSY3_ECOLI	LEUCYL-TRNA SYNTHETASE	ESCHERICHIA COLI	220-247								
PSY4_ECOLI	METHIONYL-TRNA SYNTHETASE	BACILLUS STEAROTHERIOPHILUS	69-99								
PSY5_ECOLI	METHIONYL-TRNA SYNTHETASE	ESCHERICHIA COLI	87-124								
PSY6_ECOLI	PROLYL-TRNA SYNTHETASE	ESCHERICHIA COLI	541-568								
PSY7_ECOLI	GLUTAMINYL-TRNA SYNTHETASE	ESCHERICHIA COLI	394-421								
PSY8_ECOLI	SYRD PROTEIN	PSEUDOMONAS SYRINGAE	449-483								
PSY9_ECOLI	ARGINYL-TRNA SYNTHETASE	ESCHERICHIA COLI	500-574								
PSY10_ECOLI	THREONYL-TRNA SYNTHETASE	BACILLUS SUBTILIS	401-428	605-639							
PSY11_ECOLI	VALYL-TRNA SYNTHETASE	BACILLUS STEAROTHERIOPHILUS	601-630	809-843							
PSY12_ECOLI	VALYL-TRNA SYNTHETASE	ESCHERICHIA COLI	300-327	883-912	924-951						
PSY13_ECOLI	TRYPHANYL-TRNA SYNTHETASE	BACILLUS STEAROTHERIOPHILUS	204-231	239-266							
PSY14_ECOLI	TYROSYL-TRNA SYNTHETASE 1	BACILLUS SUBTILIS	81-115	375-409							
PSY15_ECOLI	TYROSYL-TRNA SYNTHETASE 2	BACILLUS SUBTILIS	69-96								
PSY16_ECOLI	TYROSYL-TRNA SYNTHETASE	BACILLUS CALDOTENAX	295-322	372-416							
PSY17_ECOLI	TYROSYL-TRNA SYNTHETASE	ESCHERICHIA COLI	126-167	405-432							
PSY18_ECOLI	ENZYME ECOR1240 1 M PROTEIN	ESCHERICHIA COLI	405-432	485-512							
PSY19_ECOLI	ENZYME ECOR1240 R PROTEIN	ESCHERICHIA COLI	30-57	624-651	702-736	768-795	843-870	966-1000			
PSY20_ECOLI	ENZYME ECOR1240 R PROTEIN	ESCHERICHIA COLI	158-263								
PSY21_ECOLI	ENZYME ECOR1240 1 SPECIFICITY PROTEIN	ESCHERICHIA COLI	154-181								
PSY22_ECOLI	ENZYME ECOR1240 1 SPECIFICITY PROTEIN	ESCHERICHIA COLI	279-306								
PSY23_ECOLI	ENZYME ECOR1240 1 SPECIFICITY PROTEIN	ESCHERICHIA COLI	278-312								
PSY24_ECOLI	ENZYME ECOD1 SPECIFICITY PROTEIN	ESCHERICHIA COLI	249-283								
PSY25_ECOLI	ENZYME ECOD1 SPECIFICITY PROTEIN	ESCHERICHIA COLI	279-306								
PSY26_ECOLI	ENZYME ECOD1 SPECIFICITY PROTEIN	SALMONELLA POTSDAM	396-423								
PSY27_ECOLI	ENZYME ECOD1 SPECIFICITY PROTEIN	SALMONELLA TYPHIMURUM	194-221	276-304	402-429						
PSY28_ECOLI	TYPE II RESTRICTION ENZYME ACCI	ESCHERICHIA COLI	138-196	265-295	406-440	639-682	687-728	926-954			
PSY29_ECOLI	TYPE II RESTRICTION ENZYME BSUI	ACINETOBACTER CALCOACETICUS	49-76								
PSY30_ECOLI	TYPE II RESTRICTION ENZYME BSUI	BACILLUS SUBTILIS	1-43	135-223	236-280						
PSY31_ECOLI	TYPE II RESTRICTION ENZYME BSUI	BACILLUS SUBTILIS	1-45	338-384	401-440	532-559					
PSY32_ECOLI	TYPE II RESTRICTION ENZYME CFBI	CITROBACTER FREUNDII	35-62								
PSY33_ECOLI	TYPE II RESTRICTION ENZYME HGCI	HEPOTOSIPHON AURANTIACUS	176-215								
PSY34_ECOLI	TYPE II RESTRICTION ENZYME HGCI	HEPOTOSIPHON AURANTIACUS	243-273								
PSY35_ECOLI	TYPE II RESTRICTION ENZYME DDEI	DESULFOVIBRIO DESULFURICANS	85-122								
PSY36_ECOLI	TYPE II RESTRICTION ENZYME DPN1	STREPTOCOCCUS PNEUMONIAE	213-240								
PSY37_ECOLI	TYPE II RESTRICTION ENZYME EORI	ESCHERICHIA COLI	2-29								
PSY38_ECOLI	TYPE II RESTRICTION ENZYME EORI	ESCHERICHIA COLI	333-360								
PSY39_ECOLI	TYPE II RESTRICTION ENZYME EORI	ESCHERICHIA COLI	128-155	214-241							
PSY40_ECOLI	TYPE II RESTRICTION ENZYME FOKI	FLAVOBACTERIUM ORKANOITIS	302-336								
PSY41_ECOLI	TYPE II RESTRICTION ENZYME HIN1	HAEMOPHILUS INFLUENZAE	6-38	40-96							
PSY42_ECOLI	TYPE II RESTRICTION ENZYME HIN1	HAEMOPHILUS INFLUENZAE	77-125								
PSY43_ECOLI	TYPE II RESTRICTION ENZYME HPA1	HAEMOPHILUS PARAHYDROPHILUS	23-50								
PSY44_ECOLI	TYPE II RESTRICTION ENZYME HPA1	HAEMOPHILUS PARAHYDROPHILUS	97-138								
PSY45_ECOLI	TYPE II RESTRICTION ENZYME HPA1	HAEMOPHILUS INFLUENZAE	18-45	178-203							
PSY46_ECOLI	TYPE II RESTRICTION ENZYME KPN1	KLERSIELLA PNEUMONIAE	15-61	187-215	225-232						
PSY47_ECOLI	TYPE II RESTRICTION ENZYME MBO1	MORAXELLA BOVIS	3-30	158-185	337-364						
PSY48_ECOLI	TYPE II RESTRICTION ENZYME MBO1	MORAXELLA BOVIS	105-151								
PSY49_ECOLI	TYPE II RESTRICTION ENZYME MBO1	MORAXELLA BOVIS	117-144	231-238							
PSY50_ECOLI	TYPE II RESTRICTION ENZYME MTHZ1	NEISSERIA GONORRHOEAE	532	41-68	395-446						
PSY51_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS	206-243	258-288							
PSY52_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS	70-102								
PSY53_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS	144-181								
PSY54_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS	61-88								
PSY55_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS	147-181	203-237							
PSY56_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS	37-71	25-102	236-296	378-405					
PSY57_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS	63-89	256-283							
PSY58_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY59_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY60_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY61_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY62_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY63_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY64_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY65_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY66_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY67_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY68_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY69_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY70_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY71_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY72_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY73_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY74_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY75_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY76_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY77_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY78_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY79_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY80_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY81_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY82_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY83_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY84_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY85_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY86_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY87_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY88_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY89_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY90_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY91_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY92_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY93_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY94_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY95_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY96_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY97_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY98_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY99_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									
PSY100_ECOLI	TYPE II RESTRICTION ENZYME SSO1	STREPTOCOCCUS SANGUIS									



PGENE	1011124.4	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PTA17 TREPA	47 KD MEMBRANE ANTIGEN PRECURSOR	TREPONEMA PALLIDUM	76-53								
PTA33 TREDE	53 KD MEMBRANE ANTIGEN A PRECURSOR	TREPONEMA DENTICOLA	99-126	298-329							
PTAC3 BACAL	ALVEOLYIN PRECURSOR	BACILLUS ALVEI	272-302	374-401							
PTAC3 CLOPE	PERFRINGOLYIN O PRECURSOR	CLOSTRIDIUM PERFRINGENS	370-311	372-434							
PTAC3 LISV	IVANOLYIN PRECURSOR	LISTERIA IVANOVII	91-120	167-195	396-423						
PTAC3 LISMO	LISTERIOLYIN O PRECURSOR	LISTERIA MONOCYTOGENES	98-123	168-196	295-329	397-424					
PTAC3 LISSE	SEELIGERIOLYIN PRECURSOR	LISTERIA SEELIGERI	99-126	296-323	340-376	398-463					
PTAC3 STRN	PNEUMOLYIN	STREPTOCOCCUS PNEUMONIAE	234-272								
PTAC3 STRY	STREPTOLYIN O PRECURSOR	STREPTOCOCCUS PYOGENES	86-133	355-382	410-470						
PTAGB BACSU	TECHOIC ACID BIOSYNTHESIS PROTEIN B PREC	BACILLUS SUBTILIS	42-69								
PTAGC BACSU	TECHOIC ACID BIOSYNTHESIS PROTEIN C	BACILLUS SUBTILIS	348-375								
PTAGE BACSU	TECHOIC ACID BIOSYNTHESIS PROTEIN E	BACILLUS SUBTILIS	59-93	144-181	185-243	565-592	600-627				
PTAGE BACSU	TECHOIC ACID BIOSYNTHESIS PROTEIN F	BACILLUS SUBTILIS	182-209								
PTBPI NEGO	TRANSFERIN-BINDING PROTEIN I PRECURSOR	NEISSERIA GONORRHOEA	39-73	137-164	398-425	810-841					
PTBUD PSEP	PHENOL 2-MONOXYGENASE	PSEUDOMONAS PICKETTII	38-65	227-254	375-402						
PTCDT SALT	TRANSCRIPTIONAL REGULATORY PROTEIN TCOT	SALMONELLA TYPHIMURUM	105-132								
PTCPB VIBCH	MEMBRANE PROTEIN TCPC PRECURSOR	VIBRIO CHOLERAE	20-47	83-128	199-233	263-290	344-375	439-486			
PTCPB VIBCH	TCP PILUS BIOSYNTHESIS PROTEIN TCPE	VIBRIO CHOLERAE	24-59	77-111							
PTCPH VIBCH	TCP PILUS SECRETION PROTEIN TCPF	VIBRIO CHOLERAE	32-66	211-238							
PTCPH VIBCH	TCP PILUS BIOSYNTHESIS PROTEIN TCPH	VIBRIO CHOLERAE	95-122								
PTCPN VIBCH	TCP PILUS BIOSYNTHESIS PROTEIN TCPI	VIBRIO CHOLERAE	25-52	234-261	279-306	346-379					
PTCPO VIBCH	TCP PILUS VIRULENCE REGULATORY PROTEIN	VIBRIO CHOLERAE	48-75								
PTCPY VIBCH	TCP PILUS BIOSYNTHESIS PROTEIN TCPY	VIBRIO CHOLERAE	220-257								
PTCPZ VIBCH	TCP PILUS BIOSYNTHESIS PROTEIN TCPZ	VIBRIO CHOLERAE	121-148								
PTCR2 BACSU	TETRACYCLINE RESISTANCE PROTEIN	BACILLUS SUBTILIS	44-55								
PTCR2 BACSU	TETRACYCLINE RESISTANCE PROTEIN	BACILLUS SUBTILIS	404-434								
PTCR BACST	TETRACYCLINE RESISTANCE PROTEIN	BACILLUS STEAROTHERIOPHILUS	422-453								
PTCR STAAU	TETRACYCLINE RESISTANCE PROTEIN	STAPHYLOCOCCUS AUREUS	404-431								
PTCR STRAG	TETRACYCLINE RESISTANCE PROTEIN	STREPTOCOCCUS AGALACTIAE	422-453								
PTCR STRN	TETRACYCLINE RESISTANCE PROTEIN	STREPTOCOCCUS PNEUMONIAE	422-453								
PTDCA ECOLI	TDCA BC OPERON TRANSCRIPTIONAL ACTIVATOR	ESCHERICHIA COLI	210-239								
PTDCC ECOLI	TDCC PROTEIN	ESCHERICHIA COLI	334-361								
PTEB8 STRY	TRYPAN-RESIST SURFACE T6 PROTEIN PREC	STREPTOCOCCUS PYOGENES	137-164	361-395	400-437						
PTER1 ECOLI	TETRACYCLINE REPRESSOR PROTEIN CLASS B	ESCHERICHIA COLI	8-16								
PTER4 ECOLI	TETRACYCLINE REPRESSOR PROTEIN CLASS D	ESCHERICHIA COLI	183-210								
PTER4 ALGSP	TELLURIUM RESISTANCE PROTEIN TERA	ALCALIGENES SP	48-86								
PTES9 ECOLI	ACTL-COA THIOESTERASE II	ESCHERICHIA COLI	4-31								
PTET3 ENTFA	TETRACYCLINE RESISTANCE PROTEIN TETM	ENTEROCOCCUS FAECALIS	2-36	130-159	179-206	217-244					
PTET9 ENTFA	TETRACYCLINE RESISTANCE PROTEIN TETM	ENTEROCOCCUS FAECALIS	2-36	130-159	317-244	260-287					
PTETC ECOLI	TRANSPOSIN TNO TETC PROTEIN	ESCHERICHIA COLI	72-106	116-158							
PTETM STRLI	TETRACYCLINE RESISTANCE PROTEIN	STREPTOMYCES LIVIDANS	82-109								
PTETM UREUR	TETRACYCLINE RESISTANCE PROTEIN TETM	UREAPLASMA UREALYTICUM	2-36	130-159	217-244	260-287					
PTETO CAMCO	TETRACYCLINE RESISTANCE PROTEIN TETO	CAMPYLOBACTER JEJUNI	2-29								
PTETO CAMIE	TETRACYCLINE RESISTANCE PROTEIN TETO	CAMPYLOBACTER JEJUNI	2-26								
PTETO STRMU	TETRACYCLINE RESISTANCE PROTEIN TETO	STREPTOCOCCUS NITANS	2-29								
PTETX BACFR	TETRACYCLINE RESISTANCE PROTEIN	BACTEROIDES FRAGILIS	35-62								
PTETX CLOTE	TETANUS TOXIN PRECURSOR	CLOSTRIDIUM TETANI	274-304	540-567	615-642	692-719	983-1012	1240-1277			
PTFD0 PYRWO	TRANS INITIATION FACTOR IIB HOMOLOG	PYROCOCCUS WOESSEI	218-258								
PTFDC ALCEU	CHLOROACETOL 1,2-DIOXYGENASE	ALCALIGENES EUTROPHUS	2-33								
PTGT ECOLI	QUEUINE TRNA-RIBOSYLTRANSFERASE	ESCHERICHIA COLI	173-200								
PTHD1 LACLA	THREONINE DEHYDRATASE BIOSYNTHETIC	ESCHERICHIA COLI	267-303								
PTHD2 ECOLI	THREONINE DEHYDRATASE CATABOLIC	ESCHERICHIA COLI	291-320								
PTHD3 BACSU	FURAN OXIDATION PROTEIN THDF	BACILLUS SUBTILIS	153-180	192-226	282-316	391-418					
PTHD4 ECOLI	FURAN OXIDATION PROTEIN THDF	ESCHERICHIA COLI	226-260	404-431							
PTHD5 PSEPU	FURAN OXIDATION PROTEIN THDF	PSEUDOMONAS PUTIDA	226-260								
PTHER BACCE	THERMOLYIN	BACILLUS CEREUS	4-38	240-267							
PTHER BACST	THERMOLYIN PRECURSOR	BACILLUS STEAROTHERIOPHILUS	45-72								



PCGENE	1071171.4	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
FILENAME	PROTEIN	ORGANISM	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PTHER_BACTH	THERMOLYSIN	BACILLUS THERMOPROTEOLYTICUS	86-113								
PTHER_THERU	THERMITASE	THERMOACTINOMYCES VULGARIS	131-161								
PTHIC_ECOLI	THIC PROTEIN	ESCHERICHIA COLI	312-263	301-218							
PTHIC_ECOLI	THIC PROTEIN	ESCHERICHIA COLI	138-165								
PTHIC_ECOLI	THIC PROTEIN	SULFOLOBUS ACIDICOLARIUS	135-172	199-233							
PTHIC_ECOLI	THIC PROTEIN	BREVIDACTERIUM LACTOFERMENTUM	288-315								
PTHIC_ECOLI	THIC PROTEIN	SACCHAROPOLYSPORA ERYTHRAEA	68-96								
PTHIC_ECOLI	THIC PROTEIN	ESCHERICHIA COLI	184-171								
PTHIC_ECOLI	THIC PROTEIN	TREPONEMA PALLIDUM	236-266								
PTHIC_ECOLI	THIC PROTEIN	TREPONEMA PALLIDUM	44-71								
PTHIC_ECOLI	THIC PROTEIN	TREPONEMA PALLIDUM	41-68								
PTHIC_ECOLI	THIC PROTEIN	ESCHERICHIA COLI	74-108								
PTHIC_ECOLI	THIC PROTEIN	STAPHYLOCOCCUS AUREUS	322-349								
PTHIC_ECOLI	THIC PROTEIN	ENTEROCOCCUS FAECALIS	59-97	111-138							
PTHIC_ECOLI	THIC PROTEIN	STAPHYLOCOCCUS AUREUS	151-178								
PTHIC_ECOLI	THIC PROTEIN	STAPHYLOCOCCUS AUREUS	589-625								
PTHIC_ECOLI	THIC PROTEIN	BACILLUS THURINGIENSIS	7-62	174-201							
PTHIC_ECOLI	THIC PROTEIN	ESCHERICHIA COLI	99-126	510-537							
PTHIC_ECOLI	THIC PROTEIN	ESCHERICHIA COLI	32-59	314-341							
PTHIC_ECOLI	THIC PROTEIN	ESCHERICHIA COLI	319-366								
PTHIC_ECOLI	THIC PROTEIN	ESCHERICHIA COLI	403-490								
PTHIC_ECOLI	THIC PROTEIN	ESCHERICHIA COLI	36-60								
PTHIC_ECOLI	THIC PROTEIN	PSEUDOMONAS PUTIDA	119-153								
PTHIC_ECOLI	THIC PROTEIN	PSEUDOMONAS PUTIDA	179-213								
PTHIC_ECOLI	THIC PROTEIN	PSEUDOMONAS PUTIDA	143-170								
PTHIC_ECOLI	THIC PROTEIN	ESCHERICHIA COLI	101-138								
PTHIC_ECOLI	THIC PROTEIN	ESCHERICHIA COLI	184-178	184-211							
PTHIC_ECOLI	THIC PROTEIN	SYNECHOCOCCUS SP	203-230								
PTHIC_ECOLI	THIC PROTEIN	ESCHERICHIA COLI	797-824								
PTHIC_ECOLI	THIC PROTEIN	BORDETELLA PERTUSSIS	179-206								
PTHIC_ECOLI	THIC PROTEIN	BORDETELLA PERTUSSIS	58-85								
PTHIC_ECOLI	THIC PROTEIN	CLOSTRIDIUM DIFFICILE	20-48	99-159							
PTHIC_ECOLI	THIC PROTEIN	PSEUDOMONAS AERUGINOSA	470-497	133-163	199-241	825-869	923-950	1334-1388	1403-1433	1506-1565	1716-1747
PTHIC_ECOLI	THIC PROTEIN	CLOSTRIDIUM DIFFICILE	38-72								
PTHIC_ECOLI	THIC PROTEIN	VIBRIO CHOLERAE	13-40								
PTHIC_ECOLI	THIC PROTEIN	TREPONEMA PALLIDUM	106-143								
PTHIC_ECOLI	THIC PROTEIN	ESCHERICHIA COLI	83-110								
PTHIC_ECOLI	THIC PROTEIN	MORAXELLA SP	139-166								
PTHIC_ECOLI	THIC PROTEIN	PORPHYROMONAS GINGIVALIS	117-144								
PTHIC_ECOLI	THIC PROTEIN	AGROBACTERIUM TUMEFACIENS	239-266	501-529							
PTHIC_ECOLI	THIC PROTEIN	AGROBACTERIUM TUMEFACIENS	239-266	501-529							
PTHIC_ECOLI	THIC PROTEIN	PSEUDOMONAS SYRINGAE	41-68								
PTHIC_ECOLI	THIC PROTEIN	STAPHYLOCOCCUS AUREUS	58-113								
PTHIC_ECOLI	THIC PROTEIN	STAPHYLOCOCCUS AUREUS	11-38	58-113							
PTHIC_ECOLI	THIC PROTEIN	ESCHERICHIA COLI	721-755								
PTHIC_ECOLI	THIC PROTEIN	RHIZOBIUM MELILOTI	179-206								
PTHIC_ECOLI	THIC PROTEIN	STAPHYLOCOCCUS AUREUS	33-60	68-95							
PTHIC_ECOLI	THIC PROTEIN	ESCHERICHIA COLI	181-208	308-340	720-754						
PTHIC_ECOLI	THIC PROTEIN	ESCHERICHIA COLI	51-78	200-227	231-238						
PTHIC_ECOLI	THIC PROTEIN	SHIGELLA SONNEI	729-756								
PTHIC_ECOLI	THIC PROTEIN	ESCHERICHIA COLI	159-186								
PTHIC_ECOLI	THIC PROTEIN	MYCOBACTERIUM TUBERCULOSIS	281-308	419-446							
PTHIC_ECOLI	THIC PROTEIN	BACILLUS THURINGIENSIS	281-308	419-446							
PTHIC_ECOLI	THIC PROTEIN	BACILLUS THURINGIENSIS	431	45-72							
PTHIC_ECOLI	THIC PROTEIN	STAPHYLOCOCCUS AUREUS	281-308	419-446							
PTHIC_ECOLI	THIC PROTEIN	BACILLUS THURINGIENSIS	93-127	509-539							

PGCENE	1011714	Protein Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12
ELUAMAF	PROTEIN	ORGANISMI	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12
PTRA_PSEAE	TRANSPORSE	PSEUDOMONAS AERUGINOSA	127-134	721-755										
PTRB1_ECOLI	TRAB PROTEIN	ESCHERICHIA COLI	113-143											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	12-39											
PTRE1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	70-97											
PTRC1_ECOLI	TRAC1 PROTEIN	ESCHERICHIA COLI	1006-1038											
PTRC2_ECOLI	TRAC2 PROTEIN	ESCHERICHIA COLI	1102-1149											
PTRC3_ECOLI	TRAC3 PROTEIN	ESCHERICHIA COLI	844-931											
PTRD1_ECOLI	TRAD PROTEIN	ESCHERICHIA COLI	297-348											
PTRE1_ECOLI	PERIPLASTIC TREHALASE PRECURSOR	ESCHERICHIA COLI	362-403	477-508										
PTREC_ECOLI	ANYLOTREHALASE	ESCHERICHIA COLI	280-307											
PTRE1_ECOLI	TRFA TRANSCRIPTIONAL REPRESSOR PROTEIN	ESCHERICHIA COLI	5-12	105-132										
PTRE1_ECOLI	TRAG PROTEIN	ESCHERICHIA COLI	91-88	630-657	831-858	865-895								
PTRC3_ECOLI	TRAG PROTEIN	ESCHERICHIA COLI	196-223											
PTRC6_ECOLI	TRAG PROTEIN	ESCHERICHIA COLI	195-222	318-345										
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	155-209	397-424	882-914	1350-1377								
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	155-209	397-424	882-914	1350-1377								
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	47-74	328-371										
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	36-63											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	5-12											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	107-137											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	115-142	226-253										
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	220-247											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	241-275											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	176-203											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	79-113											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	76-103	218-245										
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	172-199											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	83-117											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	77-104	164-191										
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	56-83											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	229-256											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	205-232											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	148-175											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	346-376											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	223-250	260-294										
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	205-232											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	3-29											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	33-60											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	165-226											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	142-191											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	145-179											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	139-166											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	191-218											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	143-183	298-328										
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	9-36	34-81										
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	12-39											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	4-31											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	5-32											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	4-31											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	12-39											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	5-32											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	9-43											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	5-32											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	147-174											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	83-119											
PTRE1_ECOLI	TRAI PROTEIN	ESCHERICHIA COLI	184-221											

PCGENE	10117184	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PTV1_SALT	TRAT PROTEIN	SALMONELLA TYPHIMURUM	10-57						
PTV1_STOR	TRATIN PRECURSOR	STREPTOMYCES GRISEUS	80-107						
PTSR_STRAZ	RNA METHYLTRANSFERASE	STREPTOMYCES AZUREUS	126-153						
PTST_STAAU	TOXIC SHOCK SYNDROME TOXIN-1 PRECURSOR	STAPHYLOCOCCUS AUREUS	29-63	102-129					
PTSX_ECOLI	CHANNEL-FORMING PROTEIN TSX PRECURSOR	ESCHERICHIA COLI	232-252						
PTTX_ECOLI	HYPOTHETICAL 24.3 KD PROTEIN	ESCHERICHIA COLI	81-113						
PTUS_ECOLI	SITE-BINDING PROTEIN	ESCHERICHIA COLI	57-91	107-134					
PTYA_BACBR	TYROCIDINE SYNTHETASE I	BACILLUS BREVIS	117-147	534-561	1019-1051				
PTYL_TREPE	ANTIGEN TYPE I	TREPONEMA PENTENUE	106-143						
PTYR_BACSU	POSSIBLE PREPHENATE DEHYDROGENASE	BACILLUS SUBTILIS	244-271	312-342					
PTYR_ECOLI	CHORISMATE MUTASE	ESCHERICHIA COLI	329-370						
PTYR_ECOLI	TRANSCRIPTIONAL REGULATORY PROTEIN TYR	ESCHERICHIA COLI	483-510						
PTYSY_LACCA	THYMIDYLATE SYNTHASE	LACTOBACILLUS CASEI	139-173						
PTYSY_LACLA	THYMIDYLATE SYNTHASE	LACTOCOCCUS LACTIS	75-109						
PTYSY_STAAU	THYMIDYLATE SYNTHASE	STAPHYLOCOCCUS AUREUS	69-96						
PUIPD_ECOLI	SENSOR PROTEIN UHPB	ESCHERICHIA COLI	276-303	316-343					
PUIPB_SALT	SENSOR PROTEIN UHPB	SALMONELLA TYPHIMURUM	276-303	316-343					
PUNUC_SALT	UNAC PROTEIN	SALMONELLA TYPHIMURUM	204-231						
PUPP_ECOLI	URACIL PHOSPHORIBOSYLTRANSFERASE	ESCHERICHIA COLI	30-57						
PURAA_ECOLI	URACIL PERMEASE	ESCHERICHIA COLI	330-384						
PUREI_HELPY	UREASE ALPHA SUBUNIT	HELICOBACTER PYLORI	13-42						
PUREI_PROMI	UREASE ALPHA SUBUNIT	PROTEUS MIRABILIS	72-99						
PUREI_PROVU	UREASE ALPHA SUBUNIT	PROTEUS VULGARIS	72-99						
PUREI_UREUR	UREASE ALPHA SUBUNIT	UREAPLASMA UREAALYTICUM	13-40	483-517					
PUREI_HELPY	UREASE BETA SUBUNIT	HELICOBACTER PYLORI	62-99						
PURED_HELPY	UREASE OPERON URED PROTEIN	HELICOBACTER PYLORI	17-44						
PUREE_PROMI	UREASE ACCESSORY PROTEIN UREE	PROTEUS MIRABILIS	57-84						
PUREF_XLEAE	UREASE ACCESSORY PROTEIN UREF PRECURSOR	KLEBSIELLA AEROGENES	20-47						
PUS49_LACLA	SECRETED 45 KD PROTEIN PRECURSOR	LACTOCOCCUS LACTIS	44-98	150-223	276-303				
PUSHA_ECOLI	P-SUGAR HYDROLASE PRECURSOR	ESCHERICHIA COLI	56-83						
PUSHA_SALT	SILENT PROTEIN USHA(0) PRECURSOR	SALMONELLA TYPHIMURUM	56-83						
PUVRA_ECOLI	EXCINUCLEASE ABC SUBUNIT A	ESCHERICHIA COLI	527-554	871-898					
PUVRA_MICLU	EXCINUCLEASE ABC SUBUNIT A	MICROCOCCUS LUTEUS	579-606	619-646	614-718	922-949			
PUVRA_PARDI	EXCINUCLEASE ABC SUBUNIT A	PARACOCCUS DENITRIFICANS	33-60						
PUVRC_BACSU	EXCINUCLEASE ABC SUBUNIT C	BACILLUS SUBTILIS	342-372	311-338					
PUVRC_ECOLI	EXCINUCLEASE ABC SUBUNIT C	ESCHERICHIA COLI	37-64	333-362					
PUVRD_ECOLI	HELICASE II	ESCHERICHIA COLI	280-307						
PVANA_ENTFC	VANCOMYCIN RESISTANCE PROTEIN VANA	ENTEROCOCCUS FAECIUM	182-209						
PVANC_ENTGA	VANCOMYCIN RESISTANCE PROTEIN VANC	ENTEROCOCCUS GALLINARUM	171-211						
PVIB4_AGR13	VIRB4 PROTEIN PRECURSOR	AGROBACTERIUM TUNIEFACIENS	138-172						
PVIB4_AGR13	VIRB4 PROTEIN	AGROBACTERIUM TUNIEFACIENS	190-227						
PVIB4_AGR16	VIRB6 PROTEIN	AGROBACTERIUM TUNIEFACIENS	190-227						
PVIB4_AGR19	VIRB6 PROTEIN	AGROBACTERIUM TUNIEFACIENS	190-227						
PVIBX_AGR13	VIRB10 PROTEIN	AGROBACTERIUM TUNIEFACIENS	32-59	212-239					
PVIBX_AGR16	VIRB10 PROTEIN	AGROBACTERIUM TUNIEFACIENS	32-59	212-239					
PVIBX_AGR19	VIRB10 PROTEIN	AGROBACTERIUM TUNIEFACIENS	32-59	212-239					
PVIC1_AGR16	VIRIC1 PROTEIN	AGROBACTERIUM RHIZOGONES TUNIEFACIENS	81-108						
PVIC1_AGR13	VIRIC1 PROTEIN	AGROBACTERIUM TUNIEFACIENS	81-108						
PVIC1_AGR16	VIRIC1 PROTEIN	AGROBACTERIUM TUNIEFACIENS	81-108						
PVIB4_AGR16	WIDE HOST RANGE (VHR) VIR4 PROTEIN	AGROBACTERIUM RHIZOGONES	149-176	265-292					
PVIB4_AGR16	WIDE HOST RANGE (VHR) VIR4 PROTEIN	AGROBACTERIUM TUNIEFACIENS	42-76	113-147	637-684				
PVIB4_AGR16	WIDE HOST RANGE (VHR) VIR4 PROTEIN	AGROBACTERIUM TUNIEFACIENS	42-69	84-125	637-680				
PVIB4_AGR19	WIDE HOST RANGE (VHR) VIR4 PROTEIN	AGROBACTERIUM TUNIEFACIENS	42-69	84-125	637-680				
PVIB4_SHIP	VIRB TRANSCRIPTIONAL ACTIVATOR	SHIGELLA FLEXNERI	37-71	107-134	187-214	252-291			
PVIBF_YEREN	VIRULENCE REGULON TRANSACTIVATOR	YERSINIA ENTEROCOLITICA	16-46						
PVIRG_AGR16	VIRG REGULATORY PROTEIN	AGROBACTERIUM RHIZOGONES	34-61						
PVIRL_AGR16	LIMITED HOST RANGE (LHR) VIR4 PROTEIN	AGROBACTERIUM TUNIEFACIENS	106-137						

PCGENE	10711314	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PVISC_ECOLI	VISC PROTEIN	ESCHERICHIA COLI	47-74							
PVLP1_MYCHR	VARIANT SURFACE ANTIGEN A PRECURSOR	MYCOPLASMA HYORUMINIS	74-112							
PVMD1_BORHE	OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR	BORRELIA HERMSII	54-81							
PVMD2_BORHE	OUTER MEMBRANE LIPOPROTEIN 7 PRECURSOR	BORRELIA HERMSII	372-339							
PVMD3_BORHE	OUTER MEMBRANE LIPOPROTEIN 21 PRECURSOR	BORRELIA HERMSII	310-337							
PVMD4_BORHE	OUTER MEMBRANE LIPOPROTEIN 24 PRECURSOR	BORRELIA HERMSII	47-143							
PVMD5_BORHE	OUTER MEMBRANE LIPOPROTEIN 35 PRECURSOR	BORRELIA HERMSII	315-316							
PVNF1_AZOVI	NITROGEN FIXATION PROTEIN VNF1	AZOTOBACTER VINELANDII	158-188	218-245						
PVNF2_AZOCH	NITROGENASE VANADIUM-IRON PROTEIN	AZOTOBACTER CIRCOCOCUM MCD 1	68-95							
PVNF3_AZOVI	NITROGENASE VANADIUM-IRON PROTEIN	AZOTOBACTER VINELANDII	68-95	372-403						
PVRP1_SALDU	65 KD VIRULENCE PROTEIN	SALMONELLA CHOLERAE-SUIS	509-536							
PVRP2_SALDU	65 KD VIRULENCE PROTEIN	SALMONELLA DUBLIN	511-538							
PVVB1_VIBVU	CTOLYIN SECRETION PROTEIN	SALMONELLA DUBLIN	31-36							
PWAF1_STRAD	WALL-ASSOCIATED PROTEIN PRECURSOR	STREPTOCOCCUS MUTANS	10-75							
PWRB1_ECOLI	TRP REPRESSOR BINDING PROTEIN	ESCHERICHIA COLI	4-41	311-316						
PXI91_ECOLI	X POLYPEPTIDE	ESCHERICHIA COLI	89-116							
PXI92_ECOLI	X POLYPEPTIDE	ESCHERICHIA COLI	104-131							
PXI93_ECOLI	X POLYPEPTIDE	ESCHERICHIA COLI	104-131							
PXISA_ANASP	EXCISEASE A	ANABAENA SP	4-31	89-116	135-162					
PXPB1_ECOLI	POSSIBLE INTEGRASE/RECOMBINASE XPRB	ESCHERICHIA COLI	268-293							
PXYLA_STAXY	XYLOSE ISOMERASE	STAPHYLOCOCCUS XYLOSUS	411-438							
PXYLK_KLAE	XYLOLASE KINASE	KLEBSIELLA AEROGES	2-29							
PXYLK_LACPE	XYLOLASE KINASE	LACTOBACILLUS PENTOSUS	52-79	211-218	260-287	246-273				
PXYLR_BACSU	XYLOSE REPRESSOR	BACILLUS SUBTILIS	4-31	96-130	209-236					
PXYLR_LACPE	XYLOSE REPRESSOR	LACTOBACILLUS PENTOSUS	73-102	260-287						
PXYLR_STAXY	XYLOSE REPRESSOR	STAPHYLOCOCCUS XYLOSUS	262-289							
PXYLZ_PSEPU	ELECTRON TRANSFER COMPONENT	PSEUDOMONAS PUTIDA	20-64	101-158	181-215	221-235	274-301			
PXYM1_CALSA	PUTATIVE ENDO-1,4-BETA-XYLANASE	CALDOCELLUM SACCHAROLYTICUM	51-78	104-131						
PXYNA_BACCI	O-1,4-BETA-XYLANASE PRECURSOR	BACILLUS CIRCULANS	198-225							
PXYNA_BACG3	ENDO-1,4-BETA-XYLANASE PRECURSOR	BACILLUS SP	47-74							
PXYNA_BACSU	ENDO-1,4-BETA-XYLANASE PRECURSOR	BACILLUS SUBTILIS	173-200							
PXYNA_CALSA	ENDO-1,4-BETA-XYLANASE A PRECURSOR	CALDOCELLUM SACCHAROLYTICUM	47-74							
PXYNA_PSEFL	ENDO-1,4-BETA-XYLANASE A PRECURSOR	PSEUDOMONAS FLUORESCENS	132-159	226-256						
PXYNB_BACPU	BETA-XYLOSIDASE	BACILLUS PUMILUS	33-82							
PXYNI_CALSA	BETA-XYLOSIDASE	CALDOCELLUM SACCHAROLYTICUM	459-486							
PXYNB_PSEFL	ENDO-1,4-BETA-XYLANASE PRECURSOR	PSEUDOMONAS FLUORESCENS	460-474							
PXYNC_PSEFL	ALPHA-L-ARABINOFURANOSIDASE C PRECURSOR	PSEUDOMONAS FLUORESCENS	51-78	251-278	317-344	475-502				
PXYNC_STRLI	ENDO-1,4-BETA-XYLANASE C PRECURSOR	STREPTOMYCES LIVIDANS	51-78	251-278						
PYIAK_HALLMO	HYPOTHETICAL 14.9 KD PROTEIN	HALOCOCCUS MORRHUAE	183-210							
PYJIK_STOR	HYPOTHETICAL 23.1 KD PROTEIN	STREPTOCOCCUS ORALIS	36-83							
PYJ6K_METSM	HYPOTHETICAL 36.7 KD PROTEIN	METHANOBREVIBACTER SMITHII	78-105							
PYAAC_ECOLI	HYPOTHETICAL 14.6 KD PROTEIN	ESCHERICHIA COLI	128-163	172-218						
PYAAG_PSEFL	HYPOTHETICAL 31.9 KD PROTEIN	PSEUDOMONAS FLUORESCENS	271-298							
PYAAM_ECOLI	HYPOTHETICAL 39.1 KD PROTEIN	ESCHERICHIA COLI	274-301							
PYAAQ_ECOLI	HYPOTHETICAL 36.6 KD PROTEIN	ESCHERICHIA COLI	352-379							
PYAB1_ECOLI	HYPOTHETICAL 28.3 KD PROTEIN	ESCHERICHIA COLI	155-182							
PYAB2_ECOLI	HYPOTHETICAL 34.9 KD PROTEIN	ESCHERICHIA COLI	131-158							
PYAB3_ECOLI	HYPOTHETICAL 39.7 KD PROTEIN	ESCHERICHIA COLI	448-480	627-634						
PYAB4_ECOLI	HYPOTHETICAL 63.9 KD PROTEIN	ESCHERICHIA COLI	478-455							
PYAD1_PSEAE	HYPOTHETICAL 21.9 KD PROTEIN	PSEUDOMONAS AERUGINOSA	48-75	150-177						
PYAD2_CLOAB	HYPOTHETICAL 21.6 KD PROTEIN	CLOSTRIDIUM ACETONUTYLICUM	75-109	114-144						
PYAD3_CLOAB	HYPOTHETICAL 36.9 KD PROTEIN	CLOSTRIDIUM ACETONUTYLICUM	132-159	165-196	210-237					
PYADA_YEREN	INVASIN PRECURSOR	YERSINIA ENTEROCOLITICA	21-55							
PYADA_YEPPS	INVASIN PRECURSOR	YERSINIA PSEUDOTUBERCULOSIS	198-210	247-274	318-381					
			255-282	297-360						

PCGENE	10/17/84	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PYADC ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	13-40	101-131							
PYAE8 ECOLI	17 KD PROTEIN	RICKETTSIA RICKETTSII	102-134								
PYAFD ECOLI	HYPOTHETICAL 29.4 KD PROTEIN	ESCHERICHIA COLI	221-248								
PYAFD ECOLI	HYPOTHETICAL 29.1 KD PROTEIN	ESCHERICHIA COLI	34-71								
PYAFD ECOLI	HYPOTHETICAL 21.0 KD PROTEIN	ESCHERICHIA COLI	123-150								
PYAFD ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA FERUGSONII	2-35								
PYAFD ECOLI	PUTATIVE AMIDASE	SALMONELLA TYPHIMURUM	72-100								
PYAFD ECOLI	HYPOTHETICAL 13.9 KD PROTEIN	SYNECHOCYSTIS SP	26-60								
PYAFD ECOLI	HYPOTHETICAL PUTATIVE ATP OPERON	MYCOBACTERIUM LEPRAE	23-57	511-538							
PYAFD ECOLI	HYPOL ATP-BINDING TRANSPORT PROTEIN	BACILLUS FIRMUS	211-238								
PYAFD ECOLI	HYPOTHETICAL PROTEIN	MYCOPLASMA GALLISEPTICUM	7-41								
PYAFD ECOLI	HYPOTHETICAL PROTEIN	MYCOPLASMA GALLISEPTICUM	29-56	60-87							
PYAFD ECOLI	HYPOTHETICAL 30 KD VIRULENCE PROTEIN	XANTHOMONAS CANIPESTRIS	68-98	199-226							
PYAFD ECOLI	HYPOTHETICAL 24.1 KD PROTEIN	ESCHERICHIA COLI	49-79								
PYAFD ECOLI	HYPOTHETICAL ABC TRANSPORTER	ESCHERICHIA COLI	6-69								
PYAFD ECOLI	HYPOTHETICAL 9.8 KD PROTEIN	ESCHERICHIA COLI	51-82								
PYAFD ECOLI	HYPOTHETICAL 14.1 KD PROTEIN	ESCHERICHIA COLI	97-124								
PYAFD ECOLI	HYPOTHETICAL 24.5 KD PROTEIN	ESCHERICHIA COLI	14-61								
PYAFD ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	18-65								
PYAFD ECOLI	HYPOTHETICAL 17.3 KD PROTEIN	BACTEROIDES UNIFORMIS	66-100								
PYAFD ECOLI	HYPOTHETICAL PROTEIN	BACILLUS LAUTUS	111-138								
PYAFD ECOLI	HYPOTHETICAL 22.9 KD PROTEIN	ESCHERICHIA COLI	52-79								
PYAFD ECOLI	HYPOTHETICAL PROTEIN	ALCALIGENES EUTROPHUS	21-48								
PYAFD ECOLI	HYPOTHETICAL 20.8 KD PROTEIN	ESCHERICHIA COLI	16-43								
PYAFD ECOLI	18.6 KD PROTEIN	ESCHERICHIA COLI	7-68	134-166							
PYAFD ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	35-62								
PYAFD ECOLI	HYPOTHETICAL 43.3 KD PROTEIN	ESCHERICHIA COLI	34-81								
PYAFD ECOLI	HYPOTHETICAL 29.1 KD PROTEIN	SYNECHOCOCUS SP	194-221								
PYAFD ECOLI	HYPOTHETICAL 28.0 KD PROTEIN	SYNECHOCOCUS SP	7-34	120-154							
PYAFD ECOLI	HYPOTHETICAL 19.5 KD PROTEIN	SYNECHOCYSTIS SP	272-308								
PYAFD ECOLI	HYPOTHETICAL PROTEIN	MASTIGOCLOADUS LAMINOSUS	2-29								
PYAFD ECOLI	HYPOTHETICAL PROTEIN	PSLEUDANABANA SP	180-407								
PYAFD ECOLI	HYPOTHETICAL 29.1 KD PROTEIN	BACILLUS THURINGIENSIS	42-74	153-180							
PYAFD ECOLI	HYPOTHETICAL PROTEIN PRECURSOR	ESCHERICHIA COLI	32-59								
PYAFD ECOLI	HYPOTHETICAL PROTEIN	BACILLUS SUBTILIS	3-30	59-86							
PYAFD ECOLI	HYPOTHETICAL 68.4 KD PROTEIN	HERPESIOSIPHON AURANTIACUS	12-39	151-178	160-416						
PYAFD ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	12-66	117-144	163-216	233-267	295-329	458-485	676-717	1136-1163	1499-1530
PYAFD ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	80-107								
PYAFD ECOLI	HYPOTHETICAL 16.7 KD PROTEIN	ESCHERICHIA COLI	606-641	683-714	726-753						
PYAFD ECOLI	HYPOTHETICAL 10.8 KD PROTEIN	ESCHERICHIA COLI	373-400	421-452	621-648						
PYAFD ECOLI	HYPOTHETICAL 24.1 KD PROTEIN	ESCHERICHIA COLI	133-174								
PYAFD ECOLI	HYPOTHETICAL 20.5 KD PROTEIN	ESCHERICHIA COLI	96-130								
PYAFD ECOLI	HYPOTHETICAL 18.3 KD PROTEIN	ESCHERICHIA COLI	4-38								
PYAFD ECOLI	HYPOTHETICAL 65.3 KD PROTEIN	BORRELIA BURGDORFERI	333-360	524-551	563-592						
PYAFD ECOLI	HYPOTHETICAL 14.3 KD PROTEIN	SULFOLOBUS SOLFATARICUS	6-36								
PYAFD ECOLI	HYPOTHETICAL 16.9 KD PROTEIN	SULFOLOBUS SOLFATARICUS	17-58	71-103							
PYAFD ECOLI	HYPOTHETICAL PROTEIN	SULFOLOBUS SOLFATARICUS	11-38								
PYAFD ECOLI	HYPOTHETICAL 10.7 KD PROTEIN	ESCHERICHIA COLI	91-120								
PYAFD ECOLI	HYPOTHETICAL 38.1 KD PROTEIN	ESCHERICHIA COLI	50-77								
PYAFD ECOLI	HYPOTHETICAL 49.3 KD TRANSPORT PROTEIN	ESCHERICHIA COLI	43-70								
PYAFD ECOLI	HYPOTHETICAL IN DCD REGION	ESCHERICHIA COLI	147-174								
PYAFD ECOLI	HYPOTHETICAL 16.9 KD PROTEIN	ESCHERICHIA COLI	143-172								
PYAFD ECOLI	HYPOTHETICAL 22.3 KD PROTEIN	ESCHERICHIA COLI	69-106	283-310							
PYAFD ECOLI	HYPOTHETICAL 19.1 KD PROTEIN	ESCHERICHIA COLI	151-178	501-545							
PYAFD ECOLI	HYPOTHETICAL 141.0 KD PROTEIN	ESCHERICHIA COLI	96-123								
PYAFD ECOLI	HYPOTHETICAL 138.1 KD PROTEIN	ESCHERICHIA COLI	343-370	102-129							

PCGENE	10112144	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9	AREA.10
FILE NAME	PROTEIN	ORGANISM	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9	AREA.10
PYH1U_ECOLI	HYPOTHETICAL 43.1 KD PROTEIN	ESCHERICHIA COLI	378-353									
PYH1C_ECOLI	HYPOTHETICAL 31.6 KD PROTEIN	ESCHERICHIA COLI	46-80									
PYH1F_ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	61-38									
PYH1J_ECOLI	HYPOTHETICAL 43.4 KD PROTEIN	ESCHERICHIA COLI	15-42									
PYH1A_ECOLI	HYPOTHETICAL ABC TRANSPORTER	ESCHERICHIA COLI	81-110									
PYH1O_ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	453-480									
PYH1D_ECOLI	HYPOTHETICAL 91.2 KD PROTEIN	ESCHERICHIA COLI	399-433									
PYH1H_ECOLI	HYPOTHETICAL 40.6 KD PROTEIN	ESCHERICHIA COLI	135-202									
PYH1Z_BACST	HYPOTHETICAL 30.6 KD PROTEIN	BACILLUS STEAROTHERIOPHILUS	133-160									
PYH1X_BACST	HYPOTHETICAL PROTEIN	BRADYRHIZOBIUM JAPONICUM	109-150									
PYH1P_BACME	HYPOTHETICAL 37.7 KD PROTEIN	BACILLUS MEGATERIUM	40-67									
PYH1G_ECOLI	HYPOTHETICAL 39.4 KD PROTEIN	ESCHERICHIA COLI	214-241									
PYH1B_ECOLI	HYPOTHETICAL 30.9 KD PROTEIN	ESCHERICHIA COLI	235-252									
PYH1Q_ECOLI	HYPOTHETICAL 31.8 KD PROTEIN	ESCHERICHIA COLI	209-236									
PYH1I_ECOLI	HYPOTHETICAL 32.8 KD PROTEIN	BACILLUS THURINGIENSIS	26-61									
PYH1F_PSEPU	HYPOTHETICAL 31.4 KD PROTEIN	PSEUDOMONAS PUTIDA	145-172									
PYH1G_ECOLI	HYPOTHETICAL 48.4 KD PROTEIN	ESCHERICHIA COLI	223-264									
PYH1A_BACST	HYPOTHETICAL 35.3 KD PROTEIN	BACILLUS STEAROTHERIOPHILUS	6-33									
PYH1N_BACCE	HYPOTHETICAL PROTEIN	BACILLUS CEREUS	182-209									
PYH1N_BACCE	HYPOTHETICAL 15 KD PROTEIN	BACILLUS CEREUS	79-124									
PYH1D_BACSU	HYPOTHETICAL PROTEIN	BACILLUS SUBTILIS	20-47									
PYH1E_BACSU	HYPOTHETICAL 17.1 KD PROTEIN	BACILLUS SUBTILIS	84-111									
PYH1P_BACSU	HYPOTHETICAL 39.0 KD PROTEIN	BACILLUS SUBTILIS	98-125									
PYH1P_CLOAB	HYPOTHETICAL 31.8 KD PROTEIN	CLOSTRIDIUM ACETOBUTYLICUM	160-210									
PYH1Z_STRMU	HYPOTHETICAL PROTEIN 2	STREPTOCOCCUS MUTANS	4-40	110-138	235-262							
PYH1B_ECOLI	HYPOTHETICAL 20.6 KD PROTEIN	ESCHERICHIA COLI	20-66									
PYH1C_ECOLI	HYPOTHETICAL 43.2 KD PROTEIN	ESCHERICHIA COLI	69-96									
PYH1F_ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	44-71	138-165								
PYH1G_ECOLI	PROBABLE ABC TRANSPORTER	ESCHERICHIA COLI	176-203									
PYH1B_PSEPU	PROBABLE ABC TRANSPORTER	PSEUDOMONAS PUTIDA	74-101	106-133	147-174							
PYH1G_THIFE	PROBABLE ABC TRANSPORTER	THIOBACILLUS FERROOXIDANS	113-140									
PYH1P_ECOLI	HYPOTHETICAL 53.4 KD PROTEIN	ESCHERICHIA COLI	267-297									
PYH1M_BACSU	HYPOTHETICAL 32.0 KD PROTEIN	BACILLUS SUBTILIS	232-253									
PYH1E_ANASP	HYPOTHETICAL PROTEIN	ANABAENA SP	72-99									
PYH1A_ECOLI	HYPOTHETICAL 16.6 KD PROTEIN	ESCHERICHIA COLI	56-84									
PYH1G_ECOLI	HYPOTHETICAL 15.1 KD PROTEIN	ESCHERICHIA COLI	43-77									
PYH1H_ECOLI	HYPOTHETICAL 14.5 KD PROTEIN	ESCHERICHIA COLI	43-73									
PYH1J_LACLA	HYPOTHETICAL PROTEIN	LACTOCOCCUS LACTIS	167-194									
PYH1B_LACLA	HYPOTHETICAL 31.0 KD PROTEIN	LACTOCOCCUS LACTIS	90-124	132-159								
PYH1B_LACLA	HYPOTHETICAL 30.7 KD PROTEIN	LACTOCOCCUS LACTIS	92-148									
PYH1N_STRAII	HYPOTHETICAL PROTEIN	LACTOCOCCUS LACTIS	77-104	156-183								
PYH1L_VIBGII	HYPOTHETICAL PROTEIN	STAPHYLOCOCCUS AUREUS	16-67									
PYH1F_VIBGII	HYPOTHETICAL 18.3 KD PROTEIN	VIBRIO CHOLERAE	99-126									
PYH1F_METFE	HYPOTHETICAL 32.2 KD PROTEIN	METHANOTHERMUS FERVIDUS	106-133									
PYH1S_CLOAB	HYPOTHETICAL 11.0 KD PROTEIN	CLOSTRIDIUM ACETOBUTYLICUM	41-85									
PYH1S_CLOAB	HYPOTHETICAL 20.6 KD PROTEIN	CLOSTRIDIUM ACETOBUTYLICUM	98-125									
PYH1S_CLOAB	HYPOTHETICAL 42.4 KD PROTEIN	CLOSTRIDIUM ACETOBUTYLICUM	23-52	208-233	276-310							
PYH1V_LACII	HYPOTHETICAL PROTEIN	LACTONACILLUS THELVETICUS	91-120	137-154								
PYH1A_PSEPN	HYPOTHETICAL PROTEIN	PSEUDOMONAS SP	217-266									
PYH1J_HAJHA	ISSUE HYPOTHETICAL 38.0 KD PROTEIN	HALOBACTERIUM HALOBURUM	245-272									
PYH1Z_MYCBU	ISSUE HYPOTHETICAL 6.6 KD PROTEIN	MYCOBACTERIUM TUBERCULOSIS	19-46									
PYH1Z_PSEAY	HYPOTHETICAL 42.6 KD PROTEIN	PSEUDOMONAS AMYLODERMOSA	9-26									
PYH1Z_MEIM	ISSUE HYPOTHETICAL 48.3 KD PROTEIN	METHANOBREVIBACTER SMITHII	73-100	154-184	338-365							
PYH1Z_HAJHA	ISSUE HYPOTHETICAL 31 KD PROTEIN	HALOBACTERIUM HALOBURUM	16-113									
PYH1B_ECOLI	HYPOTHETICAL 34.0 KD PROTEIN	ESCHERICHIA COLI	202-239									
PYH1D_ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	9-43									
PYH1F_ECOLI	HYPOTHETICAL 22.6 KD PROTEIN	ESCHERICHIA COLI	131-158									

PCGENE	1051-2144	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PYIBO_ECOLI	HYPOTHETICAL 11.1 KD PROTEIN	ESCHERICHIA COLI	70-97							
PYICC_ECOLI	HYPOTHETICAL 37.2 KD PROTEIN	ESCHERICHIA COLI	143-170							
PYICD_ECOLI	HYPOTHETICAL 31.1 KD PROTEIN	ESCHERICHIA COLI	132-159							
PYICL_ECOLI	HYPOTHETICAL 62.3 KD PROTEIN	ESCHERICHIA COLI	408-435							
PYICN_ECOLI	HYPOTHETICAL 88.1 KD PROTEIN	ESCHERICHIA COLI	121-149							
PYICN_ECOLI	HYPOTHETICAL 18.2 KD PROTEIN	ESCHERICHIA COLI	76-103							
PYICN_ECOLI	HYPOTHETICAL 49.9 KD PROTEIN	ESCHERICHIA COLI	320-347							
PYIDB_ECOLI	HYPOTHETICAL 11.8 KD PROTEIN	ESCHERICHIA COLI	34-78							
PYIDE_ECOLI	HYPOTHETICAL 58.9 KD PROTEIN	ESCHERICHIA COLI	86-113	182-209	272-304					
PYIDJ_ECOLI	HYPOTHETICAL 13.7 KD PROTEIN	ESCHERICHIA COLI	56-83							
PYIDK_ECOLI	HYPOTHETICAL 62.1 KD PROTEIN	ESCHERICHIA COLI	2-39							
PYIDP_ECOLI	HYPOTHETICAL 27.3 KD PROTEIN	ESCHERICHIA COLI	63-97							
PYIEA_ECOLI	HYPOTHETICAL 49.2 KD PROTEIN	ESCHERICHIA COLI	221-248							
PYIEC_ECOLI	HYPOTHETICAL 60.6 KD PROTEIN	ESCHERICHIA COLI	22-67	270-297						
PYIEC_ERWCH	HYPOTHETICAL PROTEIN	ERWINIA CHRYSANTHEMI	86-120							
PYIEG_ECOLI	HYPOTHETICAL 34.8 KD PROTEIN	ESCHERICHIA COLI	293-327							
PYIEH_ECOLI	HYPOTHETICAL 46.9 KD PROTEIN	ESCHERICHIA COLI	51-78							
PYIEM_ECOLI	HYPOTHETICAL 24.7 KD PROTEIN	ESCHERICHIA COLI	73-105							
PYIEO_ECOLI	HYPOTHETICAL 51.5 KD PROTEIN	ESCHERICHIA COLI	201-242	380-407						
PYIEC_ECOLI	HYPOTHETICAL 39.6 KD PROTEIN	ESCHERICHIA COLI	175-202							
PYIGJ_ECOLI	HYPOTHETICAL 14.0 KD PROTEIN	ESCHERICHIA COLI	51-92							
PYIGM_ECOLI	HYPOTHETICAL 31.7 KD PROTEIN	ESCHERICHIA COLI	120-154							
PYIGN_ECOLI	HYPOTHETICAL 54.7 KD PROTEIN	ESCHERICHIA COLI	207-234							
PYIGO_ECOLI	HYPOTHETICAL 28.1 KD PROTEIN	ESCHERICHIA COLI	62-94							
PYIGP_ECOLI	HYPOTHETICAL 22.3 KD PROTEIN	ESCHERICHIA COLI	173-200							
PYIGT_ECOLI	HYPOTHETICAL 27.8 KD PROTEIN	ESCHERICHIA COLI	132-159							
PYIHB_ECOLI	HYPOTHETICAL 21.2 KD PROTEIN	ESCHERICHIA COLI	131-40							
PYIHD_ECOLI	HYPOTHETICAL 10.3 KD PROTEIN	ESCHERICHIA COLI	28-55							
PYIHR_ECOLI	HYPOTHETICAL 54.1 KD PROTEIN	ESCHERICHIA COLI	272-306							
PYIHL_ECOLI	HYPOTHETICAL 19.1 KD PROTEIN	ESCHERICHIA COLI	112-139							
PYIHK_ECOLI	HYPOTHETICAL 65.4 KD PROTEIN	ESCHERICHIA COLI	4-31							
PYIHM_ECOLI	HYPOTHETICAL 36.9 KD PROTEIN	ESCHERICHIA COLI	83-110	120-154	297-324					
PYIHO_ECOLI	HYPOTHETICAL 81.8 KD PROTEIN	ESCHERICHIA COLI	612-646							
PYIHP_ECOLI	HYPOTHETICAL 51.1 KD PROTEIN	ESCHERICHIA COLI	337-384							
PYIHV_ECOLI	HYPOTHETICAL 31.9 KD PROTEIN	ESCHERICHIA COLI	72-99							
PYIHX_ECOLI	HYPOTHETICAL 23.3 KD PROTEIN	ESCHERICHIA COLI	9-36							
PYIHZ_ECOLI	HYPOTHETICAL 15.9 KD PROTEIN	ESCHERICHIA COLI	6-33							
PYIIP_ECOLI	HYPOTHETICAL 32.9 KD PROTEIN	ESCHERICHIA COLI	22-63							
PYIUI_ECOLI	HYPOTHETICAL 9.6 KD PROTEIN	ESCHERICHIA COLI	28-71							
PYIUC_ECOLI	HYPOTHETICAL 26.6 KD PROTEIN	ESCHERICHIA COLI	136-163							
PYIUI_ECOLI	HYPOTHETICAL 78.3 KD PROTEIN	ESCHERICHIA COLI	225-263							
PYIUK_ECOLI	HYPOTHETICAL 11.2 KD PROTEIN	ESCHERICHIA COLI	26-53							
PYIUL_ECOLI	HYPOTHETICAL 22.1 KD PROTEIN	ESCHERICHIA COLI	214-241							
PYIUP_ECOLI	HYPOTHETICAL 66.6 KD PROTEIN	ESCHERICHIA COLI	110-137	419-446						
PYIUL_LISMO	HYPOTHETICAL 26.8 KD PROTEIN	LISTERIA MONOCYTOGENES	7-34							
PYIS1_SHISO	INSERTION ELEMENT IS600	SHIGELLA SONNEI	62-69							
PYIS1_STRCO	IS110 HYPOTHETICAL 41.6 KD PROTEIN	STREPTOMYCES COELICOLOR	125-152							
PYIS7_SHISO	INSERTION ELEMENT IS629	SHIGELLA SONNEI	66-100							
PYISP_BACP	HYPOTHETICAL 42.1 KD PROTEIN	BACILLUS SP	312-339							
PYIAG_ECOLI	HYPOTHETICAL 22.6 KD PROTEIN	ESCHERICHIA COLI	51-78							
PYIAI_ECOLI	HYPOTHETICAL 20.4 KD PROTEIN	ESCHERICHIA COLI	88-122							
PYIBH_ECOLI	HYPOTHETICAL 78.3 KD PROTEIN	ESCHERICHIA COLI	93-120							
PYIBL_ECOLI	HYPOTHETICAL 9.7 KD PROTEIN	ESCHERICHIA COLI	30-57							
PYIBM_ECOLI	HYPOTHETICAL 26.7 KD PROTEIN	ESCHERICHIA COLI	112-149							
PYIBO_ECOLI	HYPOTHETICAL 15.7 KD PROTEIN	ESCHERICHIA COLI	2-29							
PYICC_ECOLI	HYPOTHETICAL 60.8 KD PROTEIN	ESCHERICHIA COLI	38-65	414-441	451-492					



PCGENE	107176.4	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAVE	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PYCE_ECOLI	HYPOTHETICAL 60.3 KD PROTEIN	ESCHERICHIA COLI	434-481								
PYCO_ECOLI	HYPOTHETICAL 39.2 KD PROTEIN	ESCHERICHIA COLI	394-421								
PYIC_ECOLI	HYPOTHETICAL 35.1 KD PROTEIN	ESCHERICHIA COLI	91-118								
PYIC_ECOLI	HYPOTHETICAL 31.4 KD PROTEIN	ESCHERICHIA COLI	242-269								
PYIC_ECOLI	HYPOTHETICAL 73.7 KD PROTEIN	ESCHERICHIA COLI	366-396								
PYICW_ECOLI	HYPOTHETICAL ABC TRANSPORTER	ESCHERICHIA COLI	50-84								
PYIDA_ECOLI	HYPOTHETICAL 84.2 KD PROTEIN	ESCHERICHIA COLI	2-29	451-483							
PYIDB_ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	103-134								
PYJIA_ECOLI	HYPOTHETICAL 17.3 KD PROTEIN PRECURSOR	ESCHERICHIA COLI	35-69	88-129							
PYKAB_BACFI	HYPOTHETICAL 48.8 KD PROTEIN	BACILLUS FIRMUS	321-355								
PYLAL_LACAC	HYPOTHETICAL PROTEIN	LACTOBACILLUS ACIDOPHILUS	47-74								
PYLAL_LACAC	HYPOTHETICAL 14.3 KD PROTEIN	LACTOBACILLUS ACIDOPHILUS	15-42								
PYLAL_LACAC	HYPOTHETICAL 14.4 KD PROTEIN	LACTOBACILLUS ACIDOPHILUS	47-74								
PYLAC_SULSO	HYPOTHETICAL 24.4 KD PROTEIN	SULFOLOBUS SOLFATARICUS	21-50								
PYLPJ_PSEPU	HYPOTHETICAL 44.7 KD PROTEIN	PSEUDOMONAS PUTIDA	186-213	314-341							
PYLPJ_YEREN	YLPJ LIPOPROTEIN PRECURSOR	YERSINIA ENTEROCOLITICA	184-221								
PYLTD_ANAVA	HYPOTHETICAL 22.6 KD PROTEIN	ANABAENA VARIABILIS	172-199								
PYLTD_LACLA	HYPOTHETICAL 29.7 KD PROTEIN	LACTOCOCCUS LACTIS	35-70								
PYME2_BACSU	HYPOTHETICAL 33.3 KD PROTEIN	BACILLUS SUBTILIS	52-79								
PYMG2_MYCGE	HYPOTHETICAL 114.4 KD PROTEIN PRECURSOR	MYCOPLASMA GENTALIUM	56-83	139-193	420-445	981-1008					
PYNGA_CLOPE	HYPOTHETICAL PROTEIN	CLOSTRIDIUM PERFRINGENS	139-166								
PYNGB_CLOPE	HYPOTHETICAL 31.2 KD PROTEIN	CLOSTRIDIUM PERFRINGENS	12-49	63-97	182-211						
PYNI1_METIL	HYPOTHETICAL PROTEIN	METHANOCOCCUS THERMOLITHOTROPHICUS	55-89								
PYNOJ_PASDE	HYPOTHETICAL 9.1 KD PROTEIN	PARACOCCLUS DENITRIFICANS	52-86								
PYNT1_ANASP	HYPOTHETICAL 21.1 KD PROTEIN	ANABAENA SP	171-198								
PYNT3_ANASP	HYPOTHETICAL PROTEIN	ANABAENA SP	87-163								
PYOHG_ECOLI	HYPOTHETICAL 21.4 KD PROTEIN	ESCHERICHIA COLI	5-32								
PYOHG_ECOLI	HYPOTHETICAL 41.3 KD PROTEIN	ESCHERICHIA COLI	104-171	289-316							
PYDIA_ECOLI	HYPOTHETICAL 13.9 KD PROTEIN	ESCHERICHIA COLI	17-44								
PYDIE_ECOLI	HYPOTHETICAL 9.3 KD PROTEIN	ESCHERICHIA COLI	231-248								
PYDIF_ECOLI	HYPOTHETICAL 9.3 KD PROTEIN	ESCHERICHIA COLI	41-82								
PYDIN_ECOLI	HYPOTHETICAL 34.3 KD PROTEIN	ESCHERICHIA COLI	145-193								
PYDJI_ECOLI	HYPOTHETICAL 36.2 KD PROTEIN	ESCHERICHIA COLI	94-121								
PYOMA_PHOS9	HYPOTHETICAL PROTEIN IN OMPH 3 REGION	PHOTOBACTERIUM SP	32-59								
PYORH_YEREN	PROTEIN-TYROSINE PHOSPHATASE YOPH	YERSINIA ENTEROCOLITICA	63-103								
PYOPH_YERPS	PROTEIN-TYROSINE PHOSPHATASE YOPH	YERSINIA PSEUDOTUBERCULOSIS	63-103								
PYOPN_YERPS	OUTER MEMBRANE PROTEIN YOPN	YERSINIA PSEUDOTUBERCULOSIS	21-50	66-93	213-262						
PYOPN_YERPS	OUTER MEMBRANE PROTEIN YOPN	YERSINIA PSEUDOTUBERCULOSIS	21-50	66-93	213-262						
PYOPN_YEREN	OUTER MEMBRANE PROTEIN YOPN	YERSINIA ENTEROCOLITICA	61-88								
PYORA_HAEIN	YOPO PROTEIN PRECURSOR	HAEMOPHILUS INFLUENZAE	147-174								
PYORA_LISMO	HYPOTHETICAL 31.9 KD PROTEIN	HAEMOPHILUS INFLUENZAE	32-77								
PYORA_PYRWO	HYPOTHETICAL 23.6 KD PROTEIN	PYROCOCCLUS WOESSEI	183-210								
PYORH_HAEIN	HYPOTHETICAL 19.8 KD PROTEIN	HAEMOPHILUS INFLUENZAE	39-66								
PYORC_HAEIN	HYPOTHETICAL 19.9 KD PROTEIN	HAEMOPHILUS INFLUENZAE	49-79								
PYORE_HAEIN	8 KD PROTEIN	HAEMOPHILUS INFLUENZAE	47-74	82-109							
PYORH_HAEIN	26.8 KD PROTEIN	HAEMOPHILUS INFLUENZAE	199-229								
PYORI_HAEIN	HYPOTHETICAL 13.7 KD PROTEIN	HAEMOPHILUS INFLUENZAE	7-34								
PYORI_HAEIN	95.4 KD PROTEIN	HAEMOPHILUS INFLUENZAE	416-450	688-722							
PYORO_BACSU	HYPOTHETICAL 34 KD PROTEIN	BACILLUS SUBTILIS	148-175								
PYORZ_PYAWO	HYPOTHETICAL PROTEIN	PYROCOCCLUS WOESSEI	66-93								
PYORZ_LISMO	HYPOTHETICAL 16.9 KD PROTEIN	LISTERIA MONOCYTOGENES	22-54								
PYPJ3_STAUI	HYPOTHETICAL 15.1 KD PROTEIN	STAPHYLOCOCCUS AUREUS	71-98	110-137							
PYPJ3_BACSU	HYPOTHETICAL 22.3 KD PROTEIN	BACILLUS SUBTILIS	57-84								
PYPJ3_STAUI	HYPOTHETICAL 22.3 KD PROTEIN	STAPHYLOCOCCUS AUREUS	29-70								
PYPJ3_STAUI	HYPOTHETICAL 26.9 KD PROTEIN	STAPHYLOCOCCUS AUREUS	34-104								
PYPJ3_STAUI	HYPOTHETICAL 37.0 KD PROTEIN	STAPHYLOCOCCUS AUREUS	21-60	62-89	179-206						
PYPJ3_STAUI	HYPOTHETICAL 27.7 KD PROTEIN	STAPHYLOCOCCUS AUREUS	13-83	129-176							



PCGENE	10717844	Prokaryotic Sequences	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10
FILE NAME	PROTEIN	ORGANISM	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10
PYP1 AGRT4	HYPOTHETICAL PROTEIN 7	AGROBACTERIUM TUMEFACIENS	79-56									
PYP2 LEPN	HYPOTHETICAL PROTEIN	LEGIONELLA PNEUMOPHILA	94-135									
PYP3 ENFA	HYPOTHETICAL 13 KD PROTEIN	ENTEROCOCCUS FAECALIS	79-106									
PYP4 BACAN	HYPOTHETICAL 21.6 KD PROTEIN	BACILLUS ANTHRACIS	11-47									
PYP5 ECOLI	HYPOTHETICAL 27.6 KD PROTEIN	ESCHERICHIA COLI	5-32									
PYP6 BACSU	HYPOTHETICAL 27.3 KD PROTEIN	BACILLUS SUBTILIS	184-222									
PYP7 ECOLI	HYPOTHETICAL 12.8 KD PROTEIN	ESCHERICHIA COLI	16-43									
PYP8 STYR2	HYPOTHETICAL 18.1 KD PROTEIN	SYNECHOCOCCUS SP	34-61									
PYP9 CLOPE	HYPOTHETICAL 19.7 KD PROTEIN	CLOSTRIDIUM PERFRINGENS	7-34									
PYP10 CLOPE	HYPOTHETICAL 14.5 KD PROTEIN	CLOSTRIDIUM PERFRINGENS	2-59									
PYP11 CLOPE	HYPOTHETICAL 38.4 KD PROTEIN	CLOSTRIDIUM PERFRINGENS	110-137									
PYP12 PSEAE	HYPOTHETICAL 38.5 KD PROTEIN	PSEUDOMONAS AERUGINOSA	22-52									
PYP13 BACSU	HYPOTHETICAL PROCESSING PROTEASE	BACILLUS SUBTILIS	229-356									
PYP14 KLEPN	HYPOTHETICAL PROTEIN	KLEBSIELLA PNEUMONIAE	243-270									
PYP15 PLEBO	HYPOTHETICAL 13.1 KD PROTEIN	PLECTONEXA BORYANUM	27-54									
PYP16 METTF	HYPOTHETICAL 40.7 KD PROTEIN	METHANOBACTERIUM THERMOFORMICICUM	58-85									
PYP17 METTF	HYPOTHETICAL 22.3 KD PROTEIN	METHANOBACTERIUM THERMOFORMICICUM	3-30									
PYP18 METTF	HYPOTHETICAL 17.3 KD PROTEIN	METHANOBACTERIUM THERMOFORMICICUM	69-117									
PYP19 METTF	HYPOTHETICAL 49.6 KD PROTEIN	METHANOBACTERIUM THERMOFORMICICUM	331-360									
PYP20 BACSU	HYPOTHETICAL 72.4 KD PROTEIN	BACILLUS SUBTILIS	602-636									
PYP21 METTF	HYPOTHETICAL 40.6 KD PROTEIN	METHANOBACTERIUM THERMOFORMICICUM	58-85									
PYP22 METTF	HYPOTHETICAL 31.1 KD PROTEIN	METHANOBACTERIUM THERMOFORMICICUM	38-65									
PYP23 METTF	HYPOTHETICAL 54.1 KD PROTEIN	METHANOBACTERIUM THERMOFORMICICUM	191-220									
PYP24 METTF	HYPOTHETICAL 9.7 KD PROTEIN	METHANOBACTERIUM THERMOFORMICICUM	5-78									
PYP25 THEPE	HYPOTHETICAL 18.7 KD PROTEIN	THERMOFILUM PENDENS	82-109									
PYP26 HALCU	HYPOTHETICAL 40 KD GTP-BINDING PROTEIN	HALOBACTERIUM CUTIRUBRUM	30-51									
PYP27 SYN22	HYPOTHETICAL 24.7 KD PROTEIN	SYNECHOCOCCUS SP	49-76									
PYP28 SALTU	HYPOTHETICAL 40.6 KD PROTEIN	SALMONELLA TYPHIMURIUM	143-190									
PYP29 SALTU	HYPOTHETICAL 51.0 KD PROTEIN	SALMONELLA TYPHIMURIUM	428-435									
PYP30 SALTU	HYPOTHETICAL 20.6 KD PROTEIN	SALMONELLA TYPHIMURIUM	39-56									
PYP31 SALTU	HYPOTHETICAL 36.6 KD PROTEIN	SALMONELLA TYPHIMURIUM	130-157									
PYP32 LACLA	HYPOTHETICAL PROTEIN	LACTOCOCCUS LACTIS	140-167									
PYP33 METVA	HYPOTHETICAL PROTEIN	METHANOCOCCUS VANNIELII	40-93									
PYP34 METVA	HYPOTHETICAL 11.6 KD PROTEIN	METHANOCOCCUS VANNIELII	129-156									
PYP35 SULAC	HYPOTHETICAL 11.3 KD PROTEIN	SULFOLOBUS ACIDOCALDARIUS	13-40									
PYP36 SULAC	HYPOTHETICAL 14.3 KD PROTEIN	SULFOLOBUS ACIDOCALDARIUS	5-51									
PYP37 BACSU	HYPOTHETICAL 25.3 KD PROTEIN	BACILLUS SUBTILIS	77-71									
PYP38 BACSU	HYPOTHETICAL 11.4 KD PROTEIN	BACILLUS SUBTILIS	29-56									
PYP39 YEREN	HYPOTHETICAL YSC OPERON PROTEIN B	YERSINIA ENTEROCOLITICA	31-30									
PYP40 YEREN	YSC OPERON PROTEIN C PRECURSOR	YERSINIA ENTEROCOLITICA	90-121									
PYP41 YEREN	YSC OPERON PROTEIN D	YERSINIA ENTEROCOLITICA	38-72									
PYP42 YEREN	YSC OPERON PROTEIN E	YERSINIA ENTEROCOLITICA	242-269									
PYP43 YEREN	YSC OPERON PROTEIN F	YERSINIA ENTEROCOLITICA	28-58									
PYP44 YEREN	YSC OPERON PROTEIN G	YERSINIA ENTEROCOLITICA	28-58									
PYP45 YEREN	YSC OPERON PROTEIN H	YERSINIA ENTEROCOLITICA	49-76									
PYP46 YEREN	YSC OPERON PROTEIN I	YERSINIA ENTEROCOLITICA	49-76									
PYP47 YEREN	YSC OPERON PROTEIN J PRECURSOR	YERSINIA ENTEROCOLITICA	99-126									
PYP48 YEREN	YSC OPERON PROTEIN L	YERSINIA ENTEROCOLITICA	99-126									
PYP49 YEREN	YSC OPERON PROTEIN L	YERSINIA ENTEROCOLITICA	41-68									
PYP50 SERMA	HYPOTHETICAL 9.4 KD PROTEIN	SERATIA MARCESCENS	41-68									
PYP51 DESAM	HYPOTHETICAL 28.3 KD PROTEIN	DESULFOLOBUS AMBIVALENS	11-70									
PYP52 DESAM	HYPOTHETICAL PROTEIN	DESULFOLOBUS AMBIVALENS	68-09									
PYP53 LEPT	HYPOTHETICAL PROTEIN	LEPTOSPIRA INTERROGANS	65-153									
PYP54 MYLKY	HYPOTHETICAL PROTEIN	MYCOPLASMA MYCOIDES	6-13									
PYP55 BACSU	HYPOTHETICAL 19.6 KD PROTEIN	BACILLUS SUBTILIS	35-59									
PYP56 METTF	HYPOTHETICAL PROTEIN	METHANOTHERMUS FERVIDUS	72-99									
PYP57 STRK	HYPOTHETICAL 37.1 KD PROTEIN	STREPTOMYCES FRADIAE	78-105									
PYP58 STRK	HYPOTHETICAL 37.1 KD PROTEIN	STREPTOMYCES FRADIAE	246-273									

PCGENE	10717144	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PLEXANME	PROTEIN	ORGANISMI	244-271	279-306							
PYTDK_BACSU	HYPOTHETICAL 33.6 KD PROTEIN	BACILLUS SUBTILIS	84-113								
PYTRE_LEPBI	HYPOTHETICAL 22 KD PROTEIN	LEPTOSPIRA BIFLEXA	76-112								
PYTRP_LACLA	HYPOTHETICAL 13.3 KD PROTEIN	LACTOCOCCUS LACTIS	32-64								
PYTSI_BACSU	HYPOTHETICAL 20 KD PROTEIN	BACILLUS SUBTILIS	102-149								
PYTSF_SPHCI	HYPOTHETICAL 23.8 KD PROTEIN	SPHIROPLASMA CITRI	37-64	63-93							
PYX04_BACSU	HYPOTHETICAL 12.8 KD PROTEIN	BACILLUS SUBTILIS	142-169								
PYX06_BACSU	HYPOTHETICAL 21.0 KD PROTEIN	BACILLUS SUBTILIS	12-51								
PYX13_BACSU	HYPOTHETICAL 26.0 KD PROTEIN	BACILLUS SUBTILIS	165-207	262-289							
PYX15_BACSU	HYPOTHETICAL 61.8 KD PROTEIN	BACILLUS SUBTILIS	3-30	34-61	94-142						
PYX18_BACSU	HYPOTHETICAL 66.8 KD PROTEIN	BACILLUS SUBTILIS	56-83	85-112							
PYX19_BACSU	HYPOTHETICAL 31.3 KD PROTEIN	BACILLUS SUBTILIS	24-58								
PYX20_BACSU	HYPOTHETICAL 21.2 KD PROTEIN	BACILLUS SUBTILIS	71-104								
PYX2P_ANASP	HYPOTHETICAL 11.9 KD PROTEIN	ANABACNA SP	9-39								
PYXYB_CALSA	HYPOTHETICAL 10.7 KD PROTEIN	CALDOCELLUM SACCHAROLYTICUM	41-94								
PYXYC_CALSA	HYPOTHETICAL PROTEIN	CALDOCELLUM SACCHAROLYTICUM	41-94								
PYZEI_ECOLI	HYPOTHETICAL 16.7 KD PROTEIN	ESCHERICHIA COLI	41-78								

TABLE IX

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL HUMAN PROTEINS









PCGENE	10712124.4 Motif Search on All Human Protein Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
FILE NAME	PROTEIN	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
PC001_HUMAN	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.1.1)	353-380							
PC010_HUMAN	CYTOCHROME P450 VII (CHOLESTEROL 7-ALPHA-MONOXYGENASE)	263-290	146-173						
PC024_HUMAN	CYTOCHROME P450 IIC17 (EC 1.14.14.1) (P450-3AC) (FRAGMENT)	109-136							
PC031_HUMAN	CYTOCHROME P450 IIE1 (EC 1.14.14.1) (P450-9) (ETHANOL INDUCIBLE)	231-258							
PC034_HUMAN	CARBAMOYL-PHOSPHATE SYNTHASE (AMMONIA) MITOCHONDRIAL PRECURSOR	112-146	420-447						
PC072_HUMAN	MITOCHONDRIAL CARNITINE PALMITOYL TRANSFERASE II PRECURSOR	410-437							
PC077_HUMAN	CYTOCHROME P450 IIA1 (P450-C17) (EC 1.14.99.9) (STEROID 17-ALPHA-)	226-257							
PC081_HUMAN	CYTOCHROME P450 IIA1 (AROMATASE) (EC 1.14.14.1) (ESTROGEN)	334-371							
PC083_HUMAN	COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR)	986-1013							
PC084_HUMAN	COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN)	64-126	179-420	633-678	724-734	763-790			
PC085_HUMAN	CAMP RESPONSE ELEMENT BINDING PROTEINS A AND B (CREB-A AND CREB-B)	94-123							
PC087_HUMAN	CAMP RESPONSE ELEMENT BINDING PROTEIN CRE-BP1	380-414							
PC089_HUMAN	C-REACTIVE PROTEIN PRECURSOR	60-87	150-177						
PC091_HUMAN	CLEAVAGE SIGNAL-1 PROTEIN (CS-1)	203-233							
PC091_HUMAN	MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (M-CSF)	143-170							
PC093_HUMAN	CLEAVAGE STIMULATION FACTOR, 30 KD SUBUNIT (CSTF 30 KD SUBUNIT) (CF-1)	6-33							
PC094_HUMAN	ALPHA-CATENIN (CADHERIN-ASSOCIATED PROTEIN)	681-718							
PC096_HUMAN	ALPHA-CATENIN RELATED PROTEIN (CATENIN ALPHA-2)	680-717							
PC098_HUMAN	GAP JUNCTION BETA-2 PROTEIN (CONNEXIN 26) (CX26)	108-139							
PC099_HUMAN	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 32) (CX32) (GAP JUNCTION 28 KD)	117-144							
PC099_HUMAN	GAP JUNCTION ALPHA-4 PROTEIN (CONNEXIN 37) (CX37)	88-115							
PC099_HUMAN	CYTOCHROME B5	3-42							
PC099_HUMAN	GUANYLATE CYCLASE SOLUBLE, BETA-1 CHAIN (EC 4.6.1.2) (70 KD CHAIN)	80-107	126-153	352-396					
PC099_HUMAN	GUANYLATE CYCLASE SOLUBLE, ALPHA-2 CHAIN (EC 4.6.1.2)	106-133							
PC099_HUMAN	RETINAL GUANYL CYCLASE PRECURSOR (EC 4.6.1.2)	824-851							
PC099_HUMAN	CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)	293-320							
PC099_HUMAN	CYSTATIN A (STEIN A) (CYSTATIN A5)	27-38							
PC099_HUMAN	PROTO-ONCOGENE DBL PRECURSOR (CONTAINS: MCF2)	233-283	485-524	766-793	801-845				
PC099_HUMAN	DESNOPLAXIN I AND II (DPI AND DPII) (FRAGMENT)	153-180	272-312	217-244	269-317	382-434	437-467	528-558	563-598
PC099_HUMAN	DESNOPLAXIN I AND II (DPI AND DPII) (FRAGMENT)	31-38	485-524	766-793	801-845				
PC099_HUMAN	ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (EC 1.2.1.5)	86-116	318-365	484-511	753-780	976-1003	1012-1039	1201-1228	1364-1394
PC099_HUMAN	DYSTROPHIN	1818-1865	2138-2185	2313-2343	2732-2739	2786-2830	2912-2958	3014-3041	3499-3533
PC099_HUMAN	DNA J PROTEIN HOMOLOG	45-76							
PC099_HUMAN	DNA LIGASE (EC 6.3.1.1) (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP))	130-157	355-392	732-759					
PC099_HUMAN	DNA POLYMERASE ALPHA (EC 2.7.7.7)	25-74	1009-1037	1100-1127					
PC099_HUMAN	DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7)	729-756							
PC099_HUMAN	DIPYRIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION)	29-77	114-148						
PC099_HUMAN	DEOXYRIBONUCLEASE I PRECURSOR (EC 3.1.2.1) (IONASE I)	44-71							
PC099_HUMAN	DESMOCOLLIN JAB8 PRECURSOR (DESMOSOMAL GLYCOPROTEIN II AND III)	80-107	355-398						
PC099_HUMAN	DESMOGLEIN 1 PRECURSOR (DESMOSOMAL GLYCOPROTEIN I) (DGI)	13-42	271-298	497-531					
PC099_HUMAN	DESMOGLEIN 3 PRECURSOR (130 KD PEMPHEGUS VULGARIS ANTIGEN) (PVA)	211-248	325-352						
PC099_HUMAN	DIVALENT UPSTREAM PROTEIN (DUP)	584-618							
PC099_HUMAN	V-ERB A RELATED PROTEIN EAR-1	523-550							
PC099_HUMAN	EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 2 (EBI2)	44-78							
PC099_HUMAN	ELONGATION FACTOR I BETA (EF-1-BETA)	105-132							
PC099_HUMAN	ELONGATION FACTOR I DELTA (EF-1-DELTA)	34-118							
PC099_HUMAN	EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112)	64-91	440-467						
PC099_HUMAN	EPIDERMAL GROWTH FACTOR RECEPTOR, KIDNEY (EGF) (UROGASTRONE)	47-74							
PC099_HUMAN	ETS-RELATED TRANSCRIPTION FACTOR ELK-1	551-588							
PC099_HUMAN	ENDOPLASMIC RETICULUM PRECURSOR (94 KD GLUCOSE-REGULATED PROTEIN) (GRP94) (GRP78)	47-74	246-273						
PC099_HUMAN	RETROVIRUS RELATED ENV POLYPROTEIN	382-420							
PC099_HUMAN	IO EPSILON CHAIN C REGION	161-188							
PC099_HUMAN	EPIMORPHIN	35-62	67-94	240-283					
PC099_HUMAN	PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72)	58-85	142-169	458-485					
PC099_HUMAN	DNA EXCISION REPAIR PROTEIN ERCC-1	240-270							



PCGENE	1071784 Motif Search on All Human Protein Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
FILE NAME	PROTEIN									
PERC6 HUMAN	EXCISION REPAIR PROTEIN ERCC-4	160-209	919-971							
PESTR HUMAN	ESTROGEN RECEPTOR (ER)	451-488								
PEZ2 HUMAN	ENDOTHELIN-2 PRECURSOR (ET-2)	133-160								
PETJ HUMAN	ENDOTHELIN-3 PRECURSOR (ET-3)	182-209								
PEVA HUMAN	EVIA PROTEIN PRECURSOR	29-46								
PEZB1 HUMAN	EZBIN (P41) (GYTOVILIN) (VILIN-2)	119-146	351-392	402-429	512-539					
PFAS HUMAN	COAGULATION FACTOR V PRECURSOR	2101-2137								
PFAB HUMAN	COAGULATION FACTOR VIII PRECURSOR (PROCOAGULANT COMPONENT)	871-908	1007-1034	1194-1210						
PFAG HUMAN	COAGULATION FACTOR IX PRECURSOR (EC 3.4.21.22) (CHRISTMAS FACTOR)	271-298								
PFAB1 HUMAN	FATTY ACID-BINDING PROTEIN, INTESTINAL	98-125								
PFASA HUMAN	APOTOSIS-MEDIATING SURFACE ANTIGEN FAS PRECURSOR (APO-1 ANTIGEN)	23-50	249-301	306-333						
PFCEZ HUMAN	LOW AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR (LYMPHOCYTE IGE)	81-115								
PFCEA HUMAN	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR ALPHA-SUBUNIT (FCER)	140-174								
PFGR2 HUMAN	FIBROBLAST GROWTH FACTOR RECEPTOR 2 PRECURSOR (EC 2.1.1.112)	310-337								
PFIBA HUMAN	FIBRINOGEN ALPHA CHAIN PRECURSOR	131-165	427-457							
PFIBB HUMAN	FIBRINOGEN BETA CHAIN PRECURSOR	149-186								
PFIBG HUMAN	FIBRINOGEN GAMMA-A CHAIN PRECURSOR	59-93	125-160							
PFIBH HUMAN	FIBRINOGEN GAMMA-B CHAIN (FIBRINOGEN GAMMA)	59-93	125-160							
PFINC HUMAN	FIBRONECTIN PRECURSOR	2168-2199								
PFLI1 HUMAN	FLI-1 ONCOGENE (EBOS TRANSCRIPTION FACTOR)	172-209								
PFMO1 HUMAN	DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 1 (EC 1.14.13.4)	162-193								
PFOS HUMAN	P53-C-FOS PROTO-ONCOGENE PROTEIN	133-168								
PFRA1 HUMAN	FOS-RELATED ANTIGEN 1	149-180								
PFRA2 HUMAN	FOS-RELATED ANTIGEN 2	7-34								
PFRRH HUMAN	FERRITIN HEAVY CHAIN	7-34								
PFRL HUMAN	FERRITIN LIGHT CHAIN	3-33								
PFHR HUMAN	FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSHR)	164-195								
PFUCO HUMAN	TISSUE ALPHA-L-FUCOSIDASE PRECURSOR (EC 2.1.3.1) (ALPHA-L-FUCOSIDASE)	308-333								
PFUMH HUMAN	FUMARATE HYDATASE, MITOCHONDRIAL (EC 4.2.1.2) (FUMARASE)	424-451								
POB32 HUMAN	PUTATIVE LYMPHOCYTE GAG SWITCH PROTEIN	56-83								
POI9P HUMAN	GLUCOSE-4-PHOSPHATE ISOMERASE (GPI) (EC 5.1.1.9) (PHOSPHOGLUCOSE)	16-50								
POB12 HUMAN	MAJOR GASTROINTESTINAL TUMOR-ASSOCIATED PROTEIN GA33-2 PRECURSOR	181-215								
POAT2 HUMAN	GALACTOKINASE 2 (EC 2.7.1.6)	254-281								
POAA1 HUMAN	GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-1 SUBUNIT PRECURSOR (GABA(A) 210-237)	210-237								
POAA3 HUMAN	GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-3 SUBUNIT PRECURSOR (GABA(A) 211-255)	211-255								
POA3R HUMAN	GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR)	74-105								
POB01 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT 1	22-49								
POB02 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT 2	22-49								
POBAX HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(K), ALPHA SUBUNIT (GQ) (ALPHA-3)	22-49								
POBAS HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (ADENYLATE)	7-34								
POBAY HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(Y), ALPHA SUBUNIT (ALPHA-11)	95-122								
POBBJ HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(Y)G(S)G(T) BETA SUBUNIT 1	65-92								
POBPL HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 2 (GUANINE NUCLEOTIDE-INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 2)	110-137	235-282	289-316						
POB12 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-2 SUBUNIT (TRANSDUCIN)	22-49								
POCF HUMAN	GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9)	260-277	293-320	367-394	396-423	647-674				
PGCH1 HUMAN	GTP CYCLOHYDROLASE I (EC 3.5.4.16)	163-192								
PGCHB HUMAN	GLUCOCORTICOID RECEPTOR, ALPHA (GR)	167-194								
PGCBH HUMAN	GLUCOCORTICOID RECEPTOR, BETA (GR)	167-194								
PGCSP HUMAN	GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (EC 1.4.4.2)	460-487								
PGDN HUMAN	GLIA DERIVED NEURIN (GDN) (PROTEASE NEURIN)	83-110								
PGELS HUMAN	GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF)	701-728								
PGFAP HUMAN	GLIAL FIBRILLARY ACIDIC PROTEIN, ASTROCYTE	189-216	349-376	384-411						
PGELS HUMAN	N-ACETYL GLUCOSAMINE-6-ASULFATASE PRECURSOR (EC 3.1.6.14) (G6S)	170-221								
PGLPK HUMAN	GLYCEROL KINASE (EC 2.7.1.30) (ATP-GLYCEROL 3-PHOSPHOTRANSFERASE)	78-112	251-278							
POLY1 HUMAN	SERINE HYDROXYMETHYL TRANSFERASE, CYTOSOLIC (EC 2.1.2.1) (SERINE)	32-59	344-371							

PCGENE	10217184.Nc01 Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
GLULAMIC	PROTEIN									
PGLY72	HUMAN SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL (EC 2.3.1.1) (SERINE	417-444								
PGRT8	HUMAN 78 KD GLUCOSE REGULATED PROTEIN PRECURSOR (GRP 78) (IMMUNOGLOBULIN	564-591	598-625							
PGRA2	HUMAN GLYCINE RECEPTOR ALPHA-2 CHAIN PRECURSOR	142-169	341-368							
PGRAV	HUMAN GRAVIN (FRAGMENT)	9-41	61-88							
PGRR	HUMAN GROWTH HORMONE-RELEASING HORMONE RECEPTOR PRECURSOR (GHRH RECEPT	128-155								
PGTH2	HUMAN GLUTATHIONE S-TRANSFERASE HA SUBUNIT 2 (EC 2.3.1.18) (GTH2) (CLASS,	64-91								
PGTGA	HUMAN GTPASE-ACTIVATING PROTEIN (GAP) (RAS P21 PROTEIN ACTIVATOR)	474-501	1012-1047							
PGTR1	HUMAN GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN	274-301								
PGTR2	HUMAN GLUCOSE TRANSPORTER TYPE 2, BRAIN	272-299								
PGTR4	HUMAN GLUCOSE TRANSPORTER TYPE 4, INSULIN-RESPONSIVE	290-317								
PHIO	HUMAN HISTONE H1	44-89								
PHIA	HUMAN HISTONE H1A (H1.1)	71-104								
PHIB	HUMAN HISTONE H1B (H1.4)	70-101								
PHIC	HUMAN HISTONE H1C (H1.5)	71-102								
PHID	HUMAN HISTONE H1D (H1.2)	70-101								
PHIT	HUMAN HISTONE H1T	74-105								
PHZB0	HUMAN HISTONE H2B.1	20-47								
PHZB2	HUMAN HISTONE H2B.2	20-47								
PHZB	HUMAN HISTONE H2B (H2B.1 A)	20-47								
PHZ3	HUMAN HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ (Q) ALPHA CHAIN PRECURSOR	142-169								
PHZK	HUMAN HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR (W) BETA CHAIN PRECURSOR	56-83								
PHBP	HUMAN HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP (W) BETA CHAIN PRECURSOR	50-77								
PHBQ	HUMAN HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP (W) BETA CHAIN PRECURSOR	50-77								
PHB3	HUMAN HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, SB BETA CHAIN (FRAGMENT)	16-43								
PHBG1	HUMAN HEPARIN-BINDING GROWTH FACTOR PRECURSOR 1 (HBGF-1) (ACIDIC FIBROBLAST	102-129								
PHBG2	HUMAN HEPARIN-BINDING GROWTH FACTOR PRECURSOR 2 (HBGF-2)	61-91								
PHBG3	HUMAN FIBROBLAST GROWTH FACTOR-4 PRECURSOR (FGF-4) (HBGF-4) (HST-2)	41-75	159-186							
PHBI	HUMAN P59 PROTEIN (HSP BINDING IMMUNOPHILIN) (HBI) (POSSIBLE PEPTIDYL-PROLYL	264-312								
PHEM4	HUMAN UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.73) (UROPORPHYRINOGEN-III	74-118								
PHF2	HUMAN HEPARIN COFACTOR II PRECURSOR (HC-II) (PROTEASE INHIBITOR LEUSEPIN 2)	169-196								
PHF3	HUMAN SERINE PROTEASE HEPSEN (EC 3.4.21.-)	22-49								
PHF5A	HUMAN BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL-	356-383								
PHF5B	HUMAN BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL-BETA-	388-415								
PHMX1	HUMAN HOMEOBOX PROTEIN MSX-1 (HOX-7)	178-212								
PHNFA	HUMAN HEPATOCYTE NUCLEAR FACTOR 1-ALPHA (HNF-1A) (LIVER SPECIFIC	2-29								
PHOT	HUMAN HEMOXYGENASE I (EC 1.14.99.3) (HO-1)	197-224								
PHPTD	HUMAN 4-HYDROXYPHENYL PYRUVATE DIOXYGENASE (EC 1.13.11.27) (4HPPD)	306-333								
PHRX	HUMAN ZINC FINGER PROTEIN HBX	521-548	914-974	1637-1666	2215-2286	2289-2316	3117-3144	3448-3475		
PHS1	HUMAN HEMATOPOIETIC LINEAGE CELL SPECIFIC PROTEIN	43-70								
PHS9A	HUMAN HEAT SHOCK PROTEIN HSP 90-ALPHA (HSP 86)	443-470	640-674							
PHSER	HUMAN HEAT-STABLE ENTEROTOXIN RECEPTOR PRECURSOR (GC-C) (INTESTINAL	511-545								
PHSF1	HUMAN HEAT SHOCK FACTOR PROTEIN 1 (HSF 1) (HEAT SHOCK TRANSCRIPTION FACTOR	113-140	168-209							
PHSF2	HUMAN HEAT SHOCK FACTOR PROTEIN 2 (HSF 2) (HEAT SHOCK TRANSCRIPTION FACTOR	117-198								
PHY21	HUMAN 10 HEAVY CHAIN PRECURSOR V-J REGION (ARH-77)	67-108								
PHYT	HUMAN 10 HEAVY CHAIN V-III REGION (GAL)	47-74								
PHX11	HUMAN HOMEOBOX PROTEIN HOX-11 (TCL-3 PROTO-ONCOGENE)	262-289								
PHX87	HUMAN HOMEOBOX PROTEIN HOX-87 (HOX-1C) (RHOD.C1)	115-162								
PIAPP	HUMAN ISLET AMYLOID POLYPEPTIDE	53-80								
PIBP3	HUMAN INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 PRECURSOR (IGFBP-3)	183-210								
PICI	HUMAN PLASMA PROTEASE C1 INHIBITOR PRECURSOR (C1 INH)	231-278								
PICQ2	HUMAN INTERCELLULAR ADHESION MOLECULE-2 PRECURSOR (ICAM-2)	57-84								
PIDB	HUMAN INSULIN-DEGRADING ENZYME (EC 3.4.99.45) (INSULINASE) (INSULIN	474-504	907-941							
PIF41	HUMAN EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)	232-259	322-349							
PIF4B	HUMAN INTRINSIC FACTOR PRECURSOR (IF) (GASTRIC INTRINSIC FACTOR)	149-176	406-433							
PIF	HUMAN INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN) (ERYTHROID	308-349								
PIFBA	HUMAN INTERLEUKIN-1 ALPHA PRECURSOR (IL-1 ALPHA) (HEMA TOPOETIN-1)	80-107	183-210							
PLITA	HUMAN INTERLEUKIN-1 RECEPTOR, TYPE 1 PRECURSOR (IL-1R) (P80)	76-110	172-199							

FCG-GENE	1021784.Nr01/ Search on All Human Protein Sequences	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10
FILE NAME	PROTEIN	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10
PILIR HUMAN	INTERLEUKIN-1 RECEPTOR, TYPE I PRECURSOR (IL-1R1) (P00)	437-467									AREA 2
PILIR HUMAN	INTERLEUKIN-1 RECEPTOR, TYPE II PRECURSOR (IL-1R2)	159-186									
PILIR HUMAN	INTERLEUKIN-3 RECEPTOR ALPHA CHAIN PRECURSOR (IL-3R-ALPHA)	87-114									
PILIR HUMAN	INTERLEUKIN-4 PRECURSOR (IL-4) (B-CELL STIMULATORY FACTOR 2) (BSF-2)	112-139									
PILIR HUMAN	INTERFERON ALPHA-1 PRECURSOR	94-121									
PINAI HUMAN	INTERFERON ALPHA-1 PRECURSOR (IFN-ALPHA-REC)	90-117	164-191	300-327	508-535						
PINAI HUMAN	INTERFERON BETA PRECURSOR (FIBROBLAST)	88-129									
PINAI HUMAN	INTERFERON-INDUCED 17 KD PROTEIN (CONTAINS: INTERFERON-INDUCED 15 KD	83-121									
PINAI HUMAN	INTERFERON-INDUCED 36 KD PROTEIN (IFI-36K)	51-78	216-245	393-430							
PINAI HUMAN	INSULIN RECEPTOR PRECURSOR (EC 2.7.1.112) (IR)	592-619									
PINAI HUMAN	INVOLUCRIN	119-146	229-273	316-363	386-430						
PITX HUMAN	ID-MYO-INOSITOL-TRISPHOSPHATE 5-KINASE A (EC 2.7.1.127) (INOSITOL	121-162									
PITX HUMAN	PLASMA SERINE PROTEASE (PROTEIN C) INHIBITOR PRECURSOR (PCI)	90-117	206-233								
PITX HUMAN	INTERPHOTORECEPTOR RETINOID-BINDING PROTEIN PRECURSOR (IRBP)	670-697									
PITX HUMAN	INTERFERON REGULATORY FACTOR 2 (IRF-2)	157-193									
PITX HUMAN	25 KD INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR	235-262									
PITX HUMAN	PLATELET MEMBRANE GLYCOPROTEIN IIA PRECURSOR (GPIIb) (COLLAGEN RECEPTOR	900-927									
PITX HUMAN	FIBRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-F)	250-284	637-695	765-792							
PITX HUMAN	FIBRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-E) (CD49F)	884-911	944-974								
PITX HUMAN	LEUKOCYTE ADHESION GLYCOPROTEIN LFA-1 ALPHA CHAIN PRECURSOR (LEUKOC	256-283	310-341	795-822							
PITX HUMAN	CELL SURFACE GLYCOPROTEIN MAC-1 ALPHA SUBUNIT PRECURSOR (CR-3 ALPHA	1044-1078									
PITX HUMAN	VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V)	230-264									
PITX HUMAN	FIBRONECTIN RECEPTOR BETA SUBUNIT PRECURSOR (INTEGRIN BETA-1) (CD29)	218-245	334-399								
PITX HUMAN	CELL SURFACE ADHESION GLYCOPROTEINS LFA-1, CR3 AND P150.95, BETA-	319-366	705-732								
PITX HUMAN	PLATELET MEMBRANE GLYCOPROTEIN IIIa PRECURSOR (GPIIb) (INTEGRIN BETA-	324-351									
PITX HUMAN	INTEGRIN BETA-4 SUBUNIT PRECURSOR (GPIIb)	342-369									
PITX HUMAN	INTEGRIN BETA-3 SUBUNIT PRECURSOR	724-751									
PITX HUMAN	INTEGRIN BETA-4 SUBUNIT PRECURSOR	311-318	332-393								
PITX HUMAN	INTEGRIN BETA-8 SUBUNIT PRECURSOR	162-199	606-717								
PITX HUMAN	INTER-ALPHA-TRYPsin INHIBITOR COMPLEX COMPONENT II PRECURSOR	134-161	435-452	772-818							
PITX HUMAN	KERATIN, TYPE I CYTOSKELETAL 10 (CYTOKERATIN 10) (K10)	154-187	196-227	337-399	428-462						
PITX HUMAN	KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13)	112-142									
PITX HUMAN	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14)	122-152	306-335	393-424							
PITX HUMAN	KERATIN, TYPE I CYTOSKELETAL 15 (CYTOKERATIN 15) (K15)	112-141									
PITX HUMAN	KERATIN, TYPE I CYTOSKELETAL 16 (CYTOKERATIN 16) (K16)	308-339									
PITX HUMAN	KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17)	122-152	302-346	393-431							
PITX HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (CYTOKERATIN 18) (K18)	87-114	231-298	337-385							
PITX HUMAN	KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19)	88-118	317-362	370-397							
PITX HUMAN	KERATIN, TYPE I CYTOSKELETAL 1 (CYTOKERATIN 1) (K1)	196-226	346-384	390-467							
PITX HUMAN	KERATIN, TYPE II CYTOSKELETAL 63 KD	215-248	364-405	461-488							
PITX HUMAN	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (FRAGMENT)	42-73	126-153	189-248							
PITX HUMAN	KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (58 KD	185-246	332-373								
PITX HUMAN	KERATIN, TYPE II CYTOSKELETAL 6 (CYTOKERATIN 6) (K6) (K6B KERATIN)	178-239	335-366	422-449							
PITX HUMAN	KERATIN, TYPE II CYTOSKELETAL 8 (CYTOKERATIN 8) (K8)	140-167									
PITX HUMAN	KERATIN, TYPE II CYTOSKELETAL 36 KD (K6A KERATIN) (FRAGMENT)	7-34	170-161	217-244							
PITX HUMAN	6-PHOSPHOFRUCTOKINASE, MUSCLE TYPE (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE	140-167									
PITX HUMAN	6-PHOSPHOFRUCTOKINASE, LIVER TYPE (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE	49-80	128-159								
PITX HUMAN	PHOTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL (EC 2.7.1.112) (P150)	498-525									
PITX HUMAN	IG KAPPA CHAIN C REGION	37-85									
PITX HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (ADHESION MOLECULE-LIKE X-LINK	180-414									
PITX HUMAN	CAMP-DEPENDENT PROTEIN KINASE TYPE I-ALPHA REGULATORY CHAIN	179-208									
PITX HUMAN	CAMP-DEPENDENT PROTEIN KINASE TYPE I-BETA REGULATORY CHAIN	177-204									
PITX HUMAN	CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN	175-202	290-317								
PITX HUMAN	NUCLEAR FACTOR KAPPA-B SUBUNIT-1 (NF-KAPPA-B P105 SUBUNIT)	329-370									
PITX HUMAN	CREATINE KINASE, B CHAIN (EC 2.7.3.2)	301-328									
PITX HUMAN	TYROSINE PROTEIN KINASE ECK PRECURSOR (EC 2.7.1.113) (EPITHELIAL CELL	468-493									
PITX HUMAN	PHOTO-ONCOGENE TYROSINE-PROTEIN KINASE FER (EC 2.7.1.112) (P94-FER)	219-246	564-591								

PGCENE	10111144 Motif Search on All Human Protein Sequences	AKRA1	AKRA2	AKRA3	AKRA4	AKRA5	AKRA6	AKRA7	AKRA8	AKRA9
FILE NAME	PROTEIN	AKRA1	AKRA2	AKRA3	AKRA4	AKRA5	AKRA6	AKRA7	AKRA8	AKRA9
PKTES_HUMAN	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FES/FPS (EC 2.7.1.112) (C-FES)	101-145	295-322							
PKFLT_HUMAN	RECEPTOR-RELATED TYROSINE KINASE FLT PRECURSOR (EC 2.7.1.112)	208-235	319-353							
PKFMS_HUMAN	MACROPHAGE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (CSF-1-R)	293-320								
PKFTN_HUMAN	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN)	199-233								
PKOPB_HUMAN	CGMP-DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37)	17-34								
PKHEK_HUMAN	TYROSINE KINASE HEK RECEPTOR PRECURSOR (EC 2.7.1.112)	646-673								
PKNH_HUMAN	KINESIN HEAVY CHAIN	125-155	425-452	633-680	689-716	872-899				
PKKIT_HUMAN	KIT PROTO-ONCOGENE TYROSINE KINASE PRECURSOR (EC 2.7.1.112)	235-263								
PKMET_HUMAN	HEPATOCYTE GROWTH FACTOR RECEPTOR PRECURSOR (MET PROTO-ONCOGENE KININOGEN, HMW PRECURSOR (ALPHA-2-THIOL PROTEINASE INHIBITOR)	898-975								
PKNH_HUMAN	KININOGEN, HMW PRECURSOR (ALPHA-2-THIOL PROTEINASE INHIBITOR)	505-532								
PKP35_HUMAN	GALACTOSYLTRANSFERASE ASSOCIATED PROTEIN KINASE P35/GTA (EC 2.7.1.1)	81-108								
PKP48_HUMAN	INTERFERON-INDUCED, DOUBLE-STRANDED RNA-ACTIVATED PROTEIN KINASE	149-179	191-235	285-312						
PKP78_HUMAN	POTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.1)	582-609								
PKPCL_HUMAN	PROTEIN KINASE C, ETA TYPE (EC 2.7.1.1) (RPKC-ETA) (PKC-L)	318-345								
PKPT1_HUMAN	SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1 (EC 2.7.1.1)	149-176	208-233							
PKPY1_HUMAN	PYRUVATE KINASE M1 (MUSCLE) ISOZYME (EC 2.7.1.40) (CYTOSOLIC THYROID	243-289								
PKPY2_HUMAN	PYRUVATE KINASE M2 ISOZYME (EC 2.7.1.40)	243-289								
PKPYR_HUMAN	PYRUVATE KINASE, ISOZYME R (EC 2.7.1.40)	2-29								
PKRET_HUMAN	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE RET (EC 2.7.1.112)	183-217								
PKROS_HUMAN	ROS PROTO-ONCOGENE TYROSINE KINASE (EC 2.7.1.112) (FRAGMENT)	137-203								
PKSRC_HUMAN	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P60-SRC)	143-170								
PKU7_HUMAN	LUPUS KU AUTOANTIGEN PROTEIN P70 (70 KD SUBUNIT OF KU ANTIGEN)	235-279								
PKUB6_HUMAN	LUPUS KU AUTOANTIGEN PROTEIN P86 (86 KD SUBUNIT OF KU ANTIGEN)	238-292								
PKYES_HUMAN	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES (EC 2.7.1.112) (P61-YES)	208-243								
PLAM1_HUMAN	LAMIN B1	32-66	117-144	152-193	214-241	397-424	480-507	510-539		
PLAM2_HUMAN	LAMIN A (70 KD LAMIN)	32-68	114-165	292-343						
PLAMC_HUMAN	LAMIN C	32-68	114-165	292-343						
PLAR_HUMAN	LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48)	935-969								
PLA_HUMAN	LUPUS LA PROTEIN (SIOGREN SYNDROME TYPE B ANTIGEN (SS-B))	191-222	295-342							
PLCAT_HUMAN	PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)	131-158								
PLDIH1_HUMAN	L-LACTATE DEHYDROGENASE H CHAIN (EC 1.1.1.27) (LDH-B)	81-108	302-379							
PLDIH2_HUMAN	L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A)	235-252								
PLDLR_HUMAN	LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR	483-510								
PLECH_HUMAN	ASialoglycoprotein receptor 1 (HEPATIC LECTIN II) (ASGPR)	62-96								
PLEND_HUMAN	P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GNP-140) (PADGEM)	32-59	87-116							
PLGUL_HUMAN	LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE)	83-117								
PLIF_HUMAN	LEUKAEMIA INHIBITORY FACTOR PRECURSOR (LIF) (DIFFERENTIATION-	95-122								
PLIN1_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	152-179	232-263	298-358	671-698	874-901	1036-1066			
PLIPO_HUMAN	TRIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.3) (LIPASE, GASTRIC)	158-185								
PLIPS_HUMAN	HORMONE SENSITIVE LIPASE (EC 3.1.1.3) (HSL)	305-332								
PLKHA_HUMAN	LEUKOTRIENE A-4 HYDROLASE (EC 3.3.2.6) (LTA-4 HYDROLASE) (LEUKOTRIENE	42-83	290-324							
PLKHA_HUMAN	LAMININ A CHAIN PRECURSOR	1318-1345	1741-1771	1785-1812	1874-1851	1884-1921	1965-1999	2026-2059	2091-2118	
PLMB1_HUMAN	LAMININ B1 CHAIN PRECURSOR	1267-1314	1364-1394	1397-1631	1651-1714	1722-1781				
PLMB2_HUMAN	LAMININ B2 CHAIN PRECURSOR	1105-1135	1513-1547							
PLMP2_HUMAN	LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 2 PRECURSOR (LAMP-2)	135-182								
PLP02_HUMAN	ARACHIDONATE 12-LIPOXYGENASE (EC 1.13.11.3) (12-LOX)	341-368								
PLP03_HUMAN	ARACHIDONATE 5-LIPOXYGENASE (EC 1.13.11.34) (5-LIPOXYGENASE) (5-LO)	50-87								
PLP13_HUMAN	LACTASE-PHLOUZIN HYDROLASE PRECURSOR (EC 3.2.1.63)	776-809								
PLP16_HUMAN	PROTEIN-TYROSINE PHOSPHATASE BETA PRECURSOR (EC 3.2.1.60)	140-167	589-637							
PLP17_HUMAN	PROTEIN-TYROSINE PHOSPHATASE GAMMA PRECURSOR (EC 3.1.3.48)	1081-1108								
PLP22_HUMAN	PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR (EC 3.1.3.48) (PTP-ZETA)	553-587	1024-1051	1973-2000						
PLSHR_HUMAN	LUTROPIN-CHORIOGNADOTROPIC HORMONE RECEPTOR PRECURSOR (LHCG-R)	66-114	448-480							
PLV2B_HUMAN	IG LAMBDA CHAIN V-II REGION (NET)	61-88								
PLYAG_HUMAN	LYSOSOMAL ALPHA-GLUCOSIDASE PRECURSOR (EC 3.2.1.20) (ACID MALTASE)	183-212								
PLZAG_HUMAN	MITOCHONDRIAL 2-OXOGLUTARATE MALATE CARRIER PROTEIN (OGCP)	50-77								
PMAC3_HUMAN	GALLACTOSE-SPECIFIC LECTIN (MAC-2 ANTIGEN) (G2-BINDING PROTEIN) (S1 KD	219-246								
PMAN9_HUMAN	MAN(9)-ALPHA-MANNOSIDASE (EC 3.2.1.1)	414-441								

PCGENE	1071784 Ncift Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PMANA_HUMAN	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.1.1.9) (PHOSPHOMANNOSE ISOMERASE)	60-87								
PMANR_HUMAN	MACROPHAGE MANNOSE RECEPTOR PRECURSOR	248-284	1147-1182							
PMAP2_HUMAN	MICROTUBULE-ASSOCIATED PROTEIN 2 (FRAGMENT)	434-478								
PMAP4_HUMAN	MICROTUBULE-ASSOCIATED PROTEIN 4	408-449								
PMAX_HUMAN	MAX PROTEIN	117-144								
PMDM2_HUMAN	MDM2 PROTEIN (P53-ASSOCIATED PROTEIN)	235-288								
PMDR1_HUMAN	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)	561-595								
PMERL_HUMAN	MERLIN (SCHWANNOMIN)	377-407	532-566							
PMERO_HUMAN	MEROSIN HEAVY CHAIN (LAMININ CHAIN A2) (FRAGMENT)	71-105	139-173	431-458	791-818					
PMGMT_HUMAN	METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE (EC 2.1.1.63) (6-O-)	91-118								
PMKLP_HUMAN	MITOTIC KINESIN-LIKE PROTEIN 1	207-224	319-346	510-537	549-608					
PMKLT_HUMAN	MELANIN-CONCENTRATING HORMONE PRECURSOR	8-35								
PMKX1_HUMAN	MIXED LINEAGE KINASE 1 (EC 2.1.1-) (FRAGMENT)	130-157	321-348							
PMASA_HUMAN	METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE	393-420								
PMOES_HUMAN	MOESIN (MEMBRANE-ORGANIZING EXTENSION SPIKE PROTEIN)	119-146	351-403							
PMPCP_HUMAN	MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN PRECURSOR	286-313								
PMPI3_HUMAN	M-Phase INDUCER PHOSPHATASE 3 (EC 3.1.3.48)	72-99								
PMPKK_HUMAN	DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE (EC 2.7.1.1-)	19-50								
PMPL1_HUMAN	CATION-INDEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR (CI MAN-6)	1569-1596	2437-2478							
PMRCP_HUMAN	MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN	396-423	507-548							
PMSTR_HUMAN	MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (MELANOTROPIN	18-63								
PMKLE_HUMAN	MACROPHAGE SCAVENGER RECEPTOR TYPES I AND II (MACROPHAGE ACETYLATED	173-204	230-260							
PMIDM_HUMAN	DNA (CYTOSINE-3)-METHYLTRANSFERASE (EC 2.1.1.37) (DNA	387-414	601-628							
PMITF_HUMAN	MITOCHONDRIAL TRANSCRIPTION FACTOR 1 PRECURSOR (MTTF1)	181-212								
PMUTA_HUMAN	METHYLMALONYL-COA MUTASE PRECURSOR (EC 3.4.99.3) (MCM)	468-519								
PMQ2_HUMAN	INTERFERON-REGULATED RESISTANCE GTP-BINDING PROTEIN MAX (INTERFERON-108-150									
PMQ3_HUMAN	INTERFERON-REGULATED RESISTANCE GTP-BINDING PROTEIN MAXB (P78-RELATED	431-489	670-697							
PMYBA_HUMAN	MYB-RELATED PROTEIN A (FRAGMENT)	619-646								
PMYBB_HUMAN	MYB-RELATED PROTEIN B	87-117								
PMYCN_HUMAN	N-MYC PROTO-ONCOGENE PROTEIN	263-300	413-461							
PMYC_HUMAN	MYC PROTO-ONCOGENE PROTEIN	193-422								
PMYF4_HUMAN	MYOGENIC FACTOR MYF-4 (MYOGENIN)	119-146								
PMYF3_HUMAN	MYOGENIC FACTOR MYF-3	121-148								
PMYF2_HUMAN	MYELIN P2 PROTEIN	70-110								
PMYF1_HUMAN	MYELIN P1 PROTEIN	43-70								
PMYF7_HUMAN	MYELIN PROTEOLIPID PROTEIN (PLP) (LIPOPHILIN) (CONTAINS: MYELIN	38-25								
PMY5A_HUMAN	MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM (FRAGMENT)	48-75								
PMY5B_HUMAN	MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM	1541-1582	1640-1681	1683-1710	1801-1838					
PMY5E_HUMAN	MYOSIN HEAVY CHAIN, FAST SKELETAL MUSCLE, EMBRYONIC	46-73	860-903	932-1077	1119-1146	1193-1235	1267-1340	1364-1411	1483-1597	1641-1675
PMY5P_HUMAN	MYOSIN HEAVY CHAIN, PERINATAL CARDIAC MUSCLE (FRAGMENT)	1707-1734	1822-1858							
PMY5S_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (FRAGMENT)	50-77	95-125	141-188	215-272	403-483	507-552	586-624	685-736	784-818
PMY5SS_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (FRAGMENT)	823-907	946-987	1049-1076						
PMY5SS_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (FRAGMENT)	133-160	193-280	304-349	423-460	468-526	581-608	645-681	743-798	808-835
PMY1_HUMAN	MYELIN TRANSCRIPTION FACTOR 1 (MYT1) (FRAGMENT)	640-678								
PMY2_HUMAN	SODIUM/CALCIUM EXCHANGER PRECURSOR (NA+/CA2+-EXCHANGE PROTEIN)	492-519	594-621	705-735						
PMY3_HUMAN	NEURAL CELL ADHESION MOLECULE, PHOSPHATIDYLINOSITOL-LINKED ISOFORM	235-282								
PMY4_HUMAN	NEUTROPHIL CYTOSOL FACTOR 1 (NCF-47K) (47 KD AUTOSOMAL CHRONIC	234-261	310-337							
PMY5_HUMAN	NEUTROPHIL NADPH OXIDASE FACTOR (P67-PHOX)	532								
PMY6_HUMAN	DNA-BINDING PROTEIN NEFA PRECURSOR	50-77	82-112	343-395						
PMY7_HUMAN	NEPHLYSIN (EC 3.4.24.11) (NEUTRAL ENDOPEPTIDASE) (NEP)	170-216	644-671							
PMY8_HUMAN	NEUROFIBROMIN (NEUROFIBROMATOSIS-RELATED PROTEIN NF-1) (FRAGMENT)	1145-1172	1388-1422	1639-1666						
PMY9_HUMAN	NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)	91-128	431-490							
PMY10_HUMAN	NEUROFILAMENT TRIPLET L PROTEIN (68 KD NEUROFILAMENT PROTEIN) (NF-L)	92-126	441-468							
PMY11_HUMAN	NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M)	101-141	164-194	215-280	315-372	737-764	794-826	872-913		
PMY12_HUMAN	SUBSTANCE-P RECEPTOR (SPR) (NK-1 RECEPTOR) (NK-1R)	338-365								
PMY13_HUMAN	NATURAL KILLER CELLS PROTEIN 4 PRECURSOR	166-193								











FCG	GENE	1071784	NCBI	Search on All Human Protein Sequences	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
FILE	NAME	PROTEIN											
PTAPB	HUMAN	TRANSCRIPTION FACTOR JUN-B		296-323									
PTAPD	HUMAN	TRANSCRIPTION FACTOR JUN-D		291-313									
PTAUT	HUMAN	MICROTUBULE-ASSOCIATED PROTEIN TAU		278-305									
PTAU2	HUMAN	MICROTUBULE-ASSOCIATED PROTEIN TAU, FETAL		211-238									
PTCCL	HUMAN	TRANSCOBALAMIN 1 PRECURSOR		201-241	310-337								
PTCPL	HUMAN	T-COMPLEX PROTEIN 1 (TCP-1)		316-343									
PTDIT	HUMAN	DNA NUCLEOTIDYL-LEOTRANSFERASE (EC 2.7.7.3) (TERMINAL ADDITION ENZYME)		61-95									
PTERK	HUMAN	RECEPTOR TYROSINE KINASE TEK PRECURSOR (EC 2.7.1.112) (ITK-6)		909-996	1007-1016								
PTF2B	HUMAN	TRANSCRIPTION INITIATION FACTOR IIB (TFIIB)		135-162									
PTF2J	HUMAN	TRANSCRIPTION FACTOR E1 (FRAGMENT)		43-70	122-149	178-226							
PTFS2	HUMAN	TRANSCRIPTION ELONGATION FACTOR 3-II		29-36									
PTF52	HUMAN	TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III)		148-175									
PTGFI	HUMAN	TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1)		148-185									
PTGFI	HUMAN	TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (TGF-BETA 2) (GLI 100H AS316)		241-270									
PTGFA	HUMAN	TRANSFORMING GROWTH FACTOR ALPHA PRECURSOR (TGF-ALPHA) (EGF-LIKE TOX)		87-114									
PTGLK	HUMAN	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE K (EC 2.3.2.13)		238-285									
PTHBS	HUMAN	THROMBOSPONDIN PRECURSOR		110-165	284-314								
PTHIK	HUMAN	3-KETOACYL-COA THIOLASE PEROXISOMAL PRECURSOR (EC 2.3.1.16) (BETA-)		185-212									
PTKND	HUMAN	PROTACHININ BETA PRECURSOR (CONTAINS: SUBSTANCE P, NEUROKININ A)		11-38									
PTLEI	HUMAN	TRANSUDIN-LIKE ENHANCER PROTEIN 1		626-653									
PTLEJ	HUMAN	TRANSUDIN-LIKE ENHANCER PROTEIN 2		94-125									
PTLEA	HUMAN	TRANSUDIN-LIKE ENHANCER PROTEIN 4 (FRAGMENT)		304-331									
PTOPA	HUMAN	DNA TOPOISOMERASE II, ALPHA ISOZYME (EC 5.99.1.3)		19-46	501-532								
PTOPB	HUMAN	DNA TOPOISOMERASE II, BETA ISOZYME (EC 5.99.1.3)		35-65	616-647								
PTPM3	HUMAN	TROPOMYOSIN, FIBROBLAST ISOFORM TM3		16-74	82-116								
PTPNA	HUMAN	TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE		16-43	47-74	147-174	191-237	243-277					
PTPAB	HUMAN	TROPOMYOSIN BETA CHAIN, SKELETAL MUSCLE		32-116	191-240								
PTPMC	HUMAN	TROPOMYOSIN ALPHA CHAIN, CARDIAC MUSCLE		16-74	82-116	193-277							
PTPMF	HUMAN	TROPOMYOSIN, FIBROBLAST AND EPITHELIAL MUSCLE-TYPE (TM10) (TME1)		37-116	210-240	243-270							
PTPMG	HUMAN	TROPOMYOSIN, FIBROBLAST NON-MUSCLE TYPE (TM10PL)		46-80	111-138	158-190	207-234						
PTPNI	HUMAN	TROPOMYOSIN, CYTOSKELETAL TYPE (TM10NM)		46-80	111-138	172-197							
PTPAS	HUMAN	TROPOMYOSIN ALPHA CHAIN, SMOOTH MUSCLE (FRAGMENT)		25-59	147-174								
PTPPI	HUMAN	TRIPETIDYL-PEPTIDASE II (EC 3.4.14.10) (TPP II) (TRIPETIDYL)		133-187	1004-1031	1160-1187							
PTPR	HUMAN	TPR ONCOGENE (FRAGMENT)		82-147									
PTR36	HUMAN	TREB36 PROTEIN		18-45	242-269								
PTR6R	HUMAN	THYROTROPIN-RELEASING HORMONE RECEPTOR (TRH-R) (THYROLIBERIN)		349-383									
PTRUC	HUMAN	TROPONIN I, CARDIAC MUSCLE		36-63									
PTRKA	HUMAN	HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112)		66-93	117-148								
PTRSR	HUMAN	TRANSFERRIN RECEPTOR PROTEIN (TR) (ANTIGEN CD71) (T9)		188-215	366-393								
PTSHR	HUMAN	THYROTROPIN RECEPTOR PRECURSOR (TSH-R)		87-117	420-447								
PTTK	HUMAN	PROTEIN KINASE TKK (EC 2.7.1.1)		126-197	324-359	510-544	549-583						
PTTK2	HUMAN	NON-RECEPTOR TYROSINE-PROTEIN KINASE TYR2 (EC 2.7.1.112)		150-177									
PUBA1	HUMAN	UBIQUITIN-ACTIVATING ENZYME E1 (A159 PROTEIN)		448-475									
PUBF1	HUMAN	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UBF-1)		227-254									
PUDP	HUMAN	UDP-GLUCURONOSYLTRANSFERASE PRECURSOR, MICROSOMAL (EC 2.4.1.17)		227-254									
PUPD	HUMAN	RECEPTOR TYROSINE-PROTEIN KINASE UFO PRECURSOR (EC 2.7.1.112)		488-522									
PUSF1	HUMAN	UPSTREAM STIMULATORY FACTOR 1		251-295									
PVATC	HUMAN	VACUOLAR ATP SYNTHASE SUBUNIT C (EC 3.6.1.34) (V-ATPASE C SUBUNIT)		47-74	117-147								
PVILL	HUMAN	VILLIN		318-372	427-461	712-744							
PVIME	HUMAN	VIMENTIN		119-146	233-260								
PVINC	HUMAN	VINCULIN		108-135									
PVPRI	HUMAN	RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-)		95-174									
PWEEI	HUMAN	WEEL-LIKE PROTEIN KINASE (EC 2.7.1.113)		354-388									
PWT1	HUMAN	WILMS TUMOR PROTEIN (WT1)		247-274									
PXBPT	HUMAN	X BOX BINDING PROTEIN-1 (XBP-1) (TREB3 PROTEIN)		97-115									
PXPAC	HUMAN	DNA-REPAIR PROTEIN COMPLEMENTING XP-A CELLS (XERODERMA PIGMENTOSUM)		180-211									
PXPCC	HUMAN	DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM)		134-168	701-728								

PCGENE	107117144	Moif Search on All Human Protein Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
FILENAME	PROTEIN		AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PXPDC_HUMAN	DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM)	264-291		715-766	1047-1081						
PXPDC_HUMAN	DNA-REPAIR PROTEIN COMPLEMENTING XP-G CELLS (XERODERMA PIGMENTOSUM)	83-110									
PXRCC_HUMAN	DNA-REPAIR PROTEIN XPRCC1	23-57									
PZN10_HUMAN	ZINC FINGER PROTEIN 10 (ZINC FINGER PROTEIN KOX1) (FRAGMENT)	29-56									
PZN40_HUMAN	ZINC FINGER PROTEIN 40 (HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER)	17-62		307-334	1071-1078	1469-1500	2013-2037	2146-2180			
PZN43_HUMAN	ZINC FINGER PROTEIN 43 (URC1744) (FRAGMENT)	3-30		201-228							
PZN46_HUMAN	ZINC FINGER PROTEIN 46 (ZINC FINGER PROTEIN KUP)	121-149									

## TABLE X

Search Results Summary for PCTLZIP,  
P1CTLZIP, and P2CTLZIP Motifs



PHEMA MUMPM	133-146		PHEMA IABAN	221-237		PHEMA CVHOC	381-408
PHEMA MUMPR	133-148		PHEMA IABUD	234-260		PHEMA IAAIC	322-339
PHEMA MUMPS	133-148		PHEMA IACKA	234-260		PHEMA IABAN	308-323
PHEMA P11HW	345-380		PHEMA IACKG	231-247		PHEMA IABUD	320-337
PHEMA P12H	65-80		PHEMA IACKV	230-246		PHEMA IACKA	320-337
PHEMA P12HT	65-80		PHEMA IADA1	234-260		PHEMA IACKG	316-333
PHEMA RINDK	308-383		PHEMA IADA3	237-263		PHEMA IACKP	302-319
PHEMA SV6	7-84		PHEMA IADCC	234-260		PHEMA IACKQ	302-319
PHEMA SV6CM	7-84		PHEMA IADH1	221-237		PHEMA IACKG	316-333
PHEMA SV6CP	7-84		PHEMA IADH2	221-237		PHEMA IACKG	316-333
PHEMA SV6LN	7-84		PHEMA IADH3	221-237		PHEMA IACKV	316-333
PVENV DHV11	42-57		PHEMA IADH4	221-237		PHEMA IADA1	320-337
PVP77 CAPYK	89-104		PHEMA IADH6	221-237		PHEMA IADA3	322-339
PVRUB VACC0	72-87		PHEMA IADH6	221-237		PHEMA IADCC	320-337
PVG01 BPP22	242-267		PHEMA IADH7	221-237		PHEMA IADH1	308-323
PVG01 HBVEB	108-184		PHEMA IADM2	237-263		PHEMA IADH2	308-323
PVG01 H8V11	210-226	317-332	PHEMA IADNZ	204-260		PHEMA IADH3	308-323
PVG06 BPT4	184-198		PHEMA IAE6	221-237		PHEMA IADH4	308-323
PVG07 BPT4	895-800		PHEMA IAE7	237-263		PHEMA IADH8	308-323
PVG08 HBV11	134-149		PHEMA IAFPR	230-246		PHEMA IADH7	308-323
PVG10 BPPH2	183-188		PHEMA IAHAL	230-262		PHEMA IADM2	322-339
PVG10 BPPZA	183-188		PHEMA IAHAR	235-261		PHEMA IADNZ	320-337
PVG10 H8V8A	106-124		PHEMA IAHCB	230-246		PHEMA IAE6	308-323
PVG16 BPP1	81-88		PHEMA IAHCB	230-246		PHEMA IAE7	322-339
PVG18 BPT4	468-483		PHEMA IAHCD	230-246		PHEMA IAFPR	316-332
PVG26 BPT4	87-112		PHEMA IAHDE	230-246		PHEMA IAGRE	320-337
PVG29 HBV11	20-35		PHEMA IAHFO	235-262		PHEMA IAGUA	320-337
PVG30 BPPH8	11-84		PHEMA IAHK6	235-262		PHEMA IAHAL	318-336
PVG30 BPOX2	22-37		PHEMA IAHK7	235-262		PHEMA IAHAL	321-338
PVG36 HBV8A	106-123		PHEMA IAHLE	230-246		PHEMA IAHCB	316-332
PVG37 BPT2	1263-1288		PHEMA IAHLO	230-246		PHEMA IAHCB	316-332
PVG37 HBV11	284-289		PHEMA IAHMI	235-262		PHEMA IAHCB	316-332
PVG66 HBV11	22-37	143-168	PHEMA IAHNM	235-262		PHEMA IAHCD	316-332
PVG66 HBV11	286-283		PHEMA IAHRO	235-262		PHEMA IAHDE	316-332
PVG68 HBV11	102-117		PHEMA IAH8A	235-262		PHEMA IAHFO	321-338
PVG68 HBV11	287-282		PHEMA IAH8P	230-246		PHEMA IAHK6	321-338
PVG68 HBV11	518-533		PHEMA IAH8W	230-246		PHEMA IAHK7	321-338
PVG8 BPPH2	234-249		PHEMA IAHTE	230-262		PHEMA IAHLE	316-332
PVG8 BPPZA	234-249		PHEMA IAHTO	235-262		PHEMA IAHLO	316-332
PVG8 BPPV1R	57-72		PHEMA IAHUR	235-262		PHEMA IAHMI	321-338
PVG8 BPPHX	234-249		PHEMA IAKIE	235-261		PHEMA IAHNM	321-338
PVG12 CVBF	284-278		PHEMA IALEN	235-261		PHEMA IAHPR	316-332
PVG12 CVBL9	284-278		PHEMA IALAA	235-249		PHEMA IAHRO	321-338
PVG12 CVBLV	284-278		PHEMA IALAB	235-264		PHEMA IAH8A	321-338
PVG12 CVBM	284-278		PHEMA IALMAO	237-283		PHEMA IAH8P	316-332
PVG12 CVBQ	284-278		PHEMA IALM1	237-263		PHEMA IAH8W	316-332
PVG12 CVBV	284-278		PHEMA IALM2	237-263		PHEMA IAHTE	321-338

PVQL2 CVPF8	442-467		PHEMA JAME9	221-237				PHEMA IAHTO	321-338	
PVQL2 CVPPU	440-466	604-619	PHEMA JAMIN	86-101	231-247			PHEMA IAHRU	321-338	
PVQL2 CVPR8	218-233		PHEMA JANT6	237-263				PHEMA IAJAP	317-334	
PVQL2 CVPRM	218-233		PHEMA JAQU7	221-237				PHEMA IAMAA	318-338	
PVQL2 IBV6	1056-1071		PHEMA IARUD	234-250				PHEMA IAMAB	324-341	
PVQL2 IBV8	1055-1070		PHEMA IABE2	234-260				PHEMA IAMAO	322-338	
PVQL2 IBVD2	1056-1071		PHEMA IASH2	234-260				PHEMA IAME1	322-338	
PVQL2 IBVK	1055-1070		PHEMA IASTA	230-246				PHEMA JAME2	322-338	
PVQL2 IBVM	1056-1070		PHEMA IATAI	235-261				PHEMA JAME9	300-323	
PVQLB HSB8A	701-716		PHEMA IATKM	234-260				PHEMA JAMIN	318-333	
PVQLB PRVF	203-216		PHEMA IATKO	233-246				PHEMA JANT6	322-339	
PVQLC HSBVC	476-480		PHEMA IATKR	230-246				PHEMA IAPIL	320-337	
PVQLC HSE4	444-469		PHEMA IATKW	226-246				PHEMA JAQU7	300-323	
PVQLC HSEB	427-442		PHEMA IAUDD	237-263				PHEMA IARUD	320-337	
PVQLC PRVF	446-461		PHEMA IAU89	235-261				PHEMA IABE2	320-337	
PVQLD H8V11	78-84		PHEMA IAV17	230-264				PHEMA IASH2	321-338	
PVQLD H8V2	78-84		PHEMA IAXIA	235-261				PHEMA IASTA	316-332	
PVQLF BR8VA	286-280		PHEMA IAZCO	237-263				PHEMA IATKM	320-337	
PVQLF BR8VC	285-280		PHEMA IAZH2	221-237				PHEMA IAUDD	322-339	380-387
PVQLF BR8VR	285-280		PHEMA IAZH3	221-237				PHEMA IAV17	323-340	
PVQLF HR8V1	285-280		PHEMA IAZUK	237-263				PHEMA IAZCO	322-339	
PVQLF HR8VA	285-280		PHEMA INBAA	116-131	286-310			PHEMA IAZH2	306-323	
PVQLF HR8VL	285-280		PHEMA INBBE	123-139	303-318			PHEMA IAZH3	300-323	
PVQLF HR8VR	285-280		PHEMA INBBO	116-132	283-308			PHEMA IAZUK	322-339	
PVQLF MUMPS	8-84		PHEMA INBEN	123-139	301-316			PHEMA MUMPM	101-118	
PVQLI VZVD	278-283		PHEMA INBFU	108-124	288-301			PHEMA MUMPR	101-118	
PVQLM HANTB	800-816		PHEMA INBGL	118-136	288-311			PHEMA MUMPS	101-118	
PVQLM FTFV	743-768		PHEMA INBHK	116-132	283-308			PHEMA NDVA	93-110	
PVQLM 8EQR	801-816		PHEMA INBIB	108-124	288-303			PHEMA NDVB	93-110	
PVQLM 8EQU8	800-915		PHEMA INBID	120-136	289-314			PHEMA NDVD	93-110	
PVQLY LA88G	426-441		PHEMA INBLE	123-139	302-317			PHEMA NDVH	93-110	
PVQLY LA88J	427-442		PHEMA INBMO	113-129	282-307			PHEMA NDVI	93-110	
PVQLY MOPEI	426-440		PHEMA INBME	116-132	288-311			PHEMA NDVM	93-110	
PVM3A REOVD	621-636		PHEMA INBNA	108-124	288-303			PHEMA NDVQ	93-110	
PVM3A HPSG8	380-386		PHEMA INBOR	123-139	301-310			PHEMA NDVTQ	93-110	
PVM3A HPSV9	187-202		PHEMA INB81	123-139	301-316			PHEMA NDVV	93-110	
PVM3A WHV1	378-383		PHEMA INB9J	118-136	288-313			PHEMA PHODV	30-63	
PVM3A WHV59	383-398		PHEMA INBUS	116-132	294-309			PHEMA PI1HW	480-503	
PVM3A WHV7	383-398		PHEMA INBVI	116-132	286-311			PHEMA PI3B	111-128	
PVM3A WHV8	383-398		PHEMA INBVK	123-139	303-318			PHEMA PI3H4	111-128	
PVM3A WHV81	383-398		PHEMA INBYB	108-124	288-301			PHEMA PI3HA	111-128	
PVM3A WHVW6	234-249		PHEMA MUMPM	133-148				PHEMA PI3HT	111-128	
PVMT2 IAKIN	26-40		PHEMA MUMPR	133-148				PHEMA PI3HU	111-128	
PVMT2 IABAN	26-40		PHEMA MUMPB	133-148				PHEMA PI3HV	111-128	
PVMT2 IAFOW	26-40		PHEMA PI1HW	346-300				PHEMA PI3HW	111-128	
PVMT2 IAFPR	26-40		PHEMA PI2H	85-91				PHEMA PI3HX	111-128	
PVMT2 IAFPW	26-40		PHEMA PI2HT	85-91				PHEMA PI4HA	50-67	











## TABLE XI

Search Results Summary for P3CTLZIP, P4CTLZIP,  
P5CTLZIP, and P6CTLZIP Motifs









TABLE XII

Search Results Summary for P7CTLZIP,  
P8CTLZIP, and P9CTLZIP Motifs



PCTLZIP	LIBRARY FILE	P8CTLZIP	LIBRARY FILE	P8CTLZIP	LIBRARY FILE	P8CTLZIP	LIBRARY FILE
PENV BAELM	202-224	PENV FR9FV	380-403	PENV BLVAF	303-327		
PENV HV1B1	480-520	PENV2 FR9FV	300-403	PENV BLVAU	303-327		
PENV HV1B8	483-516	PENV BIV00	178-201	PENV BLVAV	303-327		
PENV HV1B9	494-516	PENV BIV22	207-230	PENV BLVB2	303-327		
PENV HV1B9	503-526	PENV FOAMV	004-087	PENV BLVB6	303-327		
PENV HV1EL	485-517	PENV HV123	176-180	PENV BLVJ	303-327		
PENV HV1H2	488-520	PENV HV2BE	3-20	PENV FINPE	781-806		
PENV HV1H3	488-520	PENV HV2CA	750-773	PENV FIVSD	778-803		
PENV HV1J3	510-532	PENV HV2D1	3-20	PENV FIVT2	780-804		
PENV HV1JR	480-512	PENV HV2G1	772-795	PHEMA CVBLY	381-415		
PENV HV1K8	504-526	PENV HV2NZ	777-800	PHEMA CVBVM	381-415		
PENV HV1MA	500-522	PENV JSRV	641-564	PHEMA CVBQ	381-415		
PENV HV1MF	488-518	PENV SFV1	004-087	PHEMA CVHOC	381-415		
PENV HV1ND	488-510	PENV BRV3L	081-004	PHEMA INCCA	442-468		
PENV HV1PV	488-520	PENV SIVM1	003-820	PHEMA INCEN	430-464		
PENV HV1S1	488-511	PENV SIVMK	002-025	PHEMA INCOL	430-464		
PENV HV1T2	123-146	PENV SIVML	801-024	PHEMA INCY	428-463		
PENV HV1Z6	487-518	PENV SIVB4	000-029	PHEMA INCJH	443-487		
PENV HV1Z8	506-527	PENV BIVSP	810-833	PHEMA INCKY	428-463		
PENV HV1ZH	488-520	PHEMA COVO	200-223	PHEMA INCM1	428-463		
PENV JSRV	376-388	PHEMA PI2H	06-88	PHEMA INCNA	428-463		
PENV MPV	213-236	PHEMA PI2HT	06-88	PHEMA INCP1	430-464		
PENV BRV1	213-236	PVF11 VACCC	101-184	PHEMA INCP2	430-464		
PHEMA IAIC	37-59	PVF16 VACCC	26-48	PHEMA INCP3	430-464		
PHEMA IABAN	21-43	PVF16 VACCP	3-26	PHEMA INCTA	430-464		
PHEMA IAD3	37-59	PVG1L AMEPV	313-336	PHEMA INCYA	430-464		
PHEMA IADH2	21-43	PVQ28 HSV11	401-514	PHEMA MUMPM	101-126		
PHEMA IADH3	21-43	PVG43 HSV11	322-345	PHEMA MUMPR	101-126		
PHEMA IADH4	21-43	PVQ52 HSV11	228-252	PHEMA MUMPS	101-126		
PHEMA IADH6	21-43	PVG67 HSV11	722-746	PHEMA PI1HW	28-63		
PHEMA IADH6	21-43	PVQ12 CVBF	10-33	PENV BEV	02-80		
PHEMA IADH7	21-43	PVQ12 CVBL9	661-674	PVF05 VACCC	280-304		
PHEMA IADM2	37-59	PVQ12 CVBLY	10-33	PVF05 VACCP	280-304		
PHEMA IADMA	28-60	PVQ12 CVMA4	1207-1280	PVF05 VACCV	281-306		
PHEMA IADU3	37-59	PVQ12 CVMA6	1216-1238	PVF09 VACCC	170-200		
PHEMA IADN6	21-43	PVQ12 CVMJH	1120-1149	PVF09 VACCV	170-200		
PHEMA IADN7	37-59	PVQ12 CVPF8	1274-1297	PVG01 VZVD	68-82		
PHEMA IADN8	37-59	PVQ12 CVPPU	1272-1285	PVG10 H8V8A	356-378		
PHEMA IADN9	37-59	PVQ12 CVPR8	1050-1073	PVG12 H8V9A	88-92		
PHEMA IADN9	37-59	PVQ12 CVPRM	1050-1073	PVG18 H8V11	88-112		
PHEMA IADN9	37-59	PVQ12 FIPV	1277-1300	PVG28 H8V11	173-187		
PHEMA IADN9	37-59	PVQ12 IBV6	186-218	PVG43 H8V11	108-133		
PHEMA IADN9	37-59	PVQ12 IBVB	186-218	PVG97 H8V11	108-132		
PHEMA IADN9	37-59	PVQ12 IBVD2	186-218	PVG72 H8V11	720-744		
PHEMA IADN9	37-59	PVQ12 IBVD3	186-218	PVG71 IBVB	3001-3026		

PHEMA IAV17	38-60		PVQL2 IBVK	196-218	PVQL8 H9VMD	588-813			
PHEMA IAX31	37-68		PVQL2 IBVM	196-218	PVQL8 ILTV6	587-821			
PHEMA IAZCO	37-68		PVQL2 IBVU1	178-201	PVQL8 ILTV9	607-831			
PHEMA IAZH2	21-43		PVQL2 IBVU2	178-201	PVQL8 ILTVT	607-831			
PHEMA IAZH3	21-43		PVQL2 IBVU3	178-201	PVGL8 H9V11	413-437			
PHEMA IAZUK	37-68		PVQL8 HCMVA	635-658	PVGL8 VZVD	468-483			
PHEMA PHODV	38-68		PVQL8 HCMVT	635-658	PVGLF 9V6	401-426			
PHEMA P12H	65-87		PVQL8 H9V6A	483-508	PVGLH HCMVA	574-588			
PHEMA P12HT	65-87		PVQL8 HCMV8	606-609	PVGLH HCMVT	673-687			
PVFF2 CAPVK	89-111		PVGLC H9V11	407-480	PVGLH H9V11	443-467	803-827		
PVFO8 VACC8	72-84		PVGLC H9V1K	407-480	PVGLH H9V1E	443-467	803-827		
PVGO1 H9V1	317-339		PVGLC H9V2	435-468	PVGLM BUNL7	31-55			
PVGO3 VACC8	80-72		PVGLC H9V23	438-459	PVGLM BUNSH	31-55			
PVGO3 VARV	60-72		PVGLM BUNL7	1387-1410	PVGLM HANTH	684-718			
PVGO4 VACC8	11-33		PVGLM BUNSH	1387-1410	PVGLM RVFV	344-368			
PVGO4 VARV	11-33		PVGLM UUK	905-989	PVGLM RVFVZ	344-368			
PVGO9 H9V1	89-110		PVGLY JUNIN	12-35	PVGLM UUK	501-585			
PVGO9 H9V1	173-186		PVGLY LASHG	12-35	PVGLM CMV	311-335			
PVGO9 H9V1	20-42		PVGLY LASHJ	12-35	PVGP2 EBV	657-681			
PVGO9 H9V1	134-158		PVGLY LYCVA	12-35	PVGP3 EBV	654-678			
PVGO9 H9V1	71-83		PVGLY LYCVW	12-35	PVM1 REOV	280-304			
PVGO9 H9V1	288-288		PVGLY MOPEI	12-35	PVM1 REOVL	280-304			
PVGO9 H9V1	267-289		PVGLY TACV	12-35	PVM21 REOVD	108-182			
PVGO9 H9V1	42-84		PVGLY TACV6	12-35	PVM22 REOVD	188-182			
PVGO9 H9V1	83-78		PVGLY TACV7	12-35	PVM2 REOVJ	108-182			
PVGO9 H9V1	1347-1389		PVGLY TACV7	12-35	PVM2 REOVL	188-182			
PVGO9 H9V1	80-82		PVGLM CMV	741-704	PVMAT MEAS1	67-111			
PVGL2 IBV6	1056-1078		PVM1 REOVD	324-347	PVMAT 86PVB	314-338			
PVGL2 IBV8	1056-1077		PVM1 REOVL	464-477	PVME1 CVBM	137-101			
PVGL2 IBV2	1056-1078		PVMAT MUMP8	227-250	PVME1 CVHOC	137-101			
PVGL2 IBVK	1058-1077		PVMSA HPB08	288-292	PVME1 CVTKE	137-101			
PVGL2 IBVM	1058-1077		PVMSA HPB0C	288-291	PVME1 IBV8	74-98			
PVGL8 H9V6U	117-139		PVMSA HPB0U	231-254	PVME1 IBV8	74-98			
PVGL8 H9V82	746-767		PVMSA HPB0W	288-292	PVME1 IBV82	74-98			
PVGLC H9VMB	389-421		PVMSA HPBHE	238-259	PVME1 IBVK	74-98			
PVGLC H9VMQ	389-420				PVMSA HPB08	271-285			
PVGLC H9VMH	389-421				PVMSA WHV1	200-283			
PVGLF BR8VA	265-287	482-504			PVMSA WHV69	274-288			
PVGLF BR8VC	484-508				PVMSA WHV7	274-288			
PVGLF BR8VR	484-508				PVMSA WHV8	274-288			
PVGLF HR8V1	484-508				PVMSA WHV8I	274-288			
PVGLF HR8VA	484-508				PVMSA WHVW8	125-149			
PVGLF HR8VL	484-508								
PVGLF HR8VR	484-508								
PVGLF TRV	452-474								
PVGLQ H9V	77-89								
PVGLQ VABVO	400-428								



## TABLE XIII

SEARCH RESULTS SUMMARY FOR P12LZIPC MOTIF













FCGENE	PICT121P	All Viruses (No Bacteriophages)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
ELKNAME	PROTEIN	VIRUS									
PENV SIVM1	GP160 PRECURSOR	SIMIAN IMMUNODEFICIENCY VIRUS (NM142.83 ISOLATE)	866-793	801-826							AREA.9
PENV SIVM2	GP160 PRECURSOR	SIMIAN IMMUNODEFICIENCY VIRUS (K6W ISOLATE)	135-134	765-792	802-825						
PENV SIVM3	GP160 PRECURSOR	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	135-134	764-791	801-824						
PENV SIVS4	GP160 PRECURSOR	SIMIAN IMMUNODEFICIENCY VIRUS (F2165M14 ISOLATE)	765-789	806-829							
PENV SIVS5	GP160 PRECURSOR	SIMIAN IMMUNODEFICIENCY VIRUS (PBJ0C11 ISOLATE)	773-793	810-833							
PENV SMSAV	PLUS PROTEIN	SIMIAN SARCOMA VIRUS	42-63								
PENV SRV1	ENV POLYPROTEIN	SIMIAN RETROVIRUS SRV-1	213-215								
PERBA AVIER	ERBA ONCOGENE PROTEIN	AVIAN ERYTHROBLASTOSIS VIRUS (STRAIN ES4)	227-249								
PEIT1 FOWP1	EARLY TRANSCRIPTION FACTOR	FOWLPOX VIRUS (STRAIN FP-1)	21-41	71-92							
PEIT1 SEVKA	EARLY TRANSCRIPTION FACTOR	SHOPE FIBROMA VIRUS (STRAIN KASZA)	21-41								
PEIT1 VACC	EARLY TRANSCRIPTION FACTOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	21-41								
PEIT1 VACC	EARLY TRANSCRIPTION FACTOR	VACCINIA VIRUS (STRAIN WR)	21-41								
PEIT2 VACC	EARLY TRANSCRIPTION FACTOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	50-73	101-117	165-187	283-308	558-582				
PEIT2 VACC	EARLY TRANSCRIPTION FACTOR	VACCINIA VIRUS (STRAIN WR)	50-73	101-117	165-187	283-308	558-582				
PEIT2 VARV	EARLY TRANSCRIPTION FACTOR	VARIOLA VIRUS	48-72								
PEXON HSU11	ALKALINE EXONUCLEASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	50-73								
PEXON HSU2	ALKALINE EXONUCLEASE	HERPES SIMPLEX VIRUS (TYPE 2)	165-180								
PEXON HSU3	ALKALINE EXONUCLEASE	EQUINE HERPES VIRUS (TYPE 1 / STRAIN AB4P)	155-170								
PEXON PRVNS	ALKALINE EXONUCLEASE	PSEUDORABIES VIRUS (STRAIN NIA-3)	278-291								
PEXON VZVD	ALKALINE EXONUCLEASE	VARIICELLA-ZOSTER VIRUS (STRAIN HUMAS)	36-51								
PFIB2 ADEA0	41.4 KD FIBER PROTEIN	HUMAN ADENOVIRUS TYPE 40	28-44	217-262							
PFIB2 ADEA1	41.4 KD FIBER PROTEIN	HUMAN ADENOVIRUS TYPE 41	116-133								
PFIB2 ADEB0	FIBER PROTEIN	HUMAN ADENOVIRUS TYPE 41	116-133								
PFIB2 ADEB1	FIBER PROTEIN	HUMAN ADENOVIRUS TYPE 41	152-173								
PFIB2 ADEB2	FIBER PROTEIN	HUMAN ADENOVIRUS TYPE 41	447-473								
PFIB2 ADEB3	FIBER PROTEIN	HUMAN ADENOVIRUS TYPE 41	347-372	715-801							
PFIB2 ADEB4	FIBER PROTEIN	BOVINE ADENOVIRUS TYPE 1 (MAST ADENOVIRUS D053)	382-397								
PFIB2 ADEB5	FIBER PROTEIN	BOVINE ADENOVIRUS TYPE 1 (STRAIN GLAXO)	191-215	227-252	403-513	548-571	579-599				
PFIB2 ADEB6	FIBER PROTEIN	MOUSE ADENOVIRUS TYPE 1	53-78								
PFIB2 ADEB7	FIBER PROTEIN	AVIAN ENDOGENOUS VIRUS EV-1	2-27								
PFIB2 ADEB8	FIBER PROTEIN	AVIAN ENDOGENOUS VIRUS ASSOCIATED VIRUS-0	53-78								
PFIB2 ADEB9	FIBER PROTEIN	AVIAN MYELOCYTOMATOSIS VIRUS MC29	53-78								
PFIB2 ADEB10	FIBER PROTEIN	AVIAN MYELOCYTOMATOSIS VIRUS IBI	53-78								
PFIB2 ADEB11	FIBER PROTEIN	AVIAN SARCOMA VIRUS (STRAIN UR2)	53-78								
PFIB2 ADEB12	FIBER PROTEIN	AVIAN SARCOMA VIRUS (STRAIN Y71)	53-78								
PFIB2 ADEB13	FIBER PROTEIN	BABOON ENDOGENOUS VIRUS (STRAIN M7)	397-422								
PFIB2 ADEB14	FIBER PROTEIN	BOVINE LEUKEMIA VIRUS (AUSTRALIAN ISOLATE)	212-238								
PFIB2 ADEB15	FIBER PROTEIN	BOVINE LEUKEMIA VIRUS (JAPANESE ISOLATE BLV-1)	213-239								
PFIB2 ADEB16	FIBER PROTEIN	CAPRIE ARTIRITIS ENCEPHALITIS VIRUS (STRAIN CORK)	102-119								
PFIB2 ADEB17	FIBER PROTEIN	FUJINAMI SARCOMA VIRUS	53-78								
PFIB2 ADEB18	FIBER PROTEIN	HUMAN T-CELL LEUKEMIA VIRUS TYPE 1 (STRAIN ATK)	77-94								
PFIB2 ADEB19	FIBER PROTEIN	HUMAN T-CELL LEUKEMIA VIRUS TYPE 1 (CARIBBEAN ISOLATE)	77-94								
PFIB2 ADEB20	FIBER PROTEIN	HUMAN T-CELL LEUKEMIA VIRUS TYPE 1 (ISOLATE MT-2)	77-94								
PFIB2 ADEB21	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ARV2SF2 ISOLATE)	65-91								
PFIB2 ADEB22	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB23	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB24	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB25	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB26	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB27	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB28	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB29	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB30	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB31	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB32	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB33	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB34	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB35	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB36	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB37	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB38	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB39	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB40	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB41	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB42	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB43	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB44	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB45	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB46	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB47	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB48	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB49	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB50	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB51	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB52	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB53	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB54	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB55	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB56	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB57	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB58	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB59	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB60	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB61	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB62	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB63	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB64	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB65	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB66	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB67	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB68	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB69	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB70	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB71	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB72	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB73	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB74	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB75	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB76	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB77	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB78	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB79	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB80	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB81	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB82	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB83	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB84	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB85	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB86	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB87	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB88	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB89	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB90	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB91	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB92	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB93	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB94	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB95	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB96	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB97	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB98	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB99	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								
PFIB2 ADEB100	FIBER PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHI0 ISOLATE)	65-91								

CCGENSE	PICTL21P	All Viruses (No Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
EULENANT	PROTEIN	YINUS									
POAG HV1U4	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (STRAIN UGANDAN / ISO 65-91)	65-91								
POAG HV1W2	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (WNI2 ISOLATE)	65-91								
POAG HV1Z2	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (WNI2 ISOLATE)	65-91								
POAG IMA	RETROVIRUS-RELATED GAG POLYPROTEIN	MOUSE INTRACISTERNAL A-PARTICLE	757-772								
POAG IMHYB	GAG POLYPROTEIN	MOUSE MAMMARY TUMOR VIRUS (STRAIN IIR6)	82-97								
POAG IMHYC	GAG POLYPROTEIN	MOUSE MAMMARY TUMOR VIRUS (STRAIN CII)	82-97								
POAG IMHYG	GAG POLYPROTEIN	MOUSE MAMMARY TUMOR VIRUS (STRAIN GR)	82-97								
POAG RSV	GAG POLYPROTEIN	ROUS SARCOMA VIRUS (STRAIN PRAGUE C)	51-78								
POAG SCVLA	MAJOR COAT PROTEIN	SACCHAROMYCES CEREVISIAE VIRUS L-A	618-645								
POAG SFV1	GAG POLYPROTEIN	SIMIAN FOAMY VIRUS (TYPE 1)	65-101								
POAG SFV1L	GAG POLYPROTEIN	SIMIAN FOAMY VIRUS (TYPE 1 / STRAIN LK)	65-101								
POAG SIVAG	GAG POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGM153 ISOLATE)	189-213								
POAG SIVAT	GAG POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGM153 ISOLATE)	189-213								
POAG SIVCZ	GAG POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (TYO-1 ISOLATE)	189-213								
POAG SIVON	GAG POLYPROTEIN	GHIMPANZEE IMMUNODEFICIENCY VIRUS (SIV(CV72))	66-92								
POAG SIVM1	GAG POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE: (H1))	66-92								
POAG SIVRH	GAG POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (MM142-83 ISOLATE)	286-307								
PGLRX VACCC	POSSIBLE GLUTAREDOXIN	SQUIDRELL MONKEY RETROVIRUS (SMRV-1)	71-87								
PGLRX VARV	POSSIBLE GLUTAREDOXIN	VACCINIA VIRUS (STRAIN COPEHAGEN), AND (STRAIN L-IVP)	71-87								
PGBAN OVAS	GRANULIN	VARIOLA VIRUS	208-226								
PGBAN OVYN	GRANULIN	AGROTIS SEGETUM GRANULOSIS VIRUS	209-227								
PGBFA VACCC	GROWTH FACTOR	TRICHOLOPHUSIA NI GRANULOSIS VIRUS	104-124								
PGBFA VACCV	GROWTH FACTOR	VACCINIA VIRUS (STRAIN COPEHAGEN)	104-124								
PGBFA VARV	GROWTH FACTOR	VACCINIA VIRUS (STRAIN WR)	104-124								
PHELT EBV	PROBABLE HELICASE	VARIOLA VIRUS	104-122								
PHELT HCMVA	PROBABLE HELICASE	EPSTEIN-BARR VIRUS (STRAIN B95-4)	180-207								
PHELT HSV1	PROBABLE HELICASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	318-361	418-464							
PHELT HSV2	PROBABLE HELICASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	397-420	539-560	826-832						
PHELT HSVB	PROBABLE HELICASE	HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN 17)	389-408	628-646							
PHELT HSVSA	PROBABLE HELICASE	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB-9)	290-309	539-554							
PHELT VZVD	PROBABLE HELICASE	HERPESVIRUS SAIMIRI (STRAIN 11)	181-204	243-266	394-413						
PIEMA CDVO	HEMAGGLUTININ-NEURAMINIDASE	VARIOLA-ZOSTER VIRUS (STRAIN DUMA-5)	327-350	389-411	658-683						
PIEMA CVBE	HEMAGGLUTININ-ESTERASE PRECURSOR	CANINE DISTEMPER VIRUS (STRAIN ONDERSTEEPOORT)	165-189	383-402	561-578	761-786					
PIEMA CVBL	HEMAGGLUTININ-ESTERASE PRECURSOR	BOVINE CORONA VIRUS (STRAIN F1)	36-53	200-223							
PIEMA CVBM	HEMAGGLUTININ-ESTERASE PRECURSOR	BOVINE CORONA VIRUS (STRAIN LY-13)	391-415								
PIEMA CVBQ	HEMAGGLUTININ-ESTERASE PRECURSOR	BOVINE CORONA VIRUS (STRAIN MEBUS)	391-415								
PIEMA CVHC	HEMAGGLUTININ-ESTERASE PRECURSOR	BOVINE CORONA VIRUS (STRAIN QUEBEC), AND (STRAIN L9)	391-415								
PIEMA CVMS	HEMAGGLUTININ-ESTERASE PRECURSOR	HUMAN CORONA VIRUS (STRAIN OC4)	391-415								
PIEMA CVMS	HEMAGGLUTININ-ESTERASE PRECURSOR	MURINE CORONA VIRUS MHV (STRAIN A39)	403-423								
PIEMA LAAC	HEMAGGLUTININ PRECURSOR	MURINE CORONA VIRUS MHV (STRAIN A39)	403-423								
PIEMA LABAN	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICAGO/2/68)	403-418								
PIEMA LABUD	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/BANGKOK/1/79)	37-59	322-339							
PIEMA LACKO	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/BRUSSELS/1/79)	21-43	306-323							
PIEMA LACKP	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LACKQ	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LACKS	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADAI	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADCI	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADHI	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH2	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH3	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH4	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH5	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH6	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH7	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH8	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH9	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH10	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH11	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH12	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH13	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH14	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH15	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH16	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH17	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH18	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH19	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH20	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH21	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH22	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH23	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH24	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH25	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH26	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH27	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH28	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH29	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH30	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH31	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH32	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH33	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH34	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH35	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH36	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH37	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH38	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH39	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH40	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH41	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH42	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH43	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH44	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH45	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH46	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH47	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH48	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH49	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH50	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH51	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH52	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH53	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH54	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH55	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH56	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH57	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH58	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH59	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH60	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH61	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH62	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH63	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH64	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH65	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH66	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH67	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH68	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH69	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH70	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								
PIEMA LADH71	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/CHICKENVALE/ABAMA/1/75)	320-337								





FCGENE	PICT121P	All Viruses (No Bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10
PIC1A	PROTEIN	VIRUS										
PIC1A	HEXAGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN TEX95/82)	111-128	272-299	324-340							
PIC1A	HEXAGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN TEX767/81)	111-128	272-299	324-340							
PIC1A	HEXAGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN WAS1064/79)	111-128	272-299	324-340							
PIC1A	HEXAGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN WAS101/51/77)	111-128	272-299	324-340							
PIC1A	HEXAGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 4A VIRUS (STRAIN TOSHIMA)	30-67									
PIC1A	HEXAGLUTININ-NEURAMINIDASE	RINDERPEST VIRUS (STRAIN KABETE O)	368-383									
PIC1A	HEXAGLUTININ-NEURAMINIDASE	RINDERPEST VIRUS (STRAIN L)	4-30									
PIC1A	HEXAGLUTININ-NEURAMINIDASE	SENDAL VIRUS (STRAIN 2) (HOST MUTANTS)	122-142									
PIC1A	HEXAGLUTININ-NEURAMINIDASE	SENDAL VIRUS (STRAIN HUSINIH)	122-142									
PIC1A	HEXAGLUTININ-NEURAMINIDASE	SENDAL VIRUS (STRAIN HARRIS)	122-142									
PIC1A	HEXAGLUTININ-NEURAMINIDASE	SENDAL VIRUS (STRAIN HV)	322-342									
PIC1A	HEXAGLUTININ-NEURAMINIDASE	SENDAL VIRUS (STRAIN Z)	322-342									
PIC1A	HEXAGLUTININ-NEURAMINIDASE	SIMIAN VIRUS 41	55-73									
PIC1A	HEXAGLUTININ-NEURAMINIDASE	SIMIAN VIRUS 5 (STRAIN WJ)	7-28	84-101	379-400							
PIC1A	HEXAGLUTININ-NEURAMINIDASE	SIMIAN VIRUS 5 (ISOLATE CANIN/CPI)	7-28	84-101	379-400							
PIC1A	HEXAGLUTININ-NEURAMINIDASE	SIMIAN VIRUS 5 (ISOLATE CANIN/CPI)	7-28	84-101	379-400							
PIC1A	HEXAGLUTININ-NEURAMINIDASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	7-28	84-101	379-400							
PIC1A	HEXAGLUTININ-NEURAMINIDASE	VACCINIA VIRUS (STRAIN H1D-1)	171-192									
PIC1A	HEXAGLUTININ-NEURAMINIDASE	VACCINIA VIRUS (STRAIN HAN TAN)	171-192									
PIC1A	HEXAGLUTININ-NEURAMINIDASE	VACCINIA VIRUS (STRAIN WR)	171-192									
PIC1A	HEXAGLUTININ-NEURAMINIDASE	VACCINIA VIRUS	171-192									
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 2	38-61	119-140								
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 3	27-48									
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 5	38-61	119-140								
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 41	38-61	128-146								
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	MOUSE ADENOVIRUS TYPE 1	36-52									
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 7, AND 3	92-117									
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	CANINE ADENOVIRUS TYPE 2	52-77									
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	TUPAIA ADENOVIRUS	60-82									
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	COWPOX VIRUS	517-533	558-583	609-636							
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	64-83									
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	169-190									
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	60-77									
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	239-260									
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	2-29									
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	92-119									
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	EPSTEIN-BARR VIRUS (STRAIN B91-8)	101-123	131-153	759-777							
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	156-176	202-222								
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 1) (STRAIN 17)	8-29	45-61	122-143	731-768						
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 1) (STRAIN ANGELOT1)	8-29	45-61	122-143	731-768						
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 2) (STRAIN F)	8-29	122-143	746-763							
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	EQUINE HERPESVIRUS TYPE 1	12-37	130-151								
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	HERPESVIRUS SAIMIRI (STRAIN 11)	37-56	129-144	712-735							
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	MURINE CYTOMEGALOVIRUS (STRAIN SN110)	27-49	51-78	647-672							
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	MURINE CYTOMEGALOVIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER)	126-144	202-229	736-759							
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	285-307	609-718								
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 1) (STRAIN 17)	69-88	619-639	721-744							
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 2) (STRAIN 17)	668-684									
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	HERPES SIMPLEX VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER)	711-729									
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 1) (STRAIN F)	81-98	631-657								
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB42)	708-725	736-759								
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN KENTUCKY A)	708-725	736-759								
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	MAREK'S DISEASE HERPESVIRUS (STRAIN GA)	488-506	585-611	1202-1218							
PIC1A	HEXON-ASSOCIATED PROTEIN PRECURSOR	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	547-563									



CCGNE	PICTLZP	All Virus (No Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
ELN-NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PIE1 PRVIF	IMMEDIATE-EARLY PROTEIN IE10	PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKIAUSER / BECKER)	731-748								
PIE2 PRVAF	IMMEDIATE-EARLY PROTEIN IE10	PSEUDORABIES VIRUS (STRAIN KAPLAN)	726-737								
PIE3 PRVGA	TRANSCRIPTIONAL REGULATOR IE3	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	386-394								
PIE4 HSV11	TRANSCRIPTIONAL REGULATOR IE4	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	364-383								
PIE5 HSV2	TRANSCRIPTIONAL REGULATOR IE5	HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN 17)	378-394								
PIE6 HSV3	32 KD IMMEDIATE-EARLY PROTEIN IE6	EQUINE HERPESVIRUS TYPE 1 (STRAIN 17)	373-383								
PIE7 HSV4	32 KD IMMEDIATE-EARLY PROTEIN IE7	HERPESVIRUS SAIMIRI (STRAIN 11)	301-326								
PIE8 HSV5	IMMEDIATE-EARLY PROTEIN IE8	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	189-205								
PIE9 HSV6	IMMEDIATE-EARLY PROTEIN IE9	EQUINE HERPESVIRUS TYPE 4	81-104								
PIE10 PRVKA	IMMEDIATE-EARLY PROTEIN	EQUINE HERPESVIRUS TYPE 1	92-116								
PIE11 PRVLA	IMMEDIATE-EARLY PROTEIN	PSEUDORABIES VIRUS (STRAIN KAPLAN)	85-108								
PIE12 PRVMA	IMMEDIATE-EARLY PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	57-78								
PIE13 PRVNA	IMMEDIATE-EARLY PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	117-137								
PIE14 PRVPA	IMMEDIATE-EARLY PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	64-84								
PIE15 PRVQA	IMMEDIATE-EARLY PROTEIN	AVIAN ERYTHROBLASTOSIS VIRUS	293-324								
PIE16 PRVRA	IMMEDIATE-EARLY PROTEIN	FELINE SARCOMA VIRUS (STRAIN GARDNER-ARNSTEIN)	73-88								
PIE17 PRVSA	IMMEDIATE-EARLY PROTEIN	FELINE SARCOMA VIRUS (STRAIN SNYDER-TIELEN)	2-22								
PIE18 PRVTA	IMMEDIATE-EARLY PROTEIN	FELINE SARCOMA VIRUS (STRAIN GARDNER-RASHEED)	289-288								
PIE19 PRVUA	IMMEDIATE-EARLY PROTEIN	FELINE SARCOMA VIRUS (STRAIN NICDONOUGH)	141-159								
PIE20 PRVVA	IMMEDIATE-EARLY PROTEIN	AVIAN SARCOMA VIRUS (STRAIN PRC11)	243-274								
PIE21 PRVWA	IMMEDIATE-EARLY PROTEIN	FUJIMAMI SARCOMA VIRUS	239-275								
PIE22 PRVXA	IMMEDIATE-EARLY PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN PA11V)	18-41								
PIE23 PRVYA	IMMEDIATE-EARLY PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8)	403-418								
PIE24 PRVZA	IMMEDIATE-EARLY PROTEIN	FISH LYMPHO CYTUS DISEASE VIRUS	96-117								
PIE25 PRVAA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	223-249								
PIE26 PRVBA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN CL101)	223-249								
PIE27 PRVCA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN IFEN)	223-249								
PIE28 PRVDA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN K05)	223-249								
PIE29 PRVFA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN SC16)	223-249								
PIE30 PRVGA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN 311)	224-250								
PIE31 PRVHA	IMMEDIATE-EARLY PROTEIN	BOVINE HERPESVIRUS TYPE 1 (STRAIN 6600)	193-219								
PIE32 PRVIA	IMMEDIATE-EARLY PROTEIN	BOVINE HERPESVIRUS TYPE 2 (STRAIN 11M-1)	180-202								
PIE33 PRVJA	IMMEDIATE-EARLY PROTEIN	BOVINE HERPESVIRUS TYPE 3 (STRAIN WC1)	181-209								
PIE34 PRVKA	IMMEDIATE-EARLY PROTEIN	BOVINE HERPESVIRUS TYPE 4 (STRAIN 0932)	194-220								
PIE35 PRVLA	IMMEDIATE-EARLY PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN 0943)	174-193								
PIE36 PRVMA	IMMEDIATE-EARLY PROTEIN	EQUINE HERPESVIRUS TYPE 2 (STRAIN 0943)	261-284								
PIE37 PRVNA	IMMEDIATE-EARLY PROTEIN	FELINE HERPESVIRUS (ISOLATE IVS23A)	171-189								
PIE38 PRVPA	IMMEDIATE-EARLY PROTEIN	FELINE HERPESVIRUS (ISOLATE IVS23A)	171-189								
PIE39 PRVQA	IMMEDIATE-EARLY PROTEIN	ICTALUND HERPESVIRUS 1	14-32								
PIE40 PRVRA	IMMEDIATE-EARLY PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	189-213								
PIE41 PRVSA	IMMEDIATE-EARLY PROTEIN	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE VIR87)	208-232								
PIE42 PRVTA	IMMEDIATE-EARLY PROTEIN	VARICELLA-ZOSTER VIRUS (ACYCLOVIR-RESISTANT STRAIN 40A2)	183-202								
PIE43 PRVUA	IMMEDIATE-EARLY PROTEIN	VARICELLA-ZOSTER VIRUS (ACYCLOVIR-RESISTANT STRAIN 7-1-3)	192-216								
PIE44 PRVVA	IMMEDIATE-EARLY PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	192-216								
PIE45 PRVWA	IMMEDIATE-EARLY PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	192-216								
PIE46 PRVXA	IMMEDIATE-EARLY PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	192-216								
PIE47 PRVYA	IMMEDIATE-EARLY PROTEIN	FELINE SARCOMA VIRUS (STRAIN HARDY-ZUCKERMAN 4)	192-216								
PIE48 PRVZA	IMMEDIATE-EARLY PROTEIN	ICTALUND HERPESVIRUS 1	151-167								
PIE49 PRVAA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE50 PRVBA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 2)	286-311								
PIE51 PRVCA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE52 PRVDA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE53 PRVFA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE54 PRVGA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE55 PRVHA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE56 PRVIA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE57 PRVJA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE58 PRVKA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE59 PRVLA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE60 PRVMA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE61 PRVNA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE62 PRVPA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE63 PRVQA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE64 PRVRA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE65 PRVSA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE66 PRVTA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE67 PRVUA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE68 PRVVA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE69 PRVWA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE70 PRVXA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE71 PRVYA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE72 PRVZA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE73 PRVAA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE74 PRVBA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE75 PRVCA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE76 PRVDA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE77 PRVFA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE78 PRVGA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE79 PRVHA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE80 PRVIA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE81 PRVJA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE82 PRVKA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE83 PRVLA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE84 PRVMA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE85 PRVNA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE86 PRVPA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE87 PRVQA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE88 PRVRA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE89 PRVSA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE90 PRVTA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE91 PRVUA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE92 PRVVA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE93 PRVWA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE94 PRVXA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE95 PRVYA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE96 PRVZA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE97 PRVAA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE98 PRVBA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE99 PRVCA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE100 PRVDA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE101 PRVFA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE102 PRVGA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE103 PRVHA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE104 PRVIA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE105 PRVJA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE106 PRVKA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE107 PRVLA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE108 PRVMA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE109 PRVNA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE110 PRVPA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE111 PRVQA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE112 PRVRA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE113 PRVSA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE114 PRVTA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE115 PRVUA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE116 PRVVA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE117 PRVWA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE118 PRVXA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE119 PRVYA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE120 PRVZA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE121 PRVAA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE122 PRVBA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE123 PRVCA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE124 PRVDA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	286-311								
PIE125 PRVFA	IMMEDIATE-EARLY PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN									













PCGENE	PICTCLZP	PROTEIN	All Viruses (No Bacteriophages)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
FILE NAME	PROTEIN											
POLN FCV6	NON-STRUCTURAL POLYPROTEIN		FELINE CALICIVIRUS (STRAIN CF168 FIV)	443-469	746-766	902-927	1066-1088	1378-1399	1545-1564			
POLN FCV7	NON-STRUCTURAL POLYPROTEIN		FELINE CALICIVIRUS (STRAIN JAPANESE F4)	300-326								
POLN FCV9	NON-STRUCTURAL POLYPROTEIN		FELINE CALICIVIRUS (STRAIN F9)	171-186	262-283	919-945	1224-1242					
POLN HEV6	NON-STRUCTURAL POLYPROTEIN		HEPATITIS E VIRUS (STRAIN RUMMA)	250-266	1274-1291							
POLN HEV7	NON-STRUCTURAL POLYPROTEIN		HEPATITIS E VIRUS (STRAIN MEXICO)	250-266	1272-1289							
POLN HEV8	NON-STRUCTURAL POLYPROTEIN		HEPATITIS E VIRUS (STRAIN MYANMAR)	250-266	1274-1291							
POLN HEV9	NON-STRUCTURAL POLYPROTEIN		HEPATITIS E VIRUS (STRAIN PAKISTAN)	249-265	1273-1290							
POLN MIDV	NON-STRUCTURAL POLYPROTEIN		MIDDLEBURY VIRUS	484-512	628-643	766-770						
POLN ONV6	NON-STRUCTURAL POLYPROTEIN		ONYONG-NYONG VIRUS (STRAIN GULL)	90-107	613-634							
POLN RUDV	NON-STRUCTURAL POLYPROTEIN		RABBIT HEMORRHAGIC DISEASE VIRUS	156-180	276-292	279-320	479-502	1471-1499				
POLN RAVN	NON-STRUCTURAL POLYPROTEIN		RABBIT HEMORRHAGIC DISEASE VIRUS (STRAIN V-351)	115-135								
POLN RAVT	NON-STRUCTURAL POLYPROTEIN		ROSS RIVER VIRUS (STRAIN T48)	89-106	611-632	2113-2128	2185-2205					
POLN RUBV	NON-STRUCTURAL POLYPROTEIN		RUBELLA VIRUS (STRAIN THIEN)	782-797	854-874							
POLN SEV	NON-STRUCTURAL POLYPROTEIN		SEMUKI FOREST VIRUS	14-37	97-113	263-279	670-694	901-918	1374-1393	2033-2052		
POLN SINDV	NON-STRUCTURAL POLYPROTEIN		SINDIBS VIRUS (SUBTYPE OCKELBO / STRAIN HUNSHYN K2-5)	91-108	617-643	2062-2077	2134-2154					
POLN SINDV	NON-STRUCTURAL POLYPROTEIN		SINDIBS VIRUS (STRAIN HIRSP)	620-646	1123-1150	1796-1814	2148-2161	2230-2240				
POLN EPV	RNA REPLICASE POLYPROTEIN		EGG PLANT MOSAIC VIRUS	620-646	1123-1150	1744-1763	1790-1812	2146-2161				
POLN OTMV	RNA REPLICASE POLYPROTEIN		ONION YELLOW MOSAIC VIRUS	808-833								
POLN TYMV	RNA REPLICASE POLYPROTEIN		TURNIP YELLOW MOSAIC VIRUS	707-727	941-962							
POLN TYMV	RNA REPLICASE POLYPROTEIN		TURNIP YELLOW MOSAIC VIRUS (AUSTRALIAN ISOLATE)	212-233	416-453	1173-1192						
POLN TYMV	RNA REPLICASE POLYPROTEIN		TURNIP YELLOW MOSAIC VIRUS (ISOLATE TYMC)	212-233	416-453	1173-1192						
POLN EEEV	STRUCTURAL POLYPROTEIN		EASTERN EQUINE ENCEPHALITIS VIRUS	315-350	211-229	491-507						
POLN EEEV	STRUCTURAL POLYPROTEIN		EASTERN EQUINE ENCEPHALITIS VIRUS	315-350	211-229	491-507						
POLN EEEV	STRUCTURAL POLYPROTEIN		VENEZUELAN EQUINE ENCEPHALITIS VIRUS (STRAIN TC-83)	32-48	214-230	492-508						
POLN EEEV	STRUCTURAL POLYPROTEIN		VENEZUELAN EQUINE ENCEPHALITIS VIRUS (STRAIN TRINIDAD DON 12-48)	32-48	214-230	492-508						
POLN EEEV	STRUCTURAL POLYPROTEIN		AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN AUSTRALIAN C1)	900-922								
POLN EEEV	STRUCTURAL POLYPROTEIN		AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN CU-1)	900-922								
POLN EEEV	STRUCTURAL POLYPROTEIN		AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN CU-1)	881-903								
POLN EEEV	STRUCTURAL POLYPROTEIN		AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN STC)	900-922								
POLN EEEV	STRUCTURAL POLYPROTEIN		ONYONG-NYONG VIRUS (STRAIN GULL)	688-708								
POLN EEEV	STRUCTURAL POLYPROTEIN		ROSS RIVER VIRUS (STRAIN T48)	1216-1243								
POLN EEEV	STRUCTURAL POLYPROTEIN		RUBELLA VIRUS (VACCINE STRAIN IPV77)	281-302								
POLN EEEV	STRUCTURAL POLYPROTEIN		RUBELLA VIRUS (VACCINE STRAIN M21)	281-302								
POLN EEEV	STRUCTURAL POLYPROTEIN		RUBELLA VIRUS (VACCINE STRAIN RA373)	281-302								
POLN EEEV	STRUCTURAL POLYPROTEIN		SEMUKI FOREST VIRUS	281-302	1041-1060							
POLN EEEV	STRUCTURAL POLYPROTEIN		SINDIBS VIRUS (SUBTYPE OCKELBO / STRAIN EDSUN 82-5)	315-32	751-772	780-801						
POLN EEEV	STRUCTURAL POLYPROTEIN		SINDIBS VIRUS (STRAIN HRSP AND IRLP)	315-32								
POLN EEEV	STRUCTURAL POLYPROTEIN		WESTERN EQUINE ENCEPHALITIS VIRUS	36-51	909-933							
POLN EEEV	STRUCTURAL POLYPROTEIN		AVIAN RETICULOENDOTHELIOSIS VIRUS	281-303								
POLN EEEV	STRUCTURAL POLYPROTEIN		BABOON ENDOGENOUS VIRUS (STRAIN M7)	526-544	973-993	999-1019	1070-1091					
POLN EEEV	STRUCTURAL POLYPROTEIN		BOVINE IMMUNODEFICIENCY VIRUS (ISOLATE 106)	101-119	742-768	868-889						
POLN EEEV	STRUCTURAL POLYPROTEIN		BOVINE IMMUNODEFICIENCY VIRUS (ISOLATE 127)	101-119	742-768	868-889						
POLN EEEV	STRUCTURAL POLYPROTEIN		BOVINE LEUKEMIA VIRUS (AUSTRALIAN ISOLATE)	487-504								
POLN EEEV	STRUCTURAL POLYPROTEIN		BOVINE LEUKEMIA VIRUS (JAPANESE ISOLATE BLV-1)	393-419	656-671							
POLN EEEV	STRUCTURAL POLYPROTEIN		CAPRINE ARTHRITIS ENCEPHALITIS VIRUS (STRAIN COK4)	184-204	380-407	471-494						
POLN EEEV	STRUCTURAL POLYPROTEIN		CAULIFLOWER MOSAIC VIRUS (STRAIN D10)	175-199	373-402	466-489						
POLN EEEV	STRUCTURAL POLYPROTEIN		CAULIFLOWER MOSAIC VIRUS (STRAIN DUC)	184-204	380-407	471-494						
POLN EEEV	STRUCTURAL POLYPROTEIN		CAULIFLOWER MOSAIC VIRUS (STRAIN NY8153)	70-97	183-203	381-408	472-495					
POLN EEEV	STRUCTURAL POLYPROTEIN		CAULIFLOWER MOSAIC VIRUS (STRAIN STRASSBOURG)	184-204	380-407	471-494						
POLN EEEV	STRUCTURAL POLYPROTEIN		CARNATION ETCHED RING VIRUS	101-186	455-478							
POLN EEEV	STRUCTURAL POLYPROTEIN		CONMELINA YELLOW MOTTLE VIRUS	320-343	1266-1311	1606-1622	1641-1665					
POLN EEEV	STRUCTURAL POLYPROTEIN		EQUINE INFECTIOUS ANEMIA VIRUS (CLONE 1369)	437-456								
POLN EEEV	STRUCTURAL POLYPROTEIN		EQUINE INFECTIOUS ANEMIA VIRUS (CLONE CL21)	437-456								

GENE	PROTEIN	ALL Viruses (No. Bacteriophages)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10
ELK-MAK	PROTEIN	VIRUS	436-435									
PPOL ELAV	POL POLYPROTEIN	EQUINE INFECTIOUS ANEMIA VIRUS (ISOLATE WYOMING)										
PPOL ENVI	POL POLYPROTEIN	FELINE ENDOGENOUS VIRUS (ICE)	381-401	856-876								
PPOL FIVE	POL POLYPROTEIN	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE PIETALUNA)	407-426	733-775								
PPOL FIVSD	POL POLYPROTEIN	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE SAN DIEGO)	407-426	733-775								
PPOL FIVT2	POL POLYPROTEIN	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE TAZ)	406-425	663-690								
PPOL FIVD	ENZYMATIC POLYPROTEIN	FIGWORT MOSAIC VIRUS (STRAIN DXS)	191-212	464-487								
PPOL FOAMY	POL POLYPROTEIN	HUMAN SPINARETROVIRUS	126-147	768-788								
PPOL GALT	POL POLYPROTEIN	GIBBON APE LEUKEMIA VIRUS	59-80	971-991								
PPOL HTLC	POL POLYPROTEIN	HUMAN T-CELL LEUKEMIA VIRUS TYPE I (STRAIN ATK)	330-346									
PPOL HTL/A	POL POLYPROTEIN	HUMAN T-CELL LEUKEMIA VIRUS TYPE I (CARIBBEAN ISOLATE)	330-346									
PPOL HTLV2	POL POLYPROTEIN	HUMAN T-CELL LEUKEMIA VIRUS TYPE II	609-627									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (ARV2SF2 ISOLATE)	860-887									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (BH10 ISOLATE)	872-899	872-899								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (BH13 ISOLATE)	872-899									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (BRU ISOLATE)	872-899									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (ELI ISOLATE)	860-887									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (HXB2 ISOLATE)	864-891									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (JRCF ISOLATE)	859-886									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (MAL ISOLATE)	859-886									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (MN ISOLATE)	861-890									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (NEW YORK-3 ISOLATE)	623-648	860-887								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (NOK ISOLATE)	623-648	859-886								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (OYL ISOLATE)	860-887									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (P221 ISOLATE)	635-660	872-899								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (REF1AT ISOLATE)	839-886									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (STRAIN UGANDAN/ISO)	839-886									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (22/CDC-234 ISOLATE)	622-647									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (ZAIRE 6 ISOLATE)	532	839-886								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE BEN)	379-406	907-934								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE CAN2)	886-913									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D194)	397-424	922-932								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D103.7)	907-934									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE GHANA-1)	359-386	887-914								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE NIH-2)	543-564	771-792								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ROD)	888-915									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE SGLISV)	159-386	887-907								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	179-406	907-934								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	166-190	198-223								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	183-201	209-236								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	102-120	128-155								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	186-213	507-526								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	133-153									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	651-671	728-744								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	333-334	978-998								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	64-84	90-110								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	340-359	983-1003								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	340-359	983-1003								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	340-359	983-1003								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	313-334	978-998								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	313-334	978-998								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	363-383	389-409								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	196-219	731-751								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	743-763									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	389-393	469-488								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	719-742									
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	891-915	1038-1083								
PPOL HTLV2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	891-915	1038-1083								



FCGENE	FILE NAME	PROTEIN	PICTLZIP	ALL Viruses (No Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		SIMIAN FOAMY VIRUS (TYPE 1)	188-204	335-356	845-869							AREA2
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		SIMIAN FOAMY VIRUS (TYPE 3 / STRAIN LK3)	186-206	337-358	847-871	976-996						AREA2
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		SIMIAN IMMUNODEFICIENCY VIRUS (AGM155 ISOLATE)	895-915									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		SIMIAN IMMUNODEFICIENCY VIRUS (AGM1 ISOLATE)	899-926	900-920								
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		SIMIAN IMMUNODEFICIENCY VIRUS (TYO-1 ISOLATE)	726-741	915-935								
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		CHIMPANZEE IMMUNODEFICIENCY VIRUS	884-911									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE GH1)	680-695	869-896								
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		SIMIAN IMMUNODEFICIENCY VIRUS (NMI142-3 ISOLATE)	380-407	908-935								
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		SIMIAN IMMUNODEFICIENCY VIRUS (K6V ISOLATE)	380-407	712-737	906-933							
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		SIMIAN IMMUNODEFICIENCY VIRUS (P2165SMH ISOLATE)	343-370	871-898								
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		SIMIAN IMMUNODEFICIENCY VIRUS (MIMC11 ISOLATE)	346-373	874-901								
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		SQUIRREL MONKEY RETROVIRUS	748-768									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		SIMIAN SARCOMA VIRUS	100-130	172-200								
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		SOYBEAN GILLOTIC NUTTLE VIRUS	131-155									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		SIMIAN RETROVIRUS	743-763									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		VISNA LENTIVIRUS (STRAIN 1514)	488-507	651-666	971-991							
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		VISNA LENTIVIRUS (STRAIN 1514 / CLONE LVI-1K51)	488-507	651-666	971-991							
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		VISNA LENTIVIRUS (STRAIN 1514 / CLONE LVI-1K53)	488-507	651-666	971-991							
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	116-141	183-210								
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	116-141	183-210								
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN G5)	158-175	396-411								
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	301-323									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	79-102									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6)	40-61									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		MOUSE MAMMARY TUMOR VIRUS (STRAIN GR)	40-61									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		MOUSE MAMMARY TUMOR VIRUS (STRAIN GR)	44-65									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		HARVEY MURINE SARCOMA VIRUS	40-61									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		RASHEED RAT SARCOMA VIRUS	56-60									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		CAMPLETTIS SONDRENSIS VIRUS	14-36									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		VACCINIA VIRUS (STRAIN WR), AND (STRAIN COPEHAGEN)	274-298	316-335	517-535							
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		VACCINIA VIRUS	274-298	316-335	517-535							
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		SIMIAN IMMUNODEFICIENCY VIRUS (AGM ISOLATE)	2-17									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE GR1)	45-72									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		AFRICAN SWINE FEVER VIRUS (ISOLATE MALAWI LIL 2001)	139-164	189-210	495-510							
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		EPSTEIN-BARR VIRUS (STRAIN B95-8)	793-812									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	192-212	669-684								
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	415-430	587-613								
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	60-85	266-288	668-694							
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		HERPESVIRUS SAIMIRI (STRAIN 11)	136-151									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		VACCINIA VIRUS (STRAIN COPEHAGEN)	36-51									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		VACCINIA VIRUS (STRAIN WR)	36-51									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		VARIOLA VIRUS	36-51									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		VARIOLA-ZOSTER VIRUS (STRAIN DUMAS)	34-58	221-247	258-280							
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		EPSTEIN-BARR VIRUS (STRAIN B95-8)	209-236									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	44-66	375-392								
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN KOS)	43-65	245-261	274-291							
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN 331)	41-63	272-289								
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		BOVINE HERPESVIRUS TYPE 1 (STRAIN 14)	244-266									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	61-88	251-273								
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		HERPESVIRUS SAIMIRI (STRAIN 11)	212-239									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		SHOPE FIBROMA VIRUS (STRAIN KASZA)	184-206	215-237								
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		VACCINIA VIRUS (STRAIN COPEHAGEN)	184-206									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		VACCINIA VIRUS (STRAIN L-1V7)	184-206									
PPOL_SFVI	PPOL_SFVI	POL POLYPROTEIN		VACCINIA VIRUS (STRAIN WR)	184-206									













PCGENE	PICTL2IP	All Viruses (No Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PUL20 PVND	UL20 MEMBRANE PROTEIN HOMOLOG	PSUDORABIES VIRUS (STRAIN NIA-3)	54-16								
PUL20 VZVD	GENE 19 MEMBRANE PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	201-224								
PUL21 HCMVA	HYPOTHEICAL PROTEIN UL21	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	91-110								
PUL21 HSV1	PROTEIN UL21	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	98-114	110-146							
PUL21 HSVIE	PROTEIN UL21	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	98-114	110-146							
PUL21 HSVEB	GENE 40 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	119-142	379-403	412-427						
PUL21 VZVD	GENE 31 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	270-293	300-327							
PUL23 HCMVA	HYPOTHEICAL PROTEIN UL23	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	44-67								
PUL24 EBV	PROTEIN BXB1	EPSTEIN-BARR VIRUS (STRAIN B95-4)	114-155								
PUL24 HCMVA	HYPOTHEICAL PROTEIN UL24	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	206-222								
PUL24 HSV1	PROTEIN UL24	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	147-166								
PUL24 TLVT	PROTEIN UL24 HOMOLOG	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE V83)	158-179								
PUL33 HCMVA	HYPOTHEICAL PROTEIN UL25	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	484-500								
PUL33 HSV1	VIRION PROTEIN UL33	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	86-101								
PUL33 HSVEB	VIRION PROTEIN UL33	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	86-101								
PUL33 HSVSA	VIRION GENE 19 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	89-104								
PUL33 ILTVT	64 I KD VIRION PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	244-263	316-336							
PUL37 HCMVA	HYPOTHEICAL PROTEIN UL27	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE V83)	320-237	316-336							
PUL39 HCMVA	HYPOTHEICAL PROTEIN UL29	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	307-324	486-507							
PUL30 HCMVA	HYPOTHEICAL PROTEIN UL30	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	339-266								
PUL31 EBV	PROTEIN B1F2	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	9-32								
PUL31 HCMVA	HYPOTHEICAL PROTEIN UL31	EPSTEIN-BARR VIRUS (STRAIN B95-4)	373-296								
PUL31 HSV1	PROTEIN UL31	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	410-437	502-602							
PUL31 HSVEB	GENE 29 PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	95-116								
PUL31 HSVSA	GENE 69 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	104-125	288-309							
PUL31 VZVD	GENE 27 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	145-161	163-190							
PUL32 HSV1	PROBABLE MAJOR ENV GLYCOPROTEIN UL32	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	117-138	295-316							
PUL32 HSVEB	MAJOR ENVELOPE GLYCOPROTEIN 300	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	127-143	564-585							
PUL33 VZVD	PROBABLE MAJOR ENV GLYCOPROTEIN 26	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	81-108								
PUL33 HCMVA	G-PROTEIN COUPLED REC HOMOLOG UL33	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	553-574								
PUL34 HCMVA	HYPOTHEICAL PROTEIN UL34	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	76-103								
PUL34 HSV1	VIRION PROTEIN UL34	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	214-232	297-321							
PUL34 HSVEB	VIRION GENE 28 PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	231-275								
PUL34 HSVSA	GENE 67 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	249-264								
PUL34 VZVD	VIRION GENE 24 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	207-229								
PUL34 HCMVA	HYPOTHEICAL PROTEIN UL35	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	244-266								
PUL35 HCMVA	HYPOTHEICAL PROTEIN UL36	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	229-252	331-348							
PUL37 EBV	PROTEIN BOLF1	EPSTEIN-BARR VIRUS (STRAIN B95-4)	143-168	387-410							
PUL37 HSV1	PROTEIN UL37	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	21-36	135-155	702-710	984-1004					
PUL37 HSVEB	GENE 21 PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	229-252	262-277	445-467	663-681	758-777				
PUL37 HSVSA	GENE 61 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	414-440	491-510	664-690	778-805	901-919	1009-1028			
PUL37 VZVD	GENE 21 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	5-20								
PUL38 HCMVA	HYPOTHEICAL PROTEIN UL38	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	4-19	104-124	140-163	168-191	196-212	229-244	248-269	670-694	776-803
PUL40 HCMVA	HYPOTHEICAL PROTEIN UL40	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	904-923								
PUL41 HCMVA	HYPOTHEICAL PROTEIN UL41	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	199-220								
PUL43 HSV1	MEMBRANE PROTEIN UL43	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	18-35								
PUL43 HSVEB	GENE 17 MEMBRANE PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	15-31	116-134	343-365	394-421					
PUL43 VZVD	GENE 13 MEMBRANE PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	41-63	139-160	343-365						
PUL43 HSV1	PROTEIN UL43	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	34-60	86-107							
PUL43 HSVIK	PROTEIN UL43	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	88-114	127-146	160-180	271-299	374-400				
PUL43 HSVIM	PROTEIN UL43	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	25-46								
PUL47 HCMVA	PROTEIN UL47	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	25-46								
PUL47 HSV1	VIRION PROTEIN UL47	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	191-218	438-464	533-556	614-640	741-766				
PUL47 HSVIF	VIRION PROTEIN UL47	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	404-425								
PUL47 HSVBP	10.7 KD ALPHA TRANS-INDUCING PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	404-425								
PUL47 HSVBA	97 KD ALPHA TRANS-INDUCING PROTEIN	BOVINE HERPESVIRUS TYPE 1 (STRAIN PB-2)	681-702								
		EQUINE HERPESVIRUS TYPE 4	580-601								

FCGENE	PL1C1L2IP	All Viruses (No Bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PUL41 HSVB	97 KD ALPHA TRANS-INDUCING PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD169)	597-608								
PUL47 VZVD	ALPHA TRANS-INDUCING FACTOR 91.8 KD PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	42-58	608-627							
PUL49 EBV	HYPOTHETICAL BFR2 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8)	336-358								
PUL49 HCMVA	HYPOTHETICAL PROTEIN UL49	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	248-264	328-343							
PUL49 HSV11	TEGUMENT PROTEIN UL49	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	226-232								
PUL49 HSVSA	HYPOTHETICAL GENE 66 PROTEIN	HERPESVIRUS SAMIRI (STRAIN 11)	232-233								
PUL50 HCMVA	PROTEIN UL50	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	96-119								
PUL51 HSV11	PROTEIN UL51	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	49-66								
PUL51 HSVB4	GENE 7 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN 1942)	109-190								
PUL51 HSVH1	GENE 8 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD169)	164-180								
PUL51 VZVD	GENE 7 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	30-49								
PUL52 EBV	PROBABLE DNA REPLICATION PROTEIN BSLF1	EPSTEIN-BARR VIRUS (STRAIN B95-8)	44-59								
PUL52 HSV11	DNA REPLICATION PROTEIN UL52	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	17-37	65-91							
PUL52 HSVB4	DNA REPLICATION PROTEIN UL52	EQUINE HERPESVIRUS TYPE 1 (STRAIN 1942)	8-27								
PUL52 HSVB	DNA REPLICATION PROTEIN UL52	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD169)	8-27	116-117							
PUL53 HSVSA	PROBABLE DNA REPLICATION GENE 56 PROTEIN	HERPESVIRUS SAMIRI (STRAIN 11)	489-508								
PUL53 VZVD	PROBABLE DNA REPLICATION GENE 6 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	446-466	645-670							
PUL53 HCMVA	PROTEIN UL53	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	173-188								
PUL53 HSV6U	UL53 PROTEIN HOMOLOG	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	64-80								
PUL60 HCMVA	HYPOTHETICAL PROTEIN UL60	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	120-141								
PUL63 HCMVA	HYPOTHETICAL PROTEIN UL63	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	63-84	176-203							
PUL68 HCMVA	HYPOTHETICAL PROTEIN UL68	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	87-107								
PUL70 HCMVA	PROBABLE DNA REPLICATION PROTEIN UL70	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	223-232								
PUL71 HCMVA	HYPOTHETICAL PROTEIN UL71	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	234-250	409-430	626-643	710-793					
PUL71 EBV	HYPOTHETICAL BLNF1 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8)	62-87								
PUL73 HSVSA	HYPOTHETICAL GENE 53 PROTEIN	HERPESVIRUS SAMIRI (STRAIN 11)	51-73								
PUL74 HCMVA	HYPOTHETICAL PROTEIN UL74	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	12-32								
PUL77 HCMVA	VIRION PROTEIN UL77	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	268-291	607-628							
PUL79 HCMVA	HYPOTHETICAL PROTEIN UL79	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	71-90	190-203							
PUL84 HCMVA	63 KD EARLY NONSTRUCTURAL PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	40-58								
PUL84 HCMVT	63 KD EARLY NONSTRUCTURAL PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	100-116								
PUL87 EBV	HYPOTHETICAL PROTEIN BCBF1	EPSTEIN-BARR VIRUS (STRAIN B95-8)	100-116								
PUL87 HCMVA	HYPOTHETICAL PROTEIN UL87	HERPESVIRUS SAMIRI (STRAIN 11)	406-422	510-537							
PUL87 HSV6U	HYPOTHETICAL PROTEIN 3R	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	203-231	109-335	606-628	633-653	737-781				
PUL87 HSVSA	HYPOTHETICAL PROTEIN 3R	HERPESVIRUS SAMIRI (STRAIN 11)	301-322	507-529							
PUL87 HCMVA	HYPOTHETICAL PROTEIN UL88	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	365-387	402-422	579-593						
PUL88 HSV6U	HYPOTHETICAL PROTEIN 6R	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	150-173	232-279							
PUL89 HCMVA	HYPOTHETICAL PROTEIN UL90	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	35-50								
PUL91 HSV6U	HYPOTHETICAL PROTEIN 1R	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	43-63								
PUL92 HCMVA	HYPOTHETICAL PROTEIN UL92	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	76-99								
PUL92 HSV6U	HYPOTHETICAL PROTEIN 9R	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	36-55	100-119							
PUL94 HCMVA	PROTEIN UL94	HERPESVIRUS SAMIRI (STRAIN 11)	48-70								
PUL95 EBV	HYPOTHETICAL PROTEIN BGLF3	EPSTEIN-BARR VIRUS (STRAIN B95-8)	201-223								
PUL95 HCMVA	HYPOTHETICAL PROTEIN UL95	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	300-326								
PUL95 HSV6U	HYPOTHETICAL PROTEIN 13R	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	6-30	328-346							
PUL95 HSVSA	HYPOTHETICAL GENE 34 PROTEIN	HERPESVIRUS SAMIRI (STRAIN 11)	182-209								
PUL97 HCMVA	GANCICLOVIR KINASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	208-228	341-367							
PUL97 HCMVA	HYPOTHETICAL PROTEIN UL102	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	168-183								
PUL97 HCMVA	PROTEIN UL103	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	26-47								
PUL97 HCMVA	VIRION PROTEIN UL104	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	315-235	473-450							
PUL98 HCMVA	HYPOTHETICAL PROTEIN UL108	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	91-118								
PUL98 HCMVA	HYPOTHETICAL PROTEIN UL111	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	60-81								
PUL98 HCMVA	HYPOTHETICAL PROTEIN UL113	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	298-319								
PUL98 HCMVA	HYPOTHETICAL PROTEIN UL117	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	178-195								
PUL98 HCMVA	HYPOTHETICAL PROTEIN UL118	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	101-130								
PUL98 HCMVA	HYPOTHETICAL PROTEIN UL121	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	179-153								





PCGENE	PICTZIP	FILENAME	PROTEIN	All Viruses (No Bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PV2A	CMV	PV2A	CMV	COWPEA CHLOROTIC MOTTLE VIRUS	206-314								
PV2A	TAV	PV2A	TAV	TOMATO ASPERMATOPHYTES VIRUS	214-235								
PV2A	TMV	PV2A	TMV	TOMATO ASPERMATOPHYTES VIRUS (STRAIN TCM)	62-82								
PV2A	TOBSV	PV2A	TOBSV	TOBACCO RATTLE VIRUS (STRAIN WC)	226-230								
PV2A	ASF	PV2A	ASF	AFRICAN SWINE FEVER VIRUS (STRAIN BAV14)	145-164								
PV2A	ASF	PV2A	ASF	AFRICAN SWINE FEVER VIRUS (STRAIN LISS7)	114-135								
PV2A	CMV	PV2A	CMV	CUCUMBER MOSAIC VIRUS (STRAIN LISS7)	160-187								
PV2A	CMV	PV2A	CMV	CUCUMBER MOSAIC VIRUS (STRAIN FNY)	214-235								
PV2A	CMV	PV2A	CMV	CUCUMBER MOSAIC VIRUS (STRAIN M)	214-235								
PV2A	CMV	PV2A	CMV	CUCUMBER MOSAIC VIRUS (STRAIN O)	214-235								
PV2A	CMV	PV2A	CMV	CUCUMBER MOSAIC VIRUS (STRAIN Q)	214-235								
PV2A	CMV	PV2A	CMV	CUCUMBER MOSAIC VIRUS (STRAIN Y)	214-235								
PV2A	IBV	PV2A	IBV	AVIAN INFLUENZA VIRUS (STRAIN DEAUDETTE)	5-28								
PV2A	IBV	PV2A	IBV	AVIAN INFLUENZA VIRUS (STRAIN N41)	5-28								
PV2A	IBV	PV2A	IBV	AVIAN INFLUENZA VIRUS (STRAIN PORTUGAL12/83)	5-28								
PV2A	IBV	PV2A	IBV	AVIAN INFLUENZA VIRUS (STRAIN UK/18/66)	5-28								
PV2A	IBV	PV2A	IBV	TOMATO ASPERMATOPHYTES VIRUS	147-168								
PV2A	IBV	PV2A	IBV	BARLEY STRIPE MOSAIC VIRUS	320-340								
PV2A	IBV	PV2A	IBV	CANINE ENTERIC CORONAVIRUS (STRAIN K378)	97-116								
PV2A	IBV	PV2A	IBV	TURNIP YELLOW MOSAIC VIRUS (AUSTRALIAN ISOLATE)	12-35								
PV2A	IBV	PV2A	IBV	ALFA MOSAIC VIRUS (STRAIN 23/1 ISOLATE LEIDEN)	44-59								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN COPENHAGEN)	217-244								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN WR)	217-244								
PV2A	IBV	PV2A	IBV	VARIOLA VIRUS	207-214								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN COPENHAGEN)	41-66								
PV2A	IBV	PV2A	IBV	VARIOLA VIRUS	41-66								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN COPENHAGEN)	21-44								
PV2A	IBV	PV2A	IBV	VARIOLA VIRUS	21-44								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN COPENHAGEN)	19-62								
PV2A	IBV	PV2A	IBV	VARIOLA VIRUS	19-62								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN COPENHAGEN)	341-362								
PV2A	IBV	PV2A	IBV	VARIOLA VIRUS	340-361								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN COPENHAGEN)	429-447								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN WR)	429-447								
PV2A	IBV	PV2A	IBV	VARIOLA VIRUS	429-447								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN COPENHAGEN)	107-131								
PV2A	IBV	PV2A	IBV	VARIOLA VIRUS	107-131								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN WR, AND (STRAIN COPENHAGEN)	38-42								
PV2A	IBV	PV2A	IBV	VARIOLA VIRUS	33-76								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN WR, AND (STRAIN COPENHAGEN)	33-76								
PV2A	IBV	PV2A	IBV	VARIOLA VIRUS	205-220								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN WR, AND (STRAIN COPENHAGEN)	175-190								
PV2A	IBV	PV2A	IBV	VARIOLA VIRUS	33-49								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN COPENHAGEN)	33-49								
PV2A	IBV	PV2A	IBV	VARIOLA VIRUS	66-90								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN COPENHAGEN)	66-90								
PV2A	IBV	PV2A	IBV	VARIOLA VIRUS	43-71								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN COPENHAGEN)	43-71								
PV2A	IBV	PV2A	IBV	VARIOLA VIRUS	47-71								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN COPENHAGEN)	47-71								
PV2A	IBV	PV2A	IBV	VARIOLA VIRUS	59-79								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN WR)	59-79								
PV2A	IBV	PV2A	IBV	VARIOLA VIRUS	201-226								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN COPENHAGEN)	201-226								
PV2A	IBV	PV2A	IBV	VARIOLA VIRUS	247-266								
PV2A	IBV	PV2A	IBV	VACCINIA VIRUS (STRAIN WR)	247-266								
PV2A	IBV	PV2A	IBV	BEEF CURLY TOP VIRUS	56-75								



PCGENE	PICTLZIP	All Viruses (No Bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
DIRNAME	PROTEIN	VIRUS	55-74									
PVAL1 CLVK	ALI PROTEIN	CASSAVA LATENT VIRUS (STRAIN WEST KENYAN 844)	55-74									
PVAL1 CLVN	ALI PROTEIN	CASSAVA LATENT VIRUS (STRAIN NIGERIAN)	55-74									
PVAL2 DCTV	ALI PROTEIN	BEEET CURLY TOP VIRUS	82-108									
PVAL3 CLVK	ALI PROTEIN	CASSAVA LATENT VIRUS (STRAIN WEST KENYAN 844)	77-97									
PVAL3 CLVN	ALI PROTEIN	CASSAVA LATENT VIRUS (STRAIN NIGERIAN)	77-97									
PVAL3 TLYCM	ALI PROTEIN	TOMATO YELLOW LEAF CURL VIRUS (STRAIN MARMANDE)	77-97									
PVAL3 TLYCV	ALI PROTEIN	TOMATO YELLOW LEAF CURL VIRUS	77-97									
PVAL4 CAMVC	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN CM-1841)	134-157									
PVAL4 CAMVD	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DRI)	134-157									
PVAL4 CAMVE	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN BIC)	134-157									
PVAL4 CAMVN	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN NY8133)	134-157									
PVAL4 CAMVP	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN PV47)	134-157									
PVAL4 CAMVS	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN STRASBOURG)	134-157									
PVAL4 CAMVW	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN W260)	141-161									
PVAL4 CERV	APHID TRANSMISSION PROTEIN	CARNATION ETCHED RING VIRUS	141-161									
PVAL4 FMDV	APHID TRANSMISSION PROTEIN	FIGWORT MOSAIC VIRUS (STRAIN DSS)	132-159									
PVB02 VACC	PROTEIN B2	VACCINIA VIRUS (STRAIN COPENHAGEN)	135-170									
PVB02 VACC	PROTEIN B2	VACCINIA VIRUS (STRAIN WR)	135-170									
PVB04 VACC	PROTEIN B4	VACCINIA VIRUS (STRAIN COPENHAGEN)	488-511									
PVB04 VACC	PROTEIN B4	VACCINIA VIRUS (STRAIN WR)	488-511									
PVB04 VARV	PROTEIN B4	VARIOLA VIRUS	488-511									
PVB05 VACC	PLAQUE-SIZE / HOST RANGE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN LG16MO)	251-271									
PVB05 VACC	PLAQUE-SIZE / HOST RANGE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	251-271									
PVB05 VACC	PLAQUE-SIZE / HOST RANGE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN LISTER)	251-271									
PVB05 VACC	PLAQUE-SIZE / HOST RANGE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN WR)	251-271									
PVB06 VACC	PROTEIN B6	VACCINIA VIRUS (STRAIN WR, AND (STRAIN COPENHAGEN)	59-82									
PVB06 VACC	PROTEIN B6	VACCINIA VIRUS (STRAIN COPENHAGEN)	59-82									
PVB06 VACC	PROTEIN B6	VACCINIA VIRUS (STRAIN WR)	121-143									
PVB06 VACC	PROTEIN B6	VACCINIA VIRUS (STRAIN COPENHAGEN)	121-143									
PVB07 VACC	PROTEIN B7	VACCINIA VIRUS (STRAIN WR)	157-179									
PVB07 VACC	PROTEIN B7	VACCINIA VIRUS (STRAIN COPENHAGEN)	157-179									
PVB07 VACC	PROTEIN B7	VACCINIA VIRUS (STRAIN WR)	34-51									
PVB07 VACC	PROTEIN B7	VACCINIA VIRUS (STRAIN COPENHAGEN)	34-51									
PVB08 VACC	PROTEIN B8	CASSAVA LATENT VIRUS (STRAIN WEST KENYAN 844)	245-268									
PVB08 VACC	PROTEIN B8	CASSAVA LATENT VIRUS (STRAIN NIGERIAN)	166-191									
PVB08 VACC	PROTEIN B8	SQUASH LEAF CURL VIRUS	166-191									
PVB08 VACC	PROTEIN B8	ABUTILON MOSAIC VIRUS (ISOLATE WEST INDIA)	166-191									
PVB08 VACC	PROTEIN B8	BEAN GOLDEN MOSAIC VIRUS	166-191									
PVB08 VACC	PROTEIN B8	POTATO YELLOW MOSAIC VIRUS (ISOLATE VENEZUELA)	191-218									
PVB08 VACC	PROTEIN B8	SQUASH LEAF CURL VIRUS	70-90									
PVB08 VACC	PROTEIN B8	VACCINIA VIRUS (STRAIN COPENHAGEN)	75-95									
PVB08 VACC	PROTEIN B8	VACCINIA VIRUS (STRAIN WR)	58-78									
PVB08 VACC	PROTEIN B8	VARIOLA VIRUS	8-31									
PVB08 VACC	PROTEIN B8	SHOPE FIBROMA VIRUS (STRAIN KASZA)	98-123									
PVB08 VACC	PROTEIN B8	SHOPE FIBROMA VIRUS (STRAIN KASZA)	182-209									
PVB08 VACC	PROTEIN B8	VACCINIA VIRUS (STRAIN COPENHAGEN)	182-209									
PVB08 VACC	PROTEIN B8	VACCINIA VIRUS (STRAIN WR)	20-47									
PVB08 VACC	PROTEIN B8	SHOPE FIBROMA VIRUS (STRAIN KASZA)	14-30									
PVB08 VACC	PROTEIN B8	SHOPE FIBROMA VIRUS (STRAIN KASZA)	40-59									
PVB08 VACC	PROTEIN B8	VACCINIA VIRUS (STRAIN COPENHAGEN)	40-59									
PVB08 VACC	PROTEIN B8	VACCINIA VIRUS (STRAIN WR)	85-109									
PVB08 VACC	PROTEIN B8	SHOPE FIBROMA VIRUS (STRAIN KASZA)	42-64									
PVB08 VACC	PROTEIN B8	VACCINIA VIRUS (STRAIN COPENHAGEN)	42-64									
PVB08 VACC	PROTEIN B8	VARIOLA VIRUS	42-64									
PVB08 VACC	PROTEIN B8	VACCINIA VIRUS (STRAIN COPENHAGEN)	41-68									
PVB08 VACC	PROTEIN B8	VACCINIA VIRUS (STRAIN COPENHAGEN)	301-326									
PVB08 VACC	PROTEIN B8	VACCINIA VIRUS (STRAIN COPENHAGEN)	3-28									
PVB08 VACC	PROTEIN B8	EPSTEIN-BARR VIRUS (STRAIN B95-4)	148-172									
PVB08 VACC	PROTEIN B8	EPSTEIN-BARR VIRUS (STRAIN B95-4)	366-381									
PVB08 VACC	PROTEIN B8	EPSTEIN-BARR VIRUS (STRAIN B95-4)	1072-1093									





PGCENE	PICTURE	FILE NAME	ALL Viruses (No Bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10
PF15 VACCP	PROTEIN F15	VACCINIA VIRUS (STRAIN L-1VP)	VIRUS	3-26									
PF15 VARV	PROTEIN F15	VACCINIA VIRUS (STRAIN L-1VP)	VIRUS	28-31									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	297-323									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	88-104									
PF17 CAPVK	PROTEIN F17	CAPRIPOX VIRUS (STRAIN KS-1)	CAPRIPOX VIRUS	89-111									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	65-90									
PF17 CAPVK	PROTEIN F17	CAPRIPOX VIRUS (STRAIN KS-1)	CAPRIPOX VIRUS	51-76									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	29-48									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	72-94									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	169-195									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	210-225									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	298-318									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	237-257									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	176-195									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	208-318									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	58-82									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	50-72									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	50-72									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	11-33									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	11-33									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	31-51									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	31-51									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	134-149									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	159-185									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	35-54									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	109-124									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	103-122									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	131-178									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	68-92									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	88-112									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	171-316									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	76-92									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	300-327									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	114-315									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	158-184									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	209-226									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	171-197									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	14-40									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	20-42									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	166-191									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	90-109									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	108-123									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	284-299									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	648-673									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	14-32									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	11-38									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	109-133									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	134-156									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	71-97									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	5-30									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	39-49									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	229-252									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	22-37									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	85-106									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	1155-1176									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	130-146									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	142-161									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	47-64									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	10-51									
PF17 FOWPV	PROTEIN F17	FOWLPOX VIRUS	FOWLPOX VIRUS	53-75									



PCGENE	PICTLZIP	All Virus (No Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (ISOLATE JIV52A) (HIV-1)	716-753								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN A01)	675-692								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN A01)	716-753								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN A04F)	716-753								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN KENTUCKY D)	716-753								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	MAREK'S DISEASE HERPESVIRUS (STRAIN RD-10)	589-613								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	HERPESVIRUS SAMIRI (STRAIN 11)	483-506	701-716							
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN 632)	256-275	597-621	740-758						
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN SA-2)	266-285	607-631	750-768						
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE VRI2)	266-285	607-631	750-768						
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	MURINE CYTOMEGALOVIRUS (STRAIN SMITH)	135-156	566-580	718-765						
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / HICKER)	203-218								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	522-538								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	1-22	467-493							
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 2)	1-22	467-493							
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 3)	435-458								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 7 / STRAIN 331)	436-459								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	BOVINE HERPESVIRUS TYPE 1 (STRAIN COOPER)	475-494								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN 1942)	444-459								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AHP) AND (STRAIN KENTUCKY D)	427-442								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	MAREK'S DISEASE HERPESVIRUS (STRAIN HC-1)	399-421								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	MAREK'S DISEASE HERPESVIRUS (STRAIN RD-10)	399-421								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	MAREK'S DISEASE HERPESVIRUS (STRAIN GA)	398-420								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	MAREK'S DISEASE HERPESVIRUS (STRAIN A01)	399-421								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / HICKER)	190-197	446-472							
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	431-449								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	VARICELLA-ZOSTER VIRUS (STRAIN SCOTT)	431-449								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	79-94								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 2)	104-129	413-437							
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	469-493								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A31908)	205-221	265-287	482-504						
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN COPIENHAGEN)	205-221	265-280	484-506						
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN BR94)	205-221	265-280	484-506						
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	CANINE DISTEMPER VIRUS (STRAIN ONDERSTPOORT)	336-361	398-414	562-589						
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN 183)	205-221	265-280	484-506						
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	205-221	265-280	484-506						
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP A / STRAIN LO)	205-221	265-280	484-506						
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN R35-2)	205-221	265-280	484-506						
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	MEASLES VIRUS (STRAIN EDMONSTON/BHD (STRAIN HALL))	274-245	286-302	451-477						
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	MEASLES VIRUS (STRAIN IP-3-CA)	227-248	286-302	451-477						
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	MEASLES VIRUS (STRAIN YAMAGATA-1)	224-245	286-302	451-477						
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	MUMPS VIRUS (STRAIN SBL-1)	5-20	276-292	446-467						
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	MUMPS VIRUS (STRAIN MIYAHARA VACCINE)	276-292	446-467							
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	MUMPS VIRUS (STRAIN RW)	276-292	446-467							
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	MUMPS VIRUS (STRAIN SBL)	5-20	276-292	446-467						
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA/2)	273-289								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN BEAUFORT C/45)	273-289								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN HER33)	273-289								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN BI-HITCHNER/41)	273-289								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN LAS/46)	273-289								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN MIYADAKI/51)	273-289								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN QUEENSLAND/66)	273-289								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN TEXAS)	273-289								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN TEXAS G B / 48)	273-289								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN ULSTER/607)	273-289								
PVGLB_HSV1E	GLYCOPROTEIN B PRECURSOR	PHOCINE DISTEMPER VIRUS	269-285	303-326	367-383	531-558					



PCGENE	FUNCTION	PROTEIN	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	VIRUS	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C19)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN C19)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN GREY)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSHIHARA)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	BOVINE PARAINFLUENZA 3 VIRUS	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN N111 47845)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	RINDERPEST VIRUS (STRAIN KAHETE C)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	RINDERPEST VIRUS (STRAIN L)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN 2, MOST MUTANTS)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN FUSIHI)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN HARRIS)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN HW)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN 2)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SIMIAN VIRUS 41	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SIMIAN VIRUS 3 (STRAIN WJ)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	TURKEY RHINOTRACHEITIS VIRUS	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	INFECTIOUS HEMATOPOIETIC NECROSIS VIRUS (STRAIN ROUND HUT)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	RABIES VIRUS (STRAIN ERA)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	RABIES VIRUS (STRAIN FV)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	RABIES VIRUS (STRAIN SAD B19)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	RABIES VIRUS (STRAIN STREET)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	TURKEY RHINOTRACHEITIS VIRUS	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	VIRAL HEMORRHAGIC SEPTICEMIA VIRUS (STRAIN 07-71)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN TOWNE)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN GS)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 4 / STRAIN 192)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD-47)mod (ISOLATE INVS3A)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HERPESVIRUS SAIMIRI (STRAIN 11)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	MURINE CYTOMEGALOVIRUS (STRAIN SMIT11)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	EQUINE HERPESVIRUS TYPE 1	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	BUNYAVIRUS GERMISTON	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	BUNYAVIRUS LA CROSSE (ISOLATE L74)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	BUNYAVIRUS SNOWSHOE HARE	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	BUNYAVIRUS VIRUS	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	DUGRE VIRUS	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN B-1)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN HO10)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN LEE)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN 76-118)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	IMPATIENS NECROTIC SPOT VIRUS (NSV)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	PROSPECT HILL VIRUS	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	PUNTA TORO PHLEBOVIRUS	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	PUMALA VIRUS (STRAIN HALLAS B1)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	PUMALA VIRUS (STRAIN SOTKANO)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	RIFT VALLEY FEVER VIRUS	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	RIFT VALLEY FEVER VIRUS (STRAIN ZH-148 B12)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SEOL VIRUS (STRAIN 00-59)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SEOL VIRUS (STRAIN K23)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SEOL VIRUS (STRAIN SR-11) (SAPPORO RAT VIRUS)	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	LUKUNEMI VIRUS	456-477								

[illegible]





ECGENE	PICT121P	All Viruses (No Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PVMA1 MEASH	MATRIX PROTEIN	MEASLES VIRUS (STRAIN VALLE)	283-309								
PVMA1 MEASU	MATRIX PROTEIN	MEASLES VIRUS (STRAIN IP-3 CA)	87-111								
PVMA1 MEASU	MATRIX PROTEIN	MEASLES VIRUS (STRAIN IU2)	283-269								
PVMA1 MUMPS	MATRIX PROTEIN	MUMPS VIRUS (STRAIN SBL-1)	191-207	227-250							
PVMA1 MUMPS	MATRIX PROTEIN	MUMPS VIRUS (STRAIN SBL)	191-207	227-250							
PVMA1 NDVA	MATRIX PROTEIN	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA/33)	135-151	190-208	309-329						
PVMA1 NDVB	MATRIX PROTEIN	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE C/45)	135-151	190-208	309-329						
PVMA1 PIHIC	MATRIX PROTEIN	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C19)	195-217								
PVMA1 PIHIB	MATRIX PROTEIN	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN TOSHIIBA) (PIV-2)	132-154	189-203	308-328						
PVMA1 PIHIB	MATRIX PROTEIN	HUMAN PARAINFLUENZA 4A VIRUS (STRAIN TOSHIIBA) (PIV-4A)	312-332								
PVMA1 BINDK	MATRIX PROTEIN	HUMAN PARAINFLUENZA 4B VIRUS (STRAIN KAIBETE O)	312-332								
PVMA1 SENDH	MATRIX PROTEIN	RINDERPEST VIRUS (STRAIN KABETE O)	208-221	279-260	283-309						
PVMA1 SENDH	MATRIX PROTEIN	SENDAL VIRUS (STRAIN FUSHIMI)	195-217								
PVMA1 SENDZ	MATRIX PROTEIN	SENDAL VIRUS (STRAIN HARRIS)	195-217								
PVMA1 SSPVB	MATRIX PROTEIN	SENDAL VIRUS (STRAIN Z)	195-217								
PVMA1 SVAT	MATRIX PROTEIN	SUBACUTE SCLEROSING PANENCEPHALITIS VIRUS (STRAIN JIKEN)	283-309	314-318							
PVMA1 SVS	MATRIX PROTEIN	SIMIAN VIRUS 41	132-154	189-203	308-328						
PVMA1 SVCV	MATRIX PROTEIN	SIMIAN VIRUS 3 (STRAIN W3)	98-114	132-148	308-335						
PVMA1 TATV	MATRIX PROTEIN	SPRING VIREMIA OF CARP VIRUS (RIJNDOVIRUS CARPIA)	141-167								
PVMA1 CYBIM	EL GLYCOPROTEIN	TURKEY RHINOTRACHEITIS VIRUS	122-143								
PVMA1 CVRH2	EL GLYCOPROTEIN	BOVINE CORONAVIRUS (STRAIN NEGUS)	9-36	137-161	171-190						
PVMA1 CVHOC	EL GLYCOPROTEIN	HUMAN CORONAVIRUS (STRAIN 229E)	136-155								
PVMA1 CVMA3	EL GLYCOPROTEIN	HUMAN CORONAVIRUS (STRAIN OC-3)	9-36	64-85	132-161						
PVMA1 CVMAH	EL GLYCOPROTEIN	MURINE CORONAVIRUS MIV (STRAIN A39)	10-37								
PVMA1 CVPPS	EL GLYCOPROTEIN	MURINE CORONAVIRUS MIV (STRAIN JIM)	10-37								
PVMA1 CVPPU	EL GLYCOPROTEIN	PORCINE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAI)	174-193								
PVMA1 CVPRM	EL GLYCOPROTEIN	PORCINE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAI)	169-193	174-193							
PVMA1 CVYKE	EL GLYCOPROTEIN	PORCINE RESPIRATORY CORONAVIRUS (STRAIN RM4)	174-193								
PVMA1 BVH	EL GLYCOPROTEIN	TURKEY ENTERIC CORONAVIRUS	9-36	137-161	171-190						
PVMA1 BVH	EL GLYCOPROTEIN	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN 6/82)	74-98								
PVMA1 BVYB	EL GLYCOPROTEIN	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTE)	74-101								
PVMA1 BVK	EL GLYCOPROTEIN	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTE N42)	74-101								
PVMA1 BVV	EL GLYCOPROTEIN	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN KR52)	74-98								
PVMA1 BVV	EL GLYCOPROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-4)	131-153	178-203							
PVMA1 BVV	EL GLYCOPROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN CA-184)	118-134	147-164	183-201						
PVMA1 BVV	EL GLYCOPROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DH)	118-134	147-164	183-201						
PVMA1 BVV	EL GLYCOPROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DHC)	118-134	147-164	183-201						
PVMA1 BVV	EL GLYCOPROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN NY133)	118-134	147-164	183-201						
PVMA1 BVV	EL GLYCOPROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN STRASBOURG)	118-134	147-164	183-201						
PVMA1 BVV	EL GLYCOPROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN W260)	118-134	147-164	183-201						
PVMA1 BVV	EL GLYCOPROTEIN	CARNATION ETCHED RING VIRUS	293-318								
PVMA1 BVV	EL GLYCOPROTEIN	FIGWORT MOSAIC VIRUS (STRAIN DX5)	115-131	180-198							
PVMA1 BVV	EL GLYCOPROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	122-147	233-259							
PVMA1 BVV	EL GLYCOPROTEIN	DUCK HEPATITIS B VIRUS (BROWN SHANGHAI DUCK ISOLATE S5)	201-228	269-295							
PVMA1 BVV	EL GLYCOPROTEIN	DUCK HEPATITIS B VIRUS (STRAIN CHINA)	194-221	268-294							
PVMA1 BVV	EL GLYCOPROTEIN	DUCK HEPATITIS B VIRUS	157-184	231-257							
PVMA1 BVV	EL GLYCOPROTEIN	DUCK HEPATITIS B VIRUS (WHITE SHANGHAI DUCK ISOLATE S11)	194-221	269-295							
PVMA1 BVV	EL GLYCOPROTEIN	GROUND SQUIRREL HEPATITIS VIRUS	209-236	271-295	380-395						
PVMA1 BVV	EL GLYCOPROTEIN	HERON HEPATITIS B VIRUS	236-262	293-320							
PVMA1 BVV	EL GLYCOPROTEIN	HEPATITIS B VIRUS	11-28	70-96							
PVMA1 BVV	EL GLYCOPROTEIN	HEPATITIS B VIRUS (SUBTYPE ADW1)	185-202	244-270							
PVMA1 BVV	EL GLYCOPROTEIN	HEPATITIS B VIRUS (SUBTYPE ADRA)	185-202	244-270							
PVMA1 BVV	EL GLYCOPROTEIN	HEPATITIS B VIRUS (SUBTYPE ADW/STRAIN 991)	244-270								
PVMA1 BVV	EL GLYCOPROTEIN	HEPATITIS B VIRUS (STRAIN ALPHA1)	174-191	233-259							
PVMA1 BVV	EL GLYCOPROTEIN	HEPATITIS B VIRUS (SUBTYPE AD)	11-28	70-96							
PVMA1 BVV	EL GLYCOPROTEIN	HEPATITIS B VIRUS (SUBTYPE ADW/STRAIN INDONESIA/PIDW420)	233-259								
PVMA1 BVV	EL GLYCOPROTEIN	HEPATITIS B VIRUS (SUBTYPE ADW/STRAIN JAPAN/PIDW233)	174-191	233-259							











PCGENE	PICTLZIP	All Viruses (No. Nucleotide Phages)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
FILE NAME	PROTEIN	VIRUS	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
PVP21 VZVD	PROBABLE CAPSID PROTEIN VP21	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	117-132							
PVP26 NPVAC	P16 PROTEIN	AUTOGRAFIA CALIFORNICA NUCLEAR POLYTHEDROSIS VIRUS	12-31	58-76	117-141					
PVP27 H5V4	OUTER CAPSID PROTEIN VP2	AFRICANA HORSE SICKNESS VIRUS (SEROTYPE 4) (STRAIN VACCINE)	868-891	974-994						
PVP2 BT10	OUTER CAPSID PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 10) (ISOLATE USA)	361-381	399-424	564-586	829-849				
PVP2 BT11	OUTER CAPSID PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 11) (ISOLATE USA)	361-381	399-424	564-586	829-849				
PVP2 BT12	OUTER CAPSID PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 12) (ISOLATE USA)	362-382	420-438	617-632	657-676				
PVP2 BT13	OUTER CAPSID PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 13) (ISOLATE USA)	361-381							
PVP2 BT14	OUTER CAPSID PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 14) (ISOLATE AUSTRALIA)	420-438	634-681						
PVP2 BT15	OUTER CAPSID PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 15) (ISOLATE SOUTH AFRICA)	14-31	117-140	420-438	654-681				
PVP2 BT16	OUTER CAPSID PROTEIN VP2	EPIZOOTIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1)	151-168	229-252						
PVP2 ROTBR	RNA-BINDING PROTEIN VP2	BOVINE ROTAVIRUS (STRAIN RF)	301-317	334-360	522-543	673-698	764-789			
PVP2 ROTBU	RNA-BINDING PROTEIN VP2	BOVINE ROTAVIRUS (STRAIN RF)	301-317	334-360	522-543	673-698	764-789			
PVP2 ROTCW	RNA-BINDING PROTEIN VP2	HUMAN ROTAVIRUS (SEROTYPE 1) (STRAIN WA)	309-325	342-363	532-553	674-700	774-799			
PVP2 ROTPC	RNA-BINDING PROTEIN VP2	PORCINE ROTAVIRUS (GROUP C) (STRAIN COWDEN)	51-75	101-119	408-435	514-533	665-691			
PVP2 ROTSI	RNA-BINDING PROTEIN VP2	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	34-57	219-240	302-318	335-361	523-544	674-700	765-790	
PVP30 MABVP	MINOR NUCLEOPROTEIN VP30	MARBURG VIRUS (STRAIN MUSOKO)	50-75							
PVP32 ASF7	PHOSPHOPROTEIN P32	AFRICANA SWINE FEVER VIRUS (STRAIN BA11V)	174-197							
PVP33 EROV	POLYMERASE COMPLEX PROTEIN VP33	EBOLA VIRUS	233-256							
PVP33 MABVM	POLYMERASE COMPLEX PROTEIN VP33	MARBURG VIRUS (STRAIN MUSOKO)	49-75	78-104						
PVP33 MABVP	POLYMERASE COMPLEX PROTEIN VP33	MARBURG VIRUS (STRAIN POMP)	49-75	78-104						
PVP33 VACCC	IMMUNODOMINANT ENVELOPE PROTEIN P33	VACCINIA VIRUS (STRAIN COPENHAGEN)	278-304							
PVP33 VACCV	IMMUNODOMINANT ENVELOPE PROTEIN P33	VACCINIA VIRUS (STRAIN WA)	278-304							
PVP33 VARV	IMMUNODOMINANT ENVELOPE PROTEIN P33	VARIOLA VIRUS	278-304							
PVP33 H5V4G	18 KD PHOSPHOPROTEIN	MARX'S DISEASE HERPESVIRUS (STRAIN GA)	235-270							
PVP33 H5V4G	18 KD PHOSPHOPROTEIN	MARX'S DISEASE HERPESVIRUS (STRAIN MD170CR2)	235-270							
PVP39 NPVAC	MAJOR CAPSID PROTEIN	AUTOGRAFIA CALIFORNICA NUCLEAR POLYTHEDROSIS VIRUS	296-311							
PVP39 NPVOP	MAJOR CAPSID PROTEIN	ORGYIA PSEUDOTUGATA MULTICAPSID POLYTHEDROSIS VIRUS	107-134	214-240	295-316					
PVP39 NPVOP	MAJOR CAPSID PROTEIN	AFRICANA HORSE SICKNESS VIRUS (SEROTYPE 4) (STRAIN VACCINE)	65-85	126-147	215-230	845-862				
PVP3 BT10	VP3 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 10) (ISOLATE USA)	133-144	212-227						
PVP3 BT11	VP3 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 11) (ISOLATE USA)	133-144	212-227						
PVP3 BT12	VP3 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 12) (ISOLATE USA)	133-144	212-227						
PVP3 BT13	VP3 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 13) (ISOLATE AUSTRALIA)	131-142	671-693						
PVP3 BT14	VP3 CORE PROTEIN	EPIZOOTIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1)	131-142	671-693						
PVP3 BT15	VP3 CORE PROTEIN	RICE DWARF VIRUS (RDV)	89-108	340-360	561-593	600-717	742-768	960-975		
PVP3 ROTPC	INNER CORE PROTEIN VP3	PORCINE ROTAVIRUS (GROUP C) (STRAIN COWDEN)	403-429							
PVP40 EBU	CAPSID PROTEIN P40	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	401-425	426-444	512-536	796-822				
PVP40 H5V11	CAPSID PROTEIN P40	EPSTEIN-BARR VIRUS (STRAIN B91.4)	429-454							
PVP40 H5V12	CAPSID PROTEIN P40	HERPES SIMPLEX VIRUS (TYPE 1) (STRAIN 17)	411-468	472-492						
PVP40 H5V13	CAPSID PROTEIN P40	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	50-67	95-119	483-504					
PVP40 ILTV	CAPSID PROTEIN P40	HERPESVIRUS SAPHIRI (STRAIN 11)	342-368							
PVP40 MABVM	CAPSID PROTEIN P40	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE VIR1)	506-528							
PVP40 MABVP	MATRIX PROTEIN VP40	MARBURG VIRUS (STRAIN MUSOKO)	94-110							
PVP40 NPVBM	STRUCTURAL GLYCOPROTEIN P40	MARBURG VIRUS (STRAIN POMP)	95-110							
PVP40 VZVD	CAPSID PROTEIN VP40	BOMBYX MORI NUCLEAR POLYTHEDROSIS VIRUS	223-242	256-272						
PVP41 NPVAC	STRUCTURAL GLYCOPROTEIN GP41	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	47-64							
PVP41 ROTSI	OUTER CAPSID PROTEIN VP4	AUTOGRAFIA CALIFORNICA NUCLEAR POLYTHEDROSIS VIRUS	229-248	262-278						
PVP42 ROTSI	OUTER CAPSID PROTEIN VP4	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	483-508							
PVP43 NPVAC	VIRAL TRANSCRIPTION REGULATOR P43	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	393-411	483-508						
PVP43 NPVOP	P43 PROTEIN	AUTOGRAFIA CALIFORNICA NUCLEAR POLYTHEDROSIS VIRUS	14-38							
PVP44 VARY	MAJOR CORE PROTEIN P44 PRECURSOR	ORGYIA PSEUDOTUGATA MULTICAPSID POLYTHEDROSIS VIRUS	136-157							
PVP44 VACCC	MAJOR CORE PROTEIN P44 PRECURSOR	VARIOLA VIRUS	273-288							
PVP44 VACCV	MAJOR CORE PROTEIN P44 PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	331-358							
PVP44 VARY	MAJOR CORE PROTEIN P44 PRECURSOR	VACCINIA VIRUS (STRAIN WA)	331-358							
PVP4 BT10	VP4 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 10) (ISOLATE USA)	174-193	233-249	545-561					
PVP4 BT11	VP4 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 11) (ISOLATE USA)	174-193	233-249	545-561					
PVP4 BT12	VP4 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 12) (ISOLATE USA)	174-193	233-249	545-561					







GENE	FUNCTION	ALL Viruses (No Bacteriophage)	AREA 1 428-430	AREA 2 431-473	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
FILE NAME	PROTEIN	VIRUS									
PS503 ROTHI	NONSTRUCTURAL PROTEIN NCVP2	HUMAN ROTAVIRUS (STRAIN 10V-40-3)									
PS503 ROTPC	NONSTRUCTURAL PROTEIN NS3	PORCINE ROTAVIRUS (GROUP C / STRAIN COWDEN)	140-157								
PS503 ROTSI	NONSTRUCTURAL PROTEIN NS3	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	140-157								
PS506 ROTBR	VP8 PROTEIN	BOVINE ROTAVIRUS (STRAIN R7)	399-414								
PS506 ROTBS	VP8 PROTEIN	BOVINE ROTAVIRUS (STRAIN R7)	202-225								
PS506 ROTBU	VP8 PROTEIN	BOVINE ROTAVIRUS (STRAIN UK)	64-85								
PS506 ROTF	VP8 PROTEIN	BOVINE ROTAVIRUS (STRAIN FL14)	202-225								
PS506 ROTEL	VP8 PROTEIN	EQUINE ROTAVIRUS (STRAIN IL-2)	202-225								
PS506 ROTGA	VP8 PROTEIN	ROTAVIRUS (GROUP B / STRAIN ADRI)	202-225								
PS506 ROTGI	VP8 PROTEIN	ROTAVIRUS (GROUP B / STRAIN ADRI)	22-40								
PS506 ROTHC	VP8 PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN 1076)	202-225								
PS506 ROTHS	VP8 PROTEIN	HUMAN ROTAVIRUS (GROUP C / STRAIN DUSTOL)	64-85								
PS506 ROTHW	VP8 PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN S3)	202-225								
PS506 ROTPC	VP8 PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	202-225								
PS506 ROTPG	VP8 PROTEIN	PORCINE ROTAVIRUS (GROUP C / STRAIN COWDEN)	64-85								
PS507 ROTBI	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (STRAIN GOTTFRIED)	202-225								
PS507 ROTC	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (STRAIN KN-4)	131-155								
PS507 ROTD	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (GROUP C / STRAIN COWDEN)	117-136								
PS507 ROTB	GLYCOPROTEIN VP7	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	274-295								
PS509 ROTBA	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (SEROTYPE 6 / STRAIN 61A)	131-155								
PS509 ROTBB	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (STRAIN A44)	131-155								
PS509 ROTBT	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (SEROTYPE 10 / STRAIN B221)	131-155								
PS509 ROTC	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (STRAIN KK)	131-155								
PS509 ROTD	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (SEROTYPE 1 / STRAIN T449)	131-155								
PS509 ROTF	GLYCOPROTEIN VP7	CHICKEN ROTAVIRUS A (SEROTYPE 7 / STRAIN C12)	134-158								
PS509 ROTG	GLYCOPROTEIN VP7	ROTAVIRUS (GROUP B / STRAIN IDIR)	205-212								
PS509 ROTHA	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN RV-4)	131-155								
PS509 ROTB	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN IU3)	192-212								
PS509 ROTC	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN DS1)	192-212								
PS509 ROTD	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN JIN126)	192-212								
PS509 ROTF	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (STRAIN L26)	131-155								
PS509 ROTG	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN M37)	192-212								
PS509 ROTH	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN NO AND STRAIN D)	131-155								
PS509 ROTI	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN P)	131-155								
PS509 ROTJ	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN RV)	131-155								
PS509 ROTK	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN S3)	192-212								
PS509 ROTL	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN VA10)	131-155								
PS509 ROTM	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 3 / STRAIN OSU)	131-155								
PS509 ROTN	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 3 / STRAIN TFR-41)	192-212								
PS509 ROTP	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 4 / STRAIN DEN-144)	192-212								
PS509 ROTQ	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 4 / STRAIN BHI-1)	131-155								
PS509 ROTR	GLYCOPROTEIN VP7	RUESUS ROTAVIRUS	131-155								
PS509 ROTS	GLYCOPROTEIN VP7	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	131-155								
PS509 ROTV	GLYCOPROTEIN VP7	ROTAVIRUS (GROUP B / STRAIN ADRI)	136-153								
PS509 ROTW	GLYCOPROTEIN VP7	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	16-41								
PS509 ROTX	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN SBL-1) AND MUMPS VIRUS (STRAIN SRL)	7-29								
PS509 ROTY	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN EDINBURGH 2 & 6)	7-29								
PS509 ROTZ	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN EDINBURGH 4)	7-29								
PS509 ROTAA	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN MATSUJAMA)	10-29								
PS509 ROTAB	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN BELFAST)	7-29								
PS509 ROTAC	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN ENDERS)	7-29								
PS509 ROTAD	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN JERYL-LYN)	7-29								
PS509 ROTAE	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN KILHAM)	7-29								
PS509 ROTAF	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN BRISTOL 1)	6-29								
PS509 ROTAG	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN MIYAHARA VACCINE)	10-29								



FCGNE	PICTLZIP	All Viruses (No Bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	VIRUS	10-27								
PIY1 SOCHV	HYPOTHETICAL 9.2 KD PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS									
PIY7 ADE07	HYPOTHETICAL 9.2 KD EARLY PROTEIN	HUMAN ADENOVIRUS TYPE 7	14-27								
PIY83 SSV1	HYPOTHETICAL 9.2 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	16-41	62-77							
PIY11 EHV	HYPOTHETICAL BAHF-ORF1 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8)	205-220								
PIY801 FOWPM	HYPOTHETICAL BAHF-ORF1 PROTEIN	FOWLPOX VIRUS (ISOLATE HP-418)(MUNICH)	354-374								
PIY807 FOWPM	HYPOTHETICAL BAHF-ORF7 PROTEIN	FOWLPOX VIRUS (ISOLATE HP-418)(MUNICH)	104-121								
PIY809 FOWPM	HYPOTHETICAL BAHF-ORF9 PROTEIN	FOWLPOX VIRUS (ISOLATE HP-418)(MUNICH)	49-67								
PIY810 FOWPM	HYPOTHETICAL BAHF-ORF10 PROTEIN	FOWLPOX VIRUS (ISOLATE HP-418)(MUNICH)	84-100								
PIY812 FOWPM	HYPOTHETICAL BAHF-ORF12 PROTEIN	FOWLPOX VIRUS (ISOLATE HP-418)(MUNICH)	114-134	134-169							
PIYBL2 SFV1	BEL-2 PROTEIN	SARAN FOAMY VIRUS (TYPE 37 STRAIN LK3)	113-128								
PIYBL3 FOAMV	BEL-3 PROTEIN	HUMAN SPONARETROVIRUS	52-78								
PIYDH1 HSVSC	HYP 28.7 KD PROTEIN IN DHFR 3 REGION	HERPESVIRUS SAIMIRI (SUBGROUP C/ STRAIN 488)	206-210								
PIYDH2 HSVSC	HYP 9.3 KD PROTEIN IN DHFR 3 REGION	HERPESVIRUS SAIMIRI (SUBGROUP C/ STRAIN 488)	69-90								
PIYEC4 EBV	HYPOTHETICAL ECRF4 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8)	200-222								
PIYGA1 HSVAB	HYPOTHETICAL 21.6 KD PROTEIN	MAREK'S DISEASE HERPESVIRUS (STRAIN BC-1)	175-190								
PIYGA1 HSVAB	HYPOTHETICAL 21.6 KD PROTEIN	MAREK'S DISEASE HERPESVIRUS (STRAIN AD5)	175-190								
PIYBL4 HCMYA	HYPOTHETICAL PROTEIN HBL4	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	101-121								
PIYH9 VACCV	HYP HOST RANGE 37.4 KD PROTEIN	VACCINIA VIRUS (STRAIN WR)	86-102								
PIY02 CYMA3	HYP PROTEIN IN NUCLEOCAPSID ORF	MURINE CORONA VIRUS MHV	141-156								
PIY08 CYM1	HYP PROTEIN IN NUCLEOCAPSID ORF	MURINE CORONA VIRUS MHV	141-156								
PIY09 CYM5	HYP PROTEIN IN NUCLEOCAPSID ORF	MURINE CORONA VIRUS MHV	7-33								
PIYK2 EBV	HYPOTHETICAL BKRF2 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8)	67-90								
PIY112 ADE41	HYPOTHETICAL 1.0 KD PROTEIN	HUMAN ADENOVIRUS TYPE 41	53-73								
PIYMA2 EBV	BKRF2 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8)	76-100	128-135	215-241	310-330					
PIYMSF IRV23	HYPOTHETICAL 13.9 KD PROTEIN	SIMULIUM IRIDESCENT VIRUS (INSECT IRIDESCENT VIRUS TYPE 22)	23-46								
PIY01 ADEG1	HYPOTHETICAL PROTEIN	AVIAN ADENOVIRUS GALI (STRAIN PHELPS) (FOWL ADENOVIRUS 1)	59-80								
PIY01 ADEG1	HYPOTHETICAL 31 KD PROTEIN	COMELINA YELLOW MOTTLE VIRUS	56-83								
PIY01 TTV1	HYPOTHETICAL 19 KD PROTEIN	THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1)	13-40								
PIY02 COYMY	HYPOTHETICAL 13 KD PROTEIN	COMELINA YELLOW MOTTLE VIRUS	21-49								
PIY03 EAV	HYPOTHETICAL 13.6 KD PROTEIN	EQUINE ARTERITIS VIRUS	165-192								
PIY03 LELV	HYPOTHETICAL 21.4 KD PROTEIN	LELYSTAD VIRUS	196-212								
PIY03 LVX	HYPOTHETICAL 11.5 KD PROTEIN	LILY VIRUS X	71-92								
PIY03 NNV	HYPOTHETICAL 14 KD PROTEIN	NARCISUS MOSAIC VIRUS	7-30								
PIY03 PVX	HYPOTHETICAL 13 KD PROTEIN	POTATO VIRUS X	11-34								
PIY03 PVXCP	HYPOTHETICAL 12 KD PROTEIN	POTATO VIRUS X (STRAIN CP)	11-34								
PIY03 WCMYM	HYPOTHETICAL 13 KD PROTEIN	WHITE CLOVER MOSAIC VIRUS (STRAIN M)	9-29								
PIY03 WCMVO	HYPOTHETICAL 13 KD PROTEIN	WHITE CLOVER MOSAIC VIRUS (STRAIN O)	9-31								
PIY03 ADEG1	HYPOTHETICAL 31.5 KD PROTEIN	AVIAN ADENOVIRUS GALI (STRAIN PHELPS) (FOWL ADENOVIRUS 1)	69-86								
PIY03 EAV	HYPOTHETICAL 28.7 KD PROTEIN	EQUINE ARTERITIS VIRUS	139-158								
PIY06 NNV	HYPOTHETICAL 10 KD PROTEIN	NARCISUS MOSAIC VIRUS	10-26								
PIY0J TTV1	HYPOTHETICAL 16.6 KD PROTEIN	THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1)	13-32								
PIY0J TTV1	HYPOTHETICAL 16.6 KD PROTEIN	THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1)	16-39								
PIY0M TTV1	HYPOTHETICAL 31.6 KD PROTEIN	THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1)	82-102	231-256							
PIY0P TTV1	HYPOTHETICAL 20.2 KD PROTEIN	THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1)	91-113								
PIY24 RTBV	HYPOTHETICAL P24 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS	2-23	104-126							
PIY41 NPVAC	HYPOTHETICAL 41.3 KD PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES)	2-23	104-126							
PIY83 NPVOP	HYPOTHETICAL 12.2 KD PROTEIN	AUTOGRAFIA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	211-234								
PIY83 NPVOP	HYPOTHETICAL 40.0 KD PROTEIN	ORGANIA PSEUDOTUGATA MULTICAPSID POLYEDROSIS VIRUS (OP)	82-108								
PIY78 TNYD	HYPOTHETICAL P78 PROTEIN	ORGANIA PSEUDOTUGATA MULTICAPSID POLYEDROSIS VIRUS (OP)	27-34	215-230							
PIY04 NPVLD	HYPOTHETICAL 5.3 KD PROTEIN	TOBACCO NECROSIS VIRUS (STRAIN D) (TNV)	13-31								
PIYF1 HSV60	HYPOTHETICAL PROTEIN RF1	LYMANTRIA DISPAR MULTICAPSID NUCLEAR POLYEDROSIS VIRUS	16-35								
PIYF2 HSV60	HYPOTHETICAL PROTEIN RF2	HERPES SIMPLEX VIRUS (TYPE 6/ STRAIN GS)	42-66								
PIYF3 HSV60	HYPOTHETICAL PROTEIN RF3	HERPES SIMPLEX VIRUS (TYPE 6/ STRAIN GS)	55-74								
PIYR1 IRV6	REPETITIVE PROTEIN ORF1	HERPES SIMPLEX VIRUS (TYPE 6/ STRAIN GS)	32-36								
PIYR4 IRV6	REPETITIVE PROTEIN ORF4	CHILLO IRIDESCENT VIRUS (CIV) (INSECT IRIDESCENT VIRUS TYPE 6)	20-43								
PIYR5 IRV6	REPETITIVE PROTEIN ORF5	CHILLO IRIDESCENT VIRUS (CIV) (INSECT IRIDESCENT VIRUS TYPE 6)	44-49								
			179-204	260-285							

PGCENE	PICTLZIP	All Viruses (No Bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
SILVADIA	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PYR1 ERV	HYPOTHETICAL BARR1 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	199-121								
PYR2 ERV	HYPOTHETICAL BARR2 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	164-182								
PYR3 ERV	HYPOTHETICAL BARR3 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	92-113								
PYR4 ERV	HYPOTHETICAL BARR4 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	181-401								
PYR5 ERV	HYPOTHETICAL BARR5 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	131-152								
PYR6 ERV	HYPOTHETICAL BARR6 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	82-99								
PYR7 ERV	HYPOTHETICAL BARR7 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	17-40								
PYR8 ERV	HYPOTHETICAL BARR8 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	31-43								
PYR9 ERV	HYPOTHETICAL BARR9 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	18-46								
PYR10 ERV	HYPOTHETICAL BARR10 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	6-28								
PYR11 ERV	HYPOTHETICAL BARR11 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	37-34								
PYR12 ERV	HYPOTHETICAL BARR12 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	18-35								
PYR13 ERV	HYPOTHETICAL BARR13 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	16-52								
PYR14 ERV	HYPOTHETICAL BARR14 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	22-38								
PYR15 ERV	HYPOTHETICAL BARR15 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	3-18								
PYR16 ERV	HYPOTHETICAL BARR16 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	44-64								
PYR17 ERV	HYPOTHETICAL BARR17 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	48-67								
PYR18 ERV	HYPOTHETICAL BARR18 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	31-42								
PYR19 ERV	HYPOTHETICAL BARR19 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	105-127								
PYR20 ERV	HYPOTHETICAL BARR20 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	54-70								
PYR21 ERV	HYPOTHETICAL BARR21 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	150-166								
PYR22 ERV	HYPOTHETICAL BARR22 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	54-80								
PYR23 ERV	HYPOTHETICAL BARR23 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	100-125								
PYR24 ERV	HYPOTHETICAL BARR24 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	50-73								
PYR25 ERV	HYPOTHETICAL BARR25 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	163-188								
PYR26 ERV	HYPOTHETICAL BARR26 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	90-106								
PYR27 ERV	HYPOTHETICAL BARR27 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	65-90								
PYR28 ERV	HYPOTHETICAL BARR28 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	122-142								
PYR29 ERV	HYPOTHETICAL BARR29 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	21-44								
PYR30 ERV	HYPOTHETICAL BARR30 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	21-36								
PYR31 ERV	HYPOTHETICAL BARR31 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	3-23								
PYR32 ERV	HYPOTHETICAL BARR32 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	96-120								
PYR33 ERV	HYPOTHETICAL BARR33 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	80-105								
PYR34 ERV	HYPOTHETICAL BARR34 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	10-27								
PYR35 ERV	HYPOTHETICAL BARR35 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	54-77								
PYR36 ERV	HYPOTHETICAL BARR36 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	16-41								
PYR37 ERV	HYPOTHETICAL BARR37 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	205-220								
PYR38 ERV	HYPOTHETICAL BARR38 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	334-374								
PYR39 ERV	HYPOTHETICAL BARR39 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	104-121								
PYR40 ERV	HYPOTHETICAL BARR40 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	49-67								
PYR41 ERV	HYPOTHETICAL BARR41 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	84-100								
PYR42 ERV	HYPOTHETICAL BARR42 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	114-134								
PYR43 ERV	HYPOTHETICAL BARR43 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	113-128								
PYR44 ERV	HYPOTHETICAL BARR44 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	52-78								
PYR45 ERV	HYPOTHETICAL BARR45 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	206-230								
PYR46 ERV	HYPOTHETICAL BARR46 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	69-90								
PYR47 ERV	HYPOTHETICAL BARR47 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	200-222								
PYR48 ERV	HYPOTHETICAL BARR48 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	173-190								
PYR49 ERV	HYPOTHETICAL BARR49 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	173-190								
PYR50 ERV	HYPOTHETICAL BARR50 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	101-121								
PYR51 ERV	HYPOTHETICAL BARR51 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	86-102								
PYR52 ERV	HYPOTHETICAL BARR52 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	141-156								
PYR53 ERV	HYPOTHETICAL BARR53 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	141-156								
PYR54 ERV	HYPOTHETICAL BARR54 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	7-33								
PYR55 ERV	HYPOTHETICAL BARR55 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	67-90								
PYR56 ERV	HYPOTHETICAL BARR56 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	15-73								
PYR57 ERV	HYPOTHETICAL BARR57 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	76-100								
PYR58 ERV	HYPOTHETICAL BARR58 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	128-155								
PYR59 ERV	HYPOTHETICAL BARR59 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	213-241								
PYR60 ERV	HYPOTHETICAL BARR60 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	330-350								
PYR61 ERV	HYPOTHETICAL BARR61 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN D95-4)	23-46								



**TABLE XIV**

**SEARCH RESULTS SUMMARY**

**FOR P23TLZIPC MOTIF**







PCGENE	PICTLZIP	All Viruses (no bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6
GENOME	PROTEIN	VIRUS						
PPOLG JAEVI	GENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN JAOAR 5082)	61-95	1231-1269	1516-1549	2779-2813	3274-3311	AREA1
PPOLG JAEVN	GENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN NAKATASIA)	1161-1197					
PPOLG KUNIM	GENOME POLYPROTEIN	KUNIN VIRUS (STRAIN NIN61C)	61-95	1519-1551	2230-2264	2166-2198	3095-3132	
PPOLG LANVT	GENOME POLYPROTEIN	LANGAT VIRUS (STRAIN TP21)	1157-1188					
PPOLG MCF A	GENOME POLYPROTEIN	MOSQUITO CELL FUSING AGENT (CFA FLAVIVIRUS)	1174-1206	1330-1359				
PPOLG JMDMV	GENOME POLYPROTEIN	MAIZE DWARF MOSAIC VIRUS (MDMV)	372-351					
PPOLG MVEV	GENOME POLYPROTEIN	MURRAY VALLEY ENCEPHALITIS VIRUS	61-95	1305-1342				
PPOLG OMV	GENOME POLYPROTEIN	ONNITHOGALLUM MOSAIC VIRUS	344-376					
PPOLG PEMVC	GENOME POLYPROTEIN	PEPPER NOTTLE VIRUS (CALIFORNIA ISOLATE) (PENV)	826-859	1086-1124				
PPOLG POLIM	GENOME POLYPROTEIN	POLIOVIRUS TYPE 1 (STRAIN MAIONEY)	1121-1158					
PPOLG POLIS	GENOME POLYPROTEIN	POLIOVIRUS TYPE 1 (STRAIN SABIN)	1122-1159					
PPOLG POL2L	GENOME POLYPROTEIN	POLIOVIRUS TYPE 2 (STRAIN LANSING)	1120-1157					
PPOLG POL2W	GENOME POLYPROTEIN	POLIOVIRUS TYPE 2 (STRAIN W-2)	1119-1156					
PPOLG POL3T	GENOME POLYPROTEIN	POLIOVIRUS TYPE 3 (STRAIN 21127)	1119-1156					
PPOLG POL3L	GENOME POLYPROTEIN	POLIOVIRUS TYPE 3 (STRAINS PLEONUT AND PLEON 12A11J)	2960-2991	3084-3113				
PPOLG PPVD	GENOME POLYPROTEIN	PLUM POX POTYVIRUS (STRAIN DJ) (PPV)	1317-1368	1461-1490				
PPOLG PPVEA	GENOME POLYPROTEIN	PLUM POX POTYVIRUS (STRAIN EL AMAR) (PPV)	2944-2975	3068-3097				
PPOLG PPVNA	GENOME POLYPROTEIN	PLUM POX POTYVIRUS (ISOLATE NAT) (PPV)	2959-2990	3083-3112				
PPOLG P3BMV	GENOME POLYPROTEIN	PEA SEED-BORNE MOSAIC VIRUS (STRAIN RANKOYIC) (PPV)	931-966	1411-1445	2149-2178			
PPOLG PVPRL	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN DPO1)	102-1316	3004-3033				
PPOLG PVTN	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN N) (PVY)	102-1316					
PPOLG PYFV1	GENOME POLYPROTEIN	PARSNIP YELLOW FLECK VIRUS (ISOLATE P-1213) (PYFV)	210-262	1110-1139	1901-1931			
PPOLG SDMVN	GENOME POLYPROTEIN	SOYBEAN MOSAIC VIRUS (STRAIN N)	245-274					
PPOLG STEVA1	GENOME POLYPROTEIN	ST. LOUIS ENCEPHALITIS VIRUS (STRAIN NR1-7)	61-95	1301-1331				
PPOLG SDVVS	GENOME POLYPROTEIN	SUGARCANE MOSAIC VIRUS (STRAIN SC)	303-336					
PPOLG SYDVH	GENOME POLYPROTEIN	SWINE VESICULAR DISEASE VIRUS (STRAIN 107-76)	1585-1617					
PPOLG TBEVS	GENOME POLYPROTEIN	SWINE VESICULAR DISEASE VIRUS (STRAIN UK G27172)	935-969	1157-1188	2166-2198	3095-3132		
PPOLG TBEVN	GENOME POLYPROTEIN	TICK-BORNE ENCEPHALITIS VIRUS (STRAIN SOFIN) (TBEV)	822-865	2998-3027				
PPOLG TIEV	GENOME POLYPROTEIN	TICK-BORNE ENCEPHALITIS VIRUS (WESTERN SUBTYPE) (TIEV)	1074-1102	1191-1221	1470-1508	1908-1939		
PPOLG TIEV3	GENOME POLYPROTEIN	THULE'S MURINE ENCEPHALITIS VIRUS (STRAIN DEAN R166)	1072-1100	1191-1219	1468-1506	1906-1937		
PPOLG TIEV4	GENOME POLYPROTEIN	THULE'S MURINE ENCEPHALITIS VIRUS (STRAIN RA)	1074-1102	1191-1221	1470-1508	1908-1939		
PPOLG TIEV5	GENOME POLYPROTEIN	THULE'S MURINE ENCEPHALITIS VIRUS (STRAIN GIV11)	1531-1602					
PPOLG TIEV6	GENOME POLYPROTEIN	TOMATO VIRUS MOTTLING VIRUS (TSMV)	3098-2731					
PPOLG WNV	GENOME POLYPROTEIN	WEST NILE VIRUS	61-95	1557-1590	2372-2389			
PPOLG YFV1	GENOME POLYPROTEIN	YELLOW FEVER VIRUS (STRAIN 171)	1157-1186	1228-1266	1495-1531	2308-2340	3092-3127	
PPOLG YFV2	GENOME POLYPROTEIN	YELLOW FEVER VIRUS (STRAIN PASTEUR 17D-204)	1157-1186	1228-1266	1495-1531	2308-2340	3092-3127	
PPOLG ZTMV	GENOME POLYPROTEIN	ZUCCHINI YELLOW MOSAIC VIRUS (ZYMV)	329-358					
PPOLG PM1A1	GENOME POLYPROTEIN	POI VIRUS TYPE 1 (STRAIN MAIONEY)	1122-1159					
PPOLG WNV2	GENOME POLYPROTEIN	WEST NILE VIRUS II	244-273					
PPOLM ECVT7	NON-STRUCTURAL POLYPROTEIN	VENEZUELAN EQUINE ENCEPHALITIS VIRUS (STRAIN TRINIDAD DONKEY)	613-648	1436-1468				
PPOLM FCV6	NON-STRUCTURAL POLYPROTEIN	FELINE CALICIVIRUS (STRAIN CHINA FIV) (FCV)	327-365					
PPOLM FCV4	NON-STRUCTURAL POLYPROTEIN	FELINE CALICIVIRUS (STRAIN JAPANESE F4) (FCV)	300-333					
PPOLM FCV9	NON-STRUCTURAL POLYPROTEIN	FELINE CALICIVIRUS (STRAIN F9) (FCV)	801-841					
PPOLM IIEV1H	NON-STRUCTURAL POLYPROTEIN	HEPATITIS E VIRUS (STRAIN IJURANA) (IIEV)	1618-1632					
PPOLM IIEV1E	NON-STRUCTURAL POLYPROTEIN	HEPATITIS E VIRUS (STRAIN MEXICO) (IIEV)	1618-1650					
PPOLM IIEV1Y	NON-STRUCTURAL POLYPROTEIN	HEPATITIS E VIRUS (STRAIN MYANMAR) (IIEV)	1618-1652					
PPOLM IIEV1A	NON-STRUCTURAL POLYPROTEIN	HEPATITIS E VIRUS (STRAIN PAKISTAN) (IIEV)	1617-1651					
PPOLM MIDOV	NON-STRUCTURAL POLYPROTEIN	MIDDLEBURY VIRUS	25-57					
PPOLM ONAVG	NON-STRUCTURAL POLYPROTEIN	ONYONG-NYONG VIRUS (STRAIN GULU) (ONN)	1144-1180	1404-1439				
PPOLM RUDV	NON-STRUCTURAL POLYPROTEIN	RABBIT HEMORRHAGIC DISEASE VIRUS (RIHDV)	299-337	1502-1594				
PPOLM SFV	NON-STRUCTURAL POLYPROTEIN	SEMLIKI FOREST VIRUS	1146-1175	1408-1441				
PPOLM SINXO	NON-STRUCTURAL POLYPROTEIN	SINDUIS VIRUS (SUBTYPE DOCKELRO) (STRAIN EISSIYN #2-5)	1454-1486					
PPOLM SINIV	NON-STRUCTURAL POLYPROTEIN	SINDUIS VIRUS (STRAIN IIRSP)	1454-1486					



PGENE	FUNCTION	PROTEIN	ALL VIRUS (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6
PRP1	PROTEIN	PROTEIN	CANIPOLIS SONORENSIS VIRUS (CSV)	131-149					AREA1
PRP2	REPEAT ELEMENT PROTEIN	REPEAT ELEMENT PROTEIN	BOVINE IMMUNODEFICIENCY VIRUS (ISOLATE 127) (BIV)	74-109					
PRP3	REV PROTEIN	REV PROTEIN	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE 1109) (EIAV)	41-79					
PRP4	REV PROTEIN	REV PROTEIN	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE CL23) (EIAV)	44-79					
PRP5	REV PROTEIN	REV PROTEIN	EQUINE INFECTIOUS ANEMIA VIRUS (ISOLATE WYONING) (EIAV)	74-109					
PRP6	REV PROTEIN	REV PROTEIN	SINIAN IMMUNODEFICIENCY VIRUS (TYOT ISOLATE) (SIV-AGN)	75-62					
PRP7	ASPN2	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CH	AFRICAN SWINE FEVER VIRUS ISOLATE NIALAWI LIL 2001 (ASFV)	630-666					
PRP8	ASPN2	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CH	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	279-311	191-430	449-477			
PRP9	ASPN2	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CH	EQUINE HERPESVIRUS TYPE 1 (STRAIN AIMP) (EHV-1)	60-92	503-531				
PRP10	VACC	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CH	VACCINIA VIRUS (STRAIN COPENHAGEN)	201-235					
PRP11	VACC	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CH	VACCINIA VIRUS (STRAIN WR)	201-235					
PRP12	VACC	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CH	VARIOLA VIRUS	201-235					
PRP13	VZV	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CH	VARIOLA-ZOSTER VIRUS (STRAIN DUNAS) (VZV)	34-72	221-234	488-516			
PRP14	AVPR	RNAI SERINE/THREONINE-PROTEIN KINASE TRANSFORM	AVIAN ROUS-ASSOCIATED VIRUS TYPE 1	149-177					
PRP15	AVPR	RNAI SERINE/THREONINE-PROTEIN KINASE TRANSFORM	AVIAN RETROVIRUS IC10	131-161					
PRP16	AVPR	RNAI SERINE/THREONINE-PROTEIN KINASE TRANSFORM	VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN)	399-427					
PRP17	AVPR	RNAI SERINE/THREONINE-PROTEIN KINASE TRANSFORM	VARIOLA VIRUS	399-427					
PRP18	VACC	RNA-DIRECTED RNA POLYMERASE 143 KD POLYPEPTIDE	VACCINIA VIRUS (STRAIN WR)	1005-1033					
PRP19	VACC	RNA-DIRECTED RNA POLYMERASE 132 KD POLYPEPTIDE	CAPRIPOX VIRUS (STRAIN KS-1)	297-333	667-696				
PRP20	VACC	RNA-DIRECTED RNA POLYMERASE 132 KD POLYPEPTIDE	COWPOX VIRUS (CPV)	202-216	542-578				
PRP21	VACC	RNA-DIRECTED RNA POLYMERASE 132 KD POLYPEPTIDE	VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN)	202-216	542-578				
PRP22	VACC	RNA-DIRECTED RNA POLYMERASE 132 KD POLYPEPTIDE	VARIOLA VIRUS	202-216	542-578				
PRP23	VACC	RNA-DIRECTED RNA POLYMERASE 19 KD POLYPEPTIDE	VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN)	31-66					
PRP24	VACC	RNA-DIRECTED RNA POLYMERASE 18 KD POLYPEPTIDE	VARIOLA VIRUS	31-66					
PRP25	LELV	RNA-DIRECTED RNA POLYMERASE	FOWLPOX VIRUS (STRAIN FP-1)	57-88					
PRP26	LELV	RNA-DIRECTED RNA POLYMERASE	ELVSTAD VIRUS (LV)	1233-1268	3133-3163	3426-3457			
PRP27	LELV	RNA-DIRECTED RNA POLYMERASE	EQUINE ARTERITIS VIRUS (EAV)	171-207	3041-3072				
PRP28	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	DHOIR VIRUS (STRAIN INDIAN/11/64) (DHO)	96-133	199-234				
PRP29	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN AVICTORIA/73)	138-170					
PRP30	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA C VIRUS (STRAIN C/1969)	564-598					
PRP31	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN ANNA ARBORE/6/60)	398-435	484-518				
PRP32	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/CHICKEN/KAIDORI/80)	484-518					
PRP33	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP34	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP35	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP36	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP37	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP38	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP39	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP40	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP41	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP42	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP43	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP44	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP45	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP46	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP47	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP48	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP49	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP50	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP51	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP52	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP53	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP54	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP55	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP56	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP57	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP58	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP59	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP60	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP61	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP62	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP63	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP64	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP65	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP66	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP67	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP68	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP69	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP70	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP71	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP72	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP73	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP74	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP75	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP76	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP77	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP78	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP79	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP80	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP81	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP82	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP83	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP84	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP85	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP86	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP87	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP88	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP89	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP90	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP91	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP92	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP93	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP94	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP95	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP96	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP97	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP98	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP99	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					
PRP100	LELV	RNA-DIRECTED RNA POLYMERASE SUBUNIT P1	INFLUENZA A VIRUS (STRAIN A/AFOWL PLAGUE VIRUS/ROSTOCK/74)	484-518					









GENE	FUNCTION	PROTEIN	ALL Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6
PUL1	HCNVA	PROTEIN UL16	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	186-223					AREA1
PUL2	HCNVA	PROTEIN UL17	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)	85-123					
PUL3	HCNVA	PROTEIN UL18	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)	102-232					
PUL4	HCNVA	PROTEIN UL19	HERPESVIRUS SAMIRI (STRAIN 11)	378-812					
PUL5	HCNVA	PROTEIN UL20	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS) (VZV)	566-602					
PUL6	HCNVA	PROTEIN UL21	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	598-629					
PUL7	HCNVA	PROTEIN UL22	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS) (VZV)	157-188					
PUL8	HCNVA	PROTEIN UL23	HERPESVIRUS SAMIRI (STRAIN 11)	274-307					
PUL9	HCNVA	PROTEIN UL24	HERPESVIRUS SAMIRI (STRAIN 11)	41-70					
PUL10	HCNVA	PROTEIN UL25	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	34-64					
PUL11	HCNVA	PROTEIN UL26	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)	418-471					
PUL12	HCNVA	PROTEIN UL27	HERPESVIRUS SAMIRI (STRAIN 11)	580-615					
PUL13	HCNVA	PROTEIN UL28	HERPESVIRUS SAMIRI (STRAIN 11)	581-622					
PUL14	HCNVA	PROTEIN UL29	HERPESVIRUS SAMIRI (STRAIN 11)	226-239					
PUL15	HCNVA	PROTEIN UL30	HERPESVIRUS SAMIRI (STRAIN 11)	135-168					
PUL16	HCNVA	PROTEIN UL31	HERPESVIRUS SAMIRI (STRAIN 11)	582-617					
PUL17	HCNVA	PROTEIN UL32	HERPESVIRUS SAMIRI (STRAIN 11)	590-620					
PUL18	HCNVA	PROTEIN UL33	HERPESVIRUS SAMIRI (STRAIN 11)	316-344					
PUL19	HCNVA	PROTEIN UL34	HERPESVIRUS SAMIRI (STRAIN 11)	374-411					
PUL20	HCNVA	PROTEIN UL35	HERPESVIRUS SAMIRI (STRAIN 11)	213-248					
PUL21	HCNVA	PROTEIN UL36	HERPESVIRUS SAMIRI (STRAIN 11)	105-139					
PUL22	HCNVA	PROTEIN UL37	HERPESVIRUS SAMIRI (STRAIN 11)	120-148					
PUL23	HCNVA	PROTEIN UL38	HERPESVIRUS SAMIRI (STRAIN 11)	36-63					
PUL24	HCNVA	PROTEIN UL39	HERPESVIRUS SAMIRI (STRAIN 11)	381-413					
PUL25	HCNVA	PROTEIN UL40	HERPESVIRUS SAMIRI (STRAIN 11)	262-290					
PUL26	HCNVA	PROTEIN UL41	HERPESVIRUS SAMIRI (STRAIN 11)	301-341					
PUL27	HCNVA	PROTEIN UL42	HERPESVIRUS SAMIRI (STRAIN 11)	138-159					
PUL28	HCNVA	PROTEIN UL43	HERPESVIRUS SAMIRI (STRAIN 11)	322-335					
PUL29	HCNVA	PROTEIN UL44	HERPESVIRUS SAMIRI (STRAIN 11)	309-337					
PUL30	HCNVA	PROTEIN UL45	HERPESVIRUS SAMIRI (STRAIN 11)	150-187					
PUL31	HCNVA	PROTEIN UL46	HERPESVIRUS SAMIRI (STRAIN 11)	33-33					
PUL32	HCNVA	PROTEIN UL47	HERPESVIRUS SAMIRI (STRAIN 11)	106-144					
PUL33	HCNVA	PROTEIN UL48	HERPESVIRUS SAMIRI (STRAIN 11)	123-137					
PUL34	HCNVA	PROTEIN UL49	HERPESVIRUS SAMIRI (STRAIN 11)	387-430					
PUL35	HCNVA	PROTEIN UL50	HERPESVIRUS SAMIRI (STRAIN 11)	111-145					
PUL36	HCNVA	PROTEIN UL51	HERPESVIRUS SAMIRI (STRAIN 11)	102-130					
PUL37	HCNVA	PROTEIN UL52	HERPESVIRUS SAMIRI (STRAIN 11)	179-183					
PUL38	HCNVA	PROTEIN UL53	HERPESVIRUS SAMIRI (STRAIN 11)	64-96					
PUL39	HCNVA	PROTEIN UL54	HERPESVIRUS SAMIRI (STRAIN 11)	66-99					
PUL40	HCNVA	PROTEIN UL55	HERPESVIRUS SAMIRI (STRAIN 11)	81-114					
PUL41	HCNVA	PROTEIN UL56	HERPESVIRUS SAMIRI (STRAIN 11)	159-189					
PUL42	HCNVA	PROTEIN UL57	HERPESVIRUS SAMIRI (STRAIN 11)	82-117					
PUL43	HCNVA	PROTEIN UL58	HERPESVIRUS SAMIRI (STRAIN 11)	82-117					
PUL44	HCNVA	PROTEIN UL59	HERPESVIRUS SAMIRI (STRAIN 11)	43-73					
PUL45	HCNVA	PROTEIN UL60	HERPESVIRUS SAMIRI (STRAIN 11)	153-190					
PUL46	HCNVA	PROTEIN UL61	HERPESVIRUS SAMIRI (STRAIN 11)	179-213					
PUL47	HCNVA	PROTEIN UL62	HERPESVIRUS SAMIRI (STRAIN 11)	137-170					
PUL48	HCNVA	PROTEIN UL63	HERPESVIRUS SAMIRI (STRAIN 11)	26-67					
PUL49	HCNVA	PROTEIN UL64	HERPESVIRUS SAMIRI (STRAIN 11)	11-45					
PUL50	HCNVA	PROTEIN UL65	HERPESVIRUS SAMIRI (STRAIN 11)	343-375					
PUL51	HCNVA	PROTEIN UL66	HERPESVIRUS SAMIRI (STRAIN 11)	151-188					
PUL52	HCNVA	PROTEIN UL67	HERPESVIRUS SAMIRI (STRAIN 11)	185-222					
PUL53	HCNVA	PROTEIN UL68	HERPESVIRUS SAMIRI (STRAIN 11)	270-299					
PUL54	HCNVA	PROTEIN UL69	HERPESVIRUS SAMIRI (STRAIN 11)	132-164					
PUL55	HCNVA	PROTEIN UL70	HERPESVIRUS SAMIRI (STRAIN 11)	247-283					
PUL56	HCNVA	PROTEIN UL71	HERPESVIRUS SAMIRI (STRAIN 11)	246-276					
PUL57	HCNVA	PROTEIN UL72	HERPESVIRUS SAMIRI (STRAIN 11)	208-246					









PCGENE	FUNCTION	PROTEIN	ALL Viruses (no bacteriophages)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7
PV01 VACCC	PROTEIN F3	PROTEIN F3	VIRUS	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7
PV02 VACCC	PROTEIN F3	PROTEIN F3	VACCINIA VIRUS (STRAIN COPENHAGEN)	2-40	61-93					
PV03 VACCC	PROTEIN F3	PROTEIN F3	VACCINIA VIRUS (STRAIN WR)	2-40	61-93					
PV04 FOWPV	PROTEIN F4	PROTEIN F4	FOWLPOX VIRUS	392-370						
PV05 FOWPV	PROTEIN F4	PROTEIN F4	FOWLPOX VIRUS	217-267						
PV06 CAPVK	PROTEIN F7	PROTEIN F7	CATRIPOX VIRUS (STRAIN KS-1)	89-118						
PV07 VACCC	14 KD FUSION PROTEIN	14 KD FUSION PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	28-61						
PV08 VACCC	14 KD FUSION PROTEIN	14 KD FUSION PROTEIN	VACCINIA VIRUS (STRAIN WR)	28-61						
PV09 VARV	14 KD FUSION PROTEIN	14 KD FUSION PROTEIN	VARIOLA VIRUS	28-61						
PV10 HSYII	HYPOTHETICAL GENE 1 PROTEIN	HYPOTHETICAL GENE 1 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	317-346						
PV11 HSYII	HYPOTHETICAL GENE 2 PROTEIN	HYPOTHETICAL GENE 2 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1)	163-196						
PV12 VACCC	ISATIN-BETA-THIOSEMICARBAZONE DEPENDENT PROTEIN	ISATIN-BETA-THIOSEMICARBAZONE DEPENDENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	92-120						
PV13 VACCC	ISATIN-BETA-THIOSEMICARBAZONE DEPENDENT PROTEIN	ISATIN-BETA-THIOSEMICARBAZONE DEPENDENT PROTEIN	VARIOLA VIRUS	92-120						
PV14 HSYII	HYPOTHETICAL GENE 3 PROTEIN	HYPOTHETICAL GENE 3 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	108-136						
PV15 HSYII	HYPOTHETICAL GENE 3 PROTEIN	HYPOTHETICAL GENE 3 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	54-83						
PV16 VACCC	HYPOTHETICAL GENE 6 MEMBRANE PROTEIN	HYPOTHETICAL GENE 6 MEMBRANE PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	99-136						
PV17 VACCC	PROTEIN G6	PROTEIN G6	VARIOLA VIRUS	99-136						
PV18 VACCC	PROTEIN G7	PROTEIN G7	VACCINIA VIRUS (STRAIN COPENHAGEN)	113-145						
PV19 VARV	PROTEIN G7	PROTEIN G7	VARIOLA VIRUS	113-145						
PV20 VACCC	PROTEIN F1	PROTEIN F1	VACCINIA VIRUS (STRAIN COPENHAGEN)	266-301						
PV21 HSYII	PROTEIN F1	PROTEIN F1	VACCINIA VIRUS (STRAIN WR)	266-301						
PV22 HSYII	PROTEIN F1	PROTEIN F1	VARIOLA VIRUS	303-338						
PV23 HSYII	HYPOTHETICAL GENE 11 ZINC-BINDING PROTEIN	HYPOTHETICAL GENE 11 ZINC-BINDING PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	303-338						
PV24 HSYII	HYPOTHETICAL GENE 12 ZINC-BINDING PROTEIN	HYPOTHETICAL GENE 12 ZINC-BINDING PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	150-183						
PV25 HSYII	HYPOTHETICAL GENE 12 ZINC-BINDING PROTEIN	HYPOTHETICAL GENE 12 ZINC-BINDING PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	206-243						
PV26 HSYII	HYPOTHETICAL GENE 12 ZINC-BINDING PROTEIN	HYPOTHETICAL GENE 12 ZINC-BINDING PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	68-106						
PV27 HSYII	HYPOTHETICAL GENE 12 ZINC-BINDING PROTEIN	HYPOTHETICAL GENE 12 ZINC-BINDING PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	354-292	303-337	414-432				
PV28 HSYII	HYPOTHETICAL GENE 22 PROTEIN	HYPOTHETICAL GENE 22 PROTEIN	SPOROPLASMA VIRUS SPV1-88A2 B	354-292	303-337	414-432				
PV29 HSYII	HYPOTHETICAL GENE 23 PROTEIN	HYPOTHETICAL GENE 23 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	300-337	647-678					
PV30 HSYII	HYPOTHETICAL GENE 23 PROTEIN	HYPOTHETICAL GENE 23 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	70-108						
PV31 HSYII	HYPOTHETICAL GENE 26 PROTEIN	HYPOTHETICAL GENE 26 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	94-125						
PV32 HSYII	HYPOTHETICAL GENE 27 PROTEIN	HYPOTHETICAL GENE 27 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	36-74						
PV33 HSYII	HYPOTHETICAL GENE 28 PROTEIN	HYPOTHETICAL GENE 28 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	491-521						
PV34 HSYII	HYPOTHETICAL GENE 28 PROTEIN	HYPOTHETICAL GENE 28 PROTEIN	AMSACTA MOOREI ENTOMOPHAGUS (AMEPV)	180-217						
PV35 HSYII	HYPOTHETICAL GENE 28 PROTEIN	HYPOTHETICAL GENE 28 PROTEIN	SPOROPLASMA VIRUS 4 (SPV4)	200-244						
PV36 HSYII	HYPOTHETICAL GENE 33 PROTEIN	HYPOTHETICAL GENE 33 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	15-46	190-226					
PV37 HSYII	POSSIBLE TYROSINE-PROTEIN KINASE	POSSIBLE TYROSINE-PROTEIN KINASE	HERPESVIRUS SAIMIRI (STRAIN 11)	131-185						
PV38 HSYII	HYPOTHETICAL GENE 39 PROTEIN	HYPOTHETICAL GENE 39 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	543-577	648-682					
PV39 HSYII	HYPOTHETICAL GENE 40 PROTEIN	HYPOTHETICAL GENE 40 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	187-216						
PV40 HSYII	HYPOTHETICAL GENE 41 PROTEIN	HYPOTHETICAL GENE 41 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	11-45	202-233					
PV41 HSYII	HYPOTHETICAL GENE 42 PROTEIN	HYPOTHETICAL GENE 42 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	91-123						
PV42 HSYII	HYPOTHETICAL GENE 43 PROTEIN	HYPOTHETICAL GENE 43 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	109-140	157-183					
PV43 HSYII	PROBABLE MAJOR GLYCOPROTEIN	PROBABLE MAJOR GLYCOPROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	888-925						
PV44 HSYII	PROBABLE MAJOR GLYCOPROTEIN	PROBABLE MAJOR GLYCOPROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	379-337						
PV45 HSYII	PROBABLE TRANSCRIPTION ACTIVATOR EDRF1	PROBABLE TRANSCRIPTION ACTIVATOR EDRF1	HERPESVIRUS SAIMIRI (STRAIN 11)	113-141						
PV46 HSYII	HYPOTHETICAL GENE 51 MEMBRANE PROTEIN	HYPOTHETICAL GENE 51 MEMBRANE PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	29-64	14-120					
PV47 HSYII	HYPOTHETICAL GENE 52 PROTEIN	HYPOTHETICAL GENE 52 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	98-134						
PV48 HSYII	HYPOTHETICAL GENE 53 PROTEIN	HYPOTHETICAL GENE 53 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	100-129						
PV49 HSYII	HYPOTHETICAL GENE 55 PROTEIN	HYPOTHETICAL GENE 55 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	364-396	611-667	1091-1126				
PV50 HSYII	HYPOTHETICAL GENE 58 PROTEIN	HYPOTHETICAL GENE 58 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	342-375	480-508					
PV51 HSYII	HYPOTHETICAL GENE 58 PROTEIN	HYPOTHETICAL GENE 58 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	25-60	195-233					
PV52 HSYII	HYPOTHETICAL GENE 59 MEMBRANE PROTEIN	HYPOTHETICAL GENE 59 MEMBRANE PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	82-118						
PV53 HSYII	HYPOTHETICAL GENE 61 PROTEIN	HYPOTHETICAL GENE 61 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	76-109						
PV54 HSYII	HYPOTHETICAL GENE 64 PROTEIN	HYPOTHETICAL GENE 64 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	55-89	163-401	420-452				
PV55 HSYII	HYPOTHETICAL GENE 65 PROTEIN	HYPOTHETICAL GENE 65 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	801-836	1146-1174	1290-1326				
PV56 HSYII	HYPOTHETICAL GENE 67 PROTEIN	HYPOTHETICAL GENE 67 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	1150-1185						
PV57 HSYII	HYPOTHETICAL GENE 67 PROTEIN	HYPOTHETICAL GENE 67 PROTEIN	SPOROPLASMA VIRUS SPV1-88A2 B	60-89						
PV58 HSYII	HYPOTHETICAL GENE 71 PROTEIN	HYPOTHETICAL GENE 71 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	128-158						
PV59 HSYII	HYPOTHETICAL GENE 72 PROTEIN	HYPOTHETICAL GENE 72 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	445-478	720-751	1158-1189	1352-1285			
PV60 HSYII	HYPOTHETICAL GENE 75 PROTEIN	HYPOTHETICAL GENE 75 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	263-291	387-422					





















PGENE	PICTZIP	All Virus (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILENAME	PROTEIN	VIRUS	63-94						
PYOR3_WCMVM	HYPOTHETICAL 13 KD PROTEIN (ORF 3)	WHITE CLOVER MOSAIC VIRUS (STRAIN N) (WCMV)	64-95						
PYOR3_WCMVO	HYPOTHETICAL 13 KD PROTEIN (ORF 3)	WHITE CLOVER MOSAIC VIRUS (STRAIN O) (WCMV)	237-272						
PYOR3_ADEGI	HYPOTHETICAL 31.3 KD PROTEIN (ORF 3)	AVIAN ADENOVIRUS GALI	5-34						
PYORG_TTV1	HYPOTHETICAL 7.1 KD PROTEIN	THEKNOTROTILUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1)	333-263						
PYORM_TTV1	HYPOTHETICAL 38.6 KD PROTEIN	THEKNOTROTILUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1)	91-124						
PYORP_TTV1	HYPOTHETICAL 20.2 KD PROTEIN	THEKNOTROTILUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1)	100-133						
PYP24_RTIV	HYPOTHETICAL P24 PROTEIN (ORF 1)	RICE TUNGRO BACILLIFORM VIRUS (RTIV)	104-133	159-191					
PYP24_RTIVP	HYPOTHETICAL P24 PROTEIN (ORF 1)	RICE TUNGRO BACILLIFORM VIRUS (RTIV)	23-51	159-191					
PYP47_NPVAC	HYPOTHETICAL 41.3 KD PROTEIN IN P47 3' REGION	AUTOGRAPIA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS (ACMPV)	180-216						
PYRF5_HSV60	HYPOTHETICAL PROTEIN BE5	HERPES SIMPLEX VIRUS (TYPE 67 STRAIN GS)	13-42						
PYRR2_EBV	HYPOTHETICAL BRG2Z PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)	92-120						
PYSR1_EBV	HYPOTHETICAL BSR1 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)	106-136						
PYTR1_EBV	HYPOTHETICAL BTR1 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)	21-53						
PYVAE_VACC	HYPOTHETICAL 18.2 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	21-49						
PYVAL_VACC	HYPOTHETICAL 9.9 KD PROTEIN	VACCINIA VIRUS (STRAIN VR), AND VACCINIA VIRUS (STRAIN COPENHAGEN)	22-53						
PYVBC_VACC	HYPOTHETICAL 10.8 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-64						
PYVDG_VACC	HYPOTHETICAL 10.4 KD PROTEIN	VACCINIA VIRUS (STRAIN WP), AND VACCINIA VIRUS (STRAIN COPENHAGEN)	8-42						
PYVEE_VACC	HYPOTHETICAL 12.9 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	7-35						
PYVFC_VACC	HYPOTHETICAL 11.5 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	29-57						
PZNF1_LYCV	ZINC FINGER PROTEIN	LYMPHOCTIC CHORIOMENINGITIS VIRUS (STRAIN ARMSTRONG)	8-32						
PZNF1_LYCV	ZINC FINGER PROTEIN (FRAGMENT)	LYMPHOCTIC CHORIOMENINGITIS VIRUS (STRAIN PASTEUR)							

TABLE XV  
RESPIRATORY SYNCYTIAL VIRUS DP107 F2 REGION ANALOG  
CARBOXY TRUNCATIONS

	X-YTS-Z
	X-YTSV-Z
5	X-YTSVI-Z
	X-YTSVIT-Z
	X-YTSVITI-Z
	X-YTSVITIE-Z
	X-YTSVITIEL-Z
	X-YTSVITIELS-Z
	X-YTSVITIELSN-Z
10	X-YTSVITIELSNI-Z
	X-YTSVITIELSNIK-Z
	X-YTSVITIELSNIKE-Z
	X-YTSVITIELSNIKEN-Z
	X-YTSVITIELSNIKENK-Z
	X-YTSVITIELSNIKENKC-Z
	X-YTSVITIELSNIKENKCN-Z
	X-YTSVITIELSNIKENKCNG-Z
15	X-YTSVITIELSNIKENKCNGT-Z
	X-YTSVITIELSNIKENKCNGTD-Z
	X-YTSVITIELSNIKENKCNGTDA-Z
	X-YTSVITIELSNIKENKCNGTDAK-Z
	X-YTSVITIELSNIKENKCNGTDAKV-Z
	X-YTSVITIELSNIKENKCNGTDAKVK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKL-Z
20	X-YTSVITIELSNIKENKCNGTDAKVKLI-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQ-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQE-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEEL-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKY-Z
25	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKN-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNA-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAV-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAVTE-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAVTEL-Z
30	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAVTELQ-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAVTELQL-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAVTELQLL-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAVTELQLLM-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAVTELQLLMQ-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAVTELQLLMQS-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAVTELQLLMQST-Z

35     The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxycarbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

10

15

20

25

30

35

TABLE XVI  
RESPIRATORY SYNCYTIAL VIRUS F2 DP178/DP107 REGION ANALOG  
AMINO TRUNCATIONS

	X-QST-Z
	X-MQST-Z
5	X-LMQST-Z
	X-LLMQST-Z
	X-QLLMQST-Z
	X-LQLLMQST-Z
	X-ELQLLMQST-Z
	X-TELQLLMQST-Z
	X-VTELQLLMQST-Z
10	X-AVTELQLLMQST-Z
	X-NAVTELQLLMQST-Z
	X-KNAVTELQLLMQST-Z
	X-YKNAVTELQLLMQST-Z
	X-KYKNAVTELQLLMQST-Z
	X-DKYKNAVTELQLLMQST-Z
	X-LDKYKNAVTELQLLMQST-Z
	X-ELDKYKNAVTELQLLMQST-Z
15	X-QELDKYKNAVTELQLLMQST-Z
	X-KQELDKYKNAVTELQLLMQST-Z
	X-IKQELDKYKNAVTELQLLMQST-Z
	X-LIKQELDKYKNAVTELQLLMQST-Z
	X-KLIKQELDKYKNAVTELQLLMQST-Z
	X-VKLIKQELDKYKNAVTELQLLMQST-Z
	X-KVKLIKQELDKYKNAVTELQLLMQST-Z
20	X-AKVLIKQELDKYKNAVTELQLLMQST-Z
	X-DAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-TDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-GTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-NGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-CNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-KCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-NKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
25	X-KENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-IKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-NIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-SNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-LSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-ELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-IELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
30	X-TIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-ITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-VITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-SVITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-TSVITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z

The one letter amino acid code is used.

35 Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

5

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

10

15

20

25

30

35



TABLE XVII  
RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG  
CARBOXY TRUNCATIONS

	X-FYD-Z
	X-FYDP-Z
	X-FYDPL-Z
5	X-FYDPLV-Z
	X-FYDPLVF-Z
	X-FYDPLVFP-Z
	X-FYDPLVFPS-Z
	X-FYDPLVFPSD-Z
	X-FYDPLVFPSDE-Z
	X-FYDPLVFPSDEF-Z
10	X-FYDPLVFPSDEFD-Z
	X-FYDPLVFPSDEFDA-Z
	X-FYDPLVFPSDEFDAS-Z
	X-FYDPLVFPSDEFDASI-Z
	X-FYDPLVFPSDEFDASIS-Z
	X-FYDPLVFPSDEFDASISQ-Z
	X-FYDPLVFPSDEFDASISQV-Z
	X-FYDPLVFPSDEFDASISQVN-Z
15	X-FYDPLVFPSDEFDASISQVNE-Z
	X-FYDPLVFPSDEFDASISQVNEK-Z
	X-FYDPLVFPSDEFDASISQVNEKI-Z
	X-FYDPLVFPSDEFDASISQVNEKIN-Z
	X-FYDPLVFPSDEFDASISQVNEKINQ-Z
	X-FYDPLVFPSDEFDASISQVNEKINQS-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSL-Z
20	X-FYDPLVFPSDEFDASISQVNEKINQSLA-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAF-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFI-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIR-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRK-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKS-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSD-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDE-Z
25	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDEL-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z

The one letter amino acid code is used.

Additionally,  
 30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier

group including but not limited to lipid-fatty acid  
conjugates, polyethylene glycol, or carbohydrates.

5

10

15

20

25

30

35

TABLE XVIII  
RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG  
AMINO TRUNCATIONS

	X-DELL-Z
	X-SDELL-Z
5	X-KSDELL-Z
	X-RKSDELL-Z
	X-IRKSDELL-Z
	X-FIRKSDELL-Z
	X-AFIRKSDELL-Z
	X-LAFIRKSDELL-Z
	X-SLAFIRKSDELL-Z
10	X-QSLAFIRKSDELL-Z
	X-NQSLAFIRKSDELL-Z
	X-INQSLAFIRKSDELL-Z
	X-KINQSLAFIRKSDELL-Z
	X-EKINQSLAFIRKSDELL-Z
	X-NEKINQSLAFIRKSDELL-Z
	X-VNEKINQSLAFIRKSDELL-Z
	X-QVNEKINQSLAFIRKSDELL-Z
15	X-SQVNEKINQSLAFIRKSDELL-Z
	X-ISQVNEKINQSLAFIRKSDELL-Z
	X-SISQVNEKINQSLAFIRKSDELL-Z
	X-ASISQVNEKINQSLAFIRKSDELL-Z
	X-DASISQVNEKINQSLAFIRKSDELL-Z
	X-FDASISQVNEKINQSLAFIRKSDELL-Z
	X-EFDASISQVNEKINQSLAFIRKSDELL-Z
20	X-DEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-SDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-PSDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-FPSDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-VFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-LVFPSEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-PLVFPSEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-DPLVFPSEFDASISQVNEKINQSLAFIRKSDELL-Z
25	X-YDPLVFPSEFDASISQVNEKINQSLAFIRKSDELL-Z

The one letter amino acid code is used.

Additionally,  
 "X" may represent an amino group, a hydrophobic group,  
 including but not limited to carbobenzoxyl, dansyl, or  
 30 T-butyloxycarbonyl; an acetyl group; a 9-  
 fluorenylmethoxy-carbonyl (Fmoc) group; a  
 macromolecular carrier group including but not limited  
 to lipid-fatty acid conjugates, polyethylene glycol,  
 or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a  
 T-butyloxycarbonyl group; a macromolecular carrier  
 35 group including but not limited to lipid-fatty acid  
 conjugates, polyethylene glycol, or carbohydrates.

TABLE XIX  
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG  
CARBOXY TRUNCATIONS

X-ITL-Z  
 X-ITLN-Z  
 X-ITLNN-Z  
 5 X-ITLNNS-Z  
 X-ITLNNSV-Z  
 X-ITLNNSVA-Z  
 X-ITLNNSVAL-Z  
 X-ITLNNSVALD-Z  
 X-ITLNNSVALDP-Z  
 X-ITLNNSVALDPI-Z  
 10 X-ITLNNSVALDPID-Z  
 X-ITLNNSVALDPIDI-Z  
 X-ITLNNSVALDPIDIS-Z  
 X-ITLNNSVALDPIDISI-Z  
 X-ITLNNSVALDPIDISIE-Z  
 X-ITLNNSVALDPIDISIEL-Z  
 X-ITLNNSVALDPIDISIELN-Z  
 X-ITLNNSVALDPIDISIELNK-Z  
 15 X-ITLNNSVALDPIDISIELNKA-Z  
 X-ITLNNSVALDPIDISIELNKAK-Z  
 X-ITLNNSVALDPIDISIELNKAKS-Z  
 X-ITLNNSVALDPIDISIELNKAKSD-Z  
 X-ITLNNSVALDPIDISIELNKAKSDL-Z  
 X-ITLNNSVALDPIDISIELNKAKSDLE-Z  
 X-ITLNNSVALDPIDISIELNKAKSDLEE-Z  
 20 X-ITLNNSVALDPIDISIELNKAKSDLEES-Z  
 X-ITLNNSVALDPIDISIELNKAKSDLEESK-Z  
 X-ITLNNSVALDPIDISIELNKAKSDLEESKE-Z  
 X-ITLNNSVALDPIDISIELNKAKSDLEESKEW-Z  
 X-ITLNNSVALDPIDISIELNKAKSDLEESKEWI-Z  
 X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIR-Z  
 X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIRR-Z  
 25 X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group,  
 including but not limited to carbobenzoxy, dansyl, or  
 T-butyloxycarbonyl; an acetyl group; a 9-  
 30 fluorenylmethoxy-carbonyl (Fmoc) group; a  
 macromolecular carrier group including but not limited  
 to lipid-fatty acid conjugates, polyethylene glycol,  
 or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a  
 T-butyloxycarbonyl group; a macromolecular carrier  
 group including but not limited to lipid-fatty acid  
 35 conjugates, polyethylene glycol, or carbohydrates.

TABLE XX  
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG  
AMINO TRUNCATIONS

	X-RRS-Z
	X-IRRS-Z
5	X-WIRRS-Z
	X-EWIRRS-Z
	X-KEWIRRS-Z
	X-SKEWIRRS-Z
	X-ESKEWIRRS-Z
	X-EESKEWIRRS-Z
	X-LEESKEWIRRS-Z
10	X-DLEESKEWIRRS-Z
	X-SDLEESKEWIRRS-Z
	X-KSDLEESKEWIRRS-Z
	X-AKSDLEESKEWIRRS-Z
	X-KAKSDLEESKEWIRRS-Z
	X-NKAKSDLEESKEWIRRS-Z
	X-LNKAKSDLEESKEWIRRS-Z
	X-ELNKAKSDLEESKEWIRRS-Z
15	X-IELNKAKSDLEESKEWIRRS-Z
	X-SIELNKAKSDLEESKEWIRRS-Z
	X-ISIELNKAKSDLEESKEWIRRS-Z
	X-DISIELNKAKSDLEESKEWIRRS-Z
	X-IDISIELNKAKSDLEESKEWIRRS-Z
	X-PIDISIELNKAKSDLEESKEWIRRS-Z
	X-DPIDISIELNKAKSDLEESKEWIRRS-Z
20	X-LDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-ALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-VALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-SVALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-NSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-NNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-LNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
25	X-TLNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XXI  
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG  
CARBOXY TRUNCATIONS

X-ALG-Z  
 X-ALGV-Z  
 X-ALGVA-Z  
 5 X-ALGVAT-Z  
 X-ALGVATS-Z  
 X-ALGVATSA-Z  
 X-ALGVATSAQ-Z  
 X-ALGVATSAQI-Z  
 X-ALGVATSAQIT-Z  
 X-ALGVATSAQITA-Z  
 10 X-ALGVATSAQITAA-Z  
 X-ALGVATSAQITA-AV-Z  
 X-ALGVATSAQITA-AVA-Z  
 X-ALGVATSAQITA-AVAL-Z  
 X-ALGVATSAQITA-AVALV-Z  
 X-ALGVATSAQITA-AVALVE-Z  
 X-ALGVATSAQITA-AVALVEA-Z  
 X-ALGVATSAQITA-AVALVEAK-Z  
 15 X-ALGVATSAQITA-AVALVEAKQ-Z  
 X-ALGVATSAQITA-AVALVEAKQA-Z  
 X-ALGVATSAQITA-AVALVEAKQAR-Z  
 X-ALGVATSAQITA-AVALVEAKQARS-Z  
 X-ALGVATSAQITA-AVALVEAKQARSD-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDI-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIE-Z  
 20 X-ALGVATSAQITA-AVALVEAKQARSDIEK-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEK-LK-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEK-LKE-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEK-LKEA-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEK-LKEAI-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEK-LKEAIR-Z

25 The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group,  
 including but not limited to carbobenzoxyl, dansyl, or  
 T-butyloxycarbonyl; an acetyl group; a 9-  
 fluorenylmethoxy-carbonyl (Fmoc) group; a  
 30 macromolecular carrier group including but not limited  
 to lipid-fatty acid conjugates, polyethylene glycol,  
 or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a  
 T-butyloxycarbonyl group; a macromolecular carrier  
 group including but not limited to lipid-fatty acid  
 conjugates, polyethylene glycol, or carbohydrates.

35

TABLE XXII  
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG  
AMINO TRUNCATIONS

	X-IRD-Z
	X-AIRD-Z
5	X-EAIRD-Z
	X-KEAIRD-Z
	X-LKEAIRD-Z
	X-KLKEAIRD-Z
	X-EKLKEAIRD-Z
	X-IEKLKEAIRD-Z
	X-DIEKLKEAIRD-Z
10	X-SDIEKLKEAIRD-Z
	X-RSDIEKLKEAIRD-Z
	X-ARSDIEKLKEAIRD-Z
	X-QARSDIEKLKEAIRD-Z
	X-KQARSDIEKLKEAIRD-Z
	X-AKQARSDIEKLKEAIRD-Z
	X-EAKQARSDIEKLKEAIRD-Z
	X-VEAKQARSDIEKLKEAIRD-Z
15	X-LVEAKQARSDIEKLKEAIRD-Z
	X-ALVEAKQARSDIEKLKEAIRD-Z
	X-VALVEAKQARSDIEKLKEAIRD-Z
	X-AVALVEAKQARSDIEKLKEAIRD-Z
	X-AAVALVEAKQARSDIEKLKEAIRD-Z
	X-TAAVALVEAKQARSDIEKLKEAIRD-Z
	X-ITAAVALVEAKQARSDIEKLKEAIRD-Z
20	X-QITAAVALVEAKQARSDIEKLKEAIRD-Z
	X-AQITAAVALVEAKQARSDIEKLKEAIRD-Z
	X-SAQITAAVALVEAKQARSDIEKLKEAIRD-Z
	X-TSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
	X-ATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
	X-VATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
	X-GVATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
25	X-LGVATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a  
30 macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier  
35 group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XXIII  
REPRESENTATIVE DP107/DP178 ANALOG ANTIVIRAL PEPTIDES

Anti-Respiratory syncytial virus peptides

X-TSVITIELSNIKENKCNCTDAKVKLIKQELDKYKN-Z  
X-SVITIELSNIKENKCNCTDAKVKLIKQELDKYKNA-Z  
5 X-VITIELSNIKENKCNCTDAKVKLIKQELDKYKNAV-Z  
X-AVSKVLHLEGEVNKIALLLSTNKAVVSLSNQVSV-Z  
X-AVSKVLHLEGEVNKIALLLSTNKAVVSLSNQVSV-Z  
X-VSKVLHLEGEVNKIALLLSTNKAVVSLSNQVSVL-Z  
X-SKVLHLEGEVNKIALLLSTNKAVVSLSNQVSVLT-Z  
X-KVLHLEGEVNKIALLLSTNKAVVSLSNQVSVLTS-Z  
X-LEGEVNKIALLLSTNKAVVSLSNQVSVLTSKVLD-Z  
10 X-GEVNKIALLLSTNKAVVSLSNQVSVLTSKVLDLK-Z  
X-EVNKIALLLSTNKAVVSLSNQVSVLTSKVLDLKN-Z  
X-VNKIALLLSTNKAVVSLSNQVSVLTSKVLDLKNY-Z  
X-NKIALLLSTNKAVVSLSNQVSVLTSKVLDLKNYI-Z  
X-KIALLLSTNKAVVSLSNQVSVLTSKVLDLKNYID-Z  
X-IALLSTNKAVVSLSNQVSVLTSKVLDLKNYIDK-Z  
X-ALLSTNKAVVSLSNQVSVLTSKVLDLKNYIDKQ-Z  
X-AVSKVLHLEGEVNKIALLLSTNKAVVSLSNQVSV-Z  
15 X-AVSKVLHLEGEVNKIALLLSTNKAVVSLSNQVSV-Z  
X-VSKVLHLEGEVNKIALLLSTNKAVVSLSNQVSVL-Z  
X-SKVLHLEGEVNKIALLLSTNKAVVSLSNQVSVLT-Z  
X-KVLHLEGEVNKIALLLSTNKAVVSLSNQVSVLTS-Z  
X-LEGEVNKIALLLSTNKAVVSLSNQVSVLTSKVLD-Z  
X-GEVNKIALLLSTNKAVVSLSNQVSVLTSKVLDLK-Z  
X-EVNKIALLLSTNKAVVSLSNQVSVLTSKVLDLKN-Z  
20 X-VNKIALLLSTNKAVVSLSNQVSVLTSKVLDLKNY-Z  
X-NKIALLLSTNKAVVSLSNQVSVLTSKVLDLKNYI-Z  
X-KIALLLSTNKAVVSLSNQVSVLTSKVLDLKNYID-Z  
X-IALLSTNKAVVSLSNQVSVLTSKVLDLKNYIDK-Z  
X-ALLSTNKAVVSLSNQVSVLTSKVLDLKNYIDKQ-Z

Anti-human parainfluenza virus 3 peptides

25 X-TLNNVALDPIDISIELNKAQSDLEESKEWIRRSN-Z  
X-LNNVALDPIDISIELNKAQSDLEESKEWIRRSNQ-Z  
X-NNNVALDPIDISIELNKAQSDLEESKEWIRRSNQK-Z  
X-NSVALDPIDISIELNKAQSDLEESKEWIRRSNQKL-Z  
X-SVALDPIDISIELNKAQSDLEESKEWIRRSNQKLD-Z  
X-VALDPIDISIELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-ALDPIDISIELNKAQSDLEESKEWIRRSNQKLDL-Z  
30 X-LDPIDISIELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-DPIDISIELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-PIDISIELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-IDISIELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-DISIELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-ISIELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-SIELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-IELNKAQSDLEESKEWIRRSNQKLDL-Z  
35 X-ELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-TAAVALVEAKQARSDIEKLKEAIRDITNKAVQSVQ-Z



X-AVALVEAKQARSDIEKLKEAIRDNTKAVQSVQSSI-Z  
 X-LVEAKQARSDIEKLKEAIRDNTKAVQSVQSSIGNL-Z  
 X-VEAKQARSDIEKLKEAIRDNTKAVQSVQSSIGNLI-Z  
 X-EAKQARSDIEKLKEAIRDNTKAVQSVQSSIGNLIV-Z  
 X-AKQARSDIEKLKEAIRDNTKAVQSVQSSIGNLIVA-Z  
 X-KQARSDIEKLKEAIRDNTKAVQSVQSSIGNLIVAI-Z  
 X-QARSDIEKLKEAIRDNTKAVQSVQSSIGNLIVAIAIK-Z  
 5 X-ARSDIEKLKEAIRDNTKAVQSVQSSIGNLIVAIAIKS-Z  
 X-RSDIEKLKEAIRDNTKAVQSVQSSIGNLIVAIAIKSV-Z  
 X-SDIEKLKEAIRDNTKAVQSVQSSIGNLIVAIAIKSVQ-Z  
 X-KLKEAIRDNTKAVQSVQSSIGNLIVAIAIKSVQDYVN-Z  
 X-LKEAIRDNTKAVQSVQSSIGNLIVAIAIKSVQDYVNVN-Z  
 X-AIRDNTKAVQSVQSSIGNLIVAIAIKSVQDYVNVNKEIV-Z

10 Anti-simian immunodeficiency virus peptides

X-WQEWERKVDVFLEENITALLEEAAQIQQEKNNMYELQK-Z  
 X-QEWERKVDVFLEENITALLEEAAQIQQEKNNMYELQKL-Z  
 X-EWERKVDVFLEENITALLEEAAQIQQEKNNMYELQKLN-Z  
 X-WERKVDVFLEENITALLEEAAQIQQEKNNMYELQKLNS-Z  
 X-ERKVDVFLEENITALLEEAAQIQQEKNNMYELQKLNSW-Z  
 X-RKVDVFLEENITALLEEAAQIQQEKNNMYELQKLNSWD-Z  
 15 X-KVDVFLEENITALLEEAAQIQQEKNNMYELQKLNSWDV-Z  
 X-VDFLEENITALLEEAAQIQQEKNNMYELQKLNSWDVF-Z  
 X-DFLEENITALLEEAAQIQQEKNNMYELQKLNSWDVFG-Z  
 X-FLEENITALLEEAAQIQQEKNNMYELQKLNSWDVFGN-Z

Anti-measles virus peptides

20 X-LHRIDLGPPISLERLDVGTNLGNIAIAKLEAKELL-Z  
 X-HRIDLGPPISLERLDVGTNLGNIAIAKLEAKELLE-Z  
 X-RIDLGPPISLERLDVGTNLGNIAIAKLEAKELLES-Z  
 X-IDLGPPISLERLDVGTNLGNIAIAKLEAKELLESS-Z  
 X-DLGPPISLERLDVGTNLGNIAIAKLEAKELLESSD-Z  
 X-LGPPISLERLDVGTNLGNIAIAKLEAKELLESSDQ-Z  
 X-GPPISLERLDVGTNLGNIAIAKLEAKELLESSDQI-Z  
 25 X-PPISLERLDVGTNLGNIAIAKLEAKELLESSDQIL-Z  
 X-PISLERLDVGTNLGNIAIAKLEAKELLESSDQILR-Z  
 X-SLERLDVGTNLGNIAIAKLEAKELLESSDQILRSM-Z  
 X-LERLDVGTNLGNIAIAKLEAKELLESSDQILRSMK-Z

The one letter amino acid code is used.

30 Additionally,  
 "X" may represent an amino group, a hydrophobic group,  
 including but not limited to carbobenzoxy, dansyl, or  
 T-butyloxycarbonyl; an acetyl group; a 9-  
 fluorenylmethoxy-carbonyl (Fmoc) group; a  
 macromolecular carrier group including but not limited  
 to lipid-fatty acid conjugates, polyethylene glycol,  
 or carbohydrates.  
 35

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

5

10

15

20

25

30

35

#### 5.4. SYNTHESIS OF PEPTIDES

The peptides of the invention may be synthesized or prepared by techniques well known in the art. See, for example, Creighton, 1983, Proteins: Structures  
5 and Molecular Principles, W.H. Freeman and Co., NY, which is incorporated herein by reference in its entirety. Short peptides, for example, can be synthesized on a solid support or in solution. Longer  
10 peptides may be made using recombinant DNA techniques. Here, the nucleotide sequences encoding the peptides of the invention may be synthesized, and/or cloned, and expressed according to techniques well known to those of ordinary skill in the art. See, for example,  
15 Sambrook, et al., 1989, Molecular Cloning, A Laboratory Manual, Vols. 1-3, Cold Spring Harbor Press, NY.

The peptides of the invention may alternatively be synthesized such that one or more of the bonds which link the amino acid residues of the peptides are  
20 non-peptide bonds. These alternative non-peptide bonds may be formed by utilizing reactions well known to those in the art, and may include, but are not limited to imino, ester, hydrazide, semicarbazide, and  
25 azo bonds, to name but a few. In yet another embodiment of the invention, peptides comprising the sequences described above may be synthesized with additional chemical groups present at their amino and/or carboxy termini, such that, for example, the  
30 stability, bioavailability, and/or inhibitory activity of the peptides is enhanced. For example, hydrophobic groups such as carbobenzoxyl, dansyl, or t-butylloxycarbonyl groups, may be added to the peptides' amino termini. Likewise, an acetyl group or a 9-fluorenylmethoxy-carbonyl group may be placed at the  
35 peptides' amino termini. (See "X" in Tables I to IV,

above.) Additionally, the hydrophobic group, t-butyloxycarbonyl, or an amido group may be added to the peptides' carboxy termini. (See "Z" in Tables I to IV, above.)

5 Further, the peptides of the invention may be synthesized such that their steric configuration is altered. For example, the D-isomer of one or more of the amino acid residues of the peptide may be used, rather than the usual L-isomer.

10 Still further, at least one of the amino acid residues of the peptides of the invention may be substituted by one of the well known non-naturally occurring amino acid residues. Alterations such as these may serve to increase the stability, bioavailability and/or inhibitory action of the  
15 peptides of the invention.

Any of the peptides described above may, additionally, have a macromolecular carrier group covalently attached to their amino and/or carboxy termini. Such macromolecular carrier groups may  
20 include, for example, lipid-fatty acid conjugates, polyethylene glycol, carbohydrates or additional peptides. "X", in Tables I to IV, above, may therefore additionally represent any of the above macromolecular carrier groups covalently attached to  
25 the amino terminus of a peptide, with an additional peptide group being preferred. Likewise, "Z", in Tables I to IV, may additionally represent any of the macromolecular carrier groups described above.

30 5.5. ASSAYS FOR ANTI-MEMBRANE FUSION ACTIVITY

Described herein, are methods for ability of a compound, such as the peptides of the invention, to inhibit membrane fusion events. Specifically, assays for cell fusion events are described in Section 5.5.1,  
35

below, and assays for antiviral activity are described in Section 5.5.2, below.

#### 5.5.1 ASSAYS FOR CELL FUSION EVENTS

5 Assays for cell fusion events are well known to those of skill in the art, and may be used in conjunction, for example, with the peptides of the invention to test the peptides' antifusogenic capabilities.

10 Cell fusion assays are generally performed in vitro. Such an assay may comprise culturing cells which, in the absence of any treatment would undergo an observable level of syncytial formation. For example, uninfected cells may be incubated in the presence of cells chronically infected with a virus  
15 that induces cell fusion. Such viruses may include, but are not limited to, HIV, SIV, or respiratory syncytial virus.

For the assay, cells are incubated in the presence of a peptide to be assayed. For each  
20 peptide, a range of peptide concentrations may be tested. This range should include a control culture wherein no peptide has been added.

Standard conditions for culturing cells, well known to those of ordinary skill in the art, are used.  
25 After incubation for an appropriate period (24 hours at 37°C, for example) the culture is examined microscopically for the presence of multinucleated giant cells, which are indicative of cell fusion and syncytial formation. Well known stains, such as  
30 crystal violet stain, may be used to facilitate the visualization of syncytial formation.

#### 5.5.2 ASSAYS FOR ANTIVIRAL ACTIVITY

35 The antiviral activity exhibited by the peptides of the invention may be measured, for example, by

easily performed in vitro assays, such as those described below, which can test the peptides' ability to inhibit syncytia formation, or their ability to inhibit infection by cell-free virus. Using these assays, such parameters as the relative antiviral activity of the peptides, exhibit against a given strain of virus and/or the strain specific inhibitory activity of the peptide can be determined.

A cell fusion assay may be utilized to test the peptides' ability to inhibit viral-induced, such as HIV-induced, syncytia formation in vitro. Such an assay may comprise culturing uninfected cells in the presence of cells chronically infected with a syncytial-inducing virus and a peptide to be assayed. For each peptide, a range of peptide concentrations may be tested. This range should include a control culture wherein no peptide has been added. Standard conditions for culturing, well known to those of ordinary skill in the art, are used. After incubation for an appropriate period (24 hours at 37°C, for example) the culture is examined microscopically for the presence of multinucleated giant cells, which are indicative of cell fusion and syncytia formation. Well known stains, such as crystal violet stain, may be used to facilitate syncytial visualization. Taking HIV as an example, such an assay would comprise CD-4<sup>+</sup> cells (such as Molt or CEM cells, for example) cultured in the presence of chronically HIV-infected cells and a peptide to be assayed.

Other well known characteristics of viral infection may also be assayed to test a peptide's antiviral capabilities. Once again taking HIV as an example, a reverse transcriptase (RT) assay may be utilized to test the peptides' ability to inhibit infection of CD-4<sup>+</sup> cells by cell-free HIV. Such an assay may comprise culturing an appropriate

concentration (i.e., TCID<sub>50</sub>) of virus and CD-4<sup>+</sup> cells in the presence of the peptide to be tested. Culture conditions well known to those in the art are used. As above, a range of peptide concentrations may be used, in addition to a control culture wherein no peptide has been added. After incubation for an appropriate period (e.g., 7 days) of culturing, a cell-free supernatant is prepared, using standard procedures, and tested for the presence of RT activity as a measure of successful infection. The RT activity may be tested using standard techniques such as those described by, for example, Goff et al. (Goff, S. et al., 1981, J. Virol. 38:239-248) and/or Willey et al. (Willey, R. et al., 1988, J. Virol. 62:139-147). These references are incorporated herein by reference in their entirety.

Standard methods which are well-known to those of skill in the art may be utilized for assaying non-retroviral activity. See, for example, Pringle et al. (Pringle, C.R. et al., 1985, J. Medical Virology 17:377-386) for a discussion of respiratory syncytial virus and parainfluenza virus activity assay techniques. Further, see, for example, "Zinsser Microbiology", 1988, Joklik, W.K. et al., eds., Appleton & Lange, Norwalk, CT, 19th ed., for a general review of such techniques. These references are incorporated by reference herein in their entirety. In addition, the Examples presented below, in Sections 17, 18, 26 and 27 each provide additional assays for the testing of a compound's antiviral capability.

In vivo assays may also be utilized to test, for example, the antiviral activity of the peptides of the invention. To test for anti-HIV activity, for example, the in vivo model described in Barnett et al. (Barnett, S.W. et al., 1994, Science 266:642-646) may be used.

5           Additionally, anti-RSV activity can be assayed in  
vivo via well known mouse models. For example, RSV  
can be administered intranasally to mice of various  
inbred strains. Virus replicates in lungs of all  
strains, but the highest titers are obtained in P/N,  
10       C57L/N and DBA/2N mice. Infection of BALB/c mice  
produces an asymptomatic bronchiolitis characterized  
by lymphocytic infiltrates and pulmonary virus titers  
of  $10^4$  to  $10^5$  pfu/g of lung tissue (Taylor, G. et al.,  
1984, Infect. Immun. 43:649-655).

10           Cotton rat models of RSV are also well known.  
Virus replicates to high titer in the nose and lungs  
of the cotton rat but produces few if any signs of  
inflammation.

15           5.6. USES OF THE PEPTIDES OF THE INVENTION

          The peptides of the invention may be utilized as  
antifusogenic or antiviral compounds, or as compounds  
which modulate intracellular processes involving  
coiled coil peptide structures. Further, such  
20       peptides may be used to identify agents which exhibit  
antifusogenic, antiviral or intracellular modulatory  
activity. Still further, the peptides of the  
invention may be utilized as organism or viral  
type/subtype-specific diagnostic tools.

25           The antifusogenic capability of the peptides of  
the invention may additionally be utilized to inhibit  
or treat/ameliorate symptoms caused by processes  
involving membrane fusion events. Such events may  
include, for example, virus transmission via cell-cell  
30       fusion, abnormal neurotransmitter exchange via cell-  
fusion, and sperm-egg fusion. Further, the peptides  
of the invention may be used to inhibit free viral,  
such as retroviral, particularly HIV, transmission to  
uninfected cells wherein such viral infection involves  
35       membrane fusion events or involves fusion of a viral



structure with a cell membrane. Among the intracellular disorders involving coiled coil peptides structures which may be ameliorated by the peptides of the invention are disorders involving, for example, bacterial toxins.

5       With respect to antiviral activity, the viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to all strains of the viruses listed above, in Tables V through VII, and IX through XIV.

10       These viruses include, for example, human retroviruses, particularly HIV-1 and HIV-2 and the human T-lymphocyte viruses (HTLV-I and II). The non-human retroviruses whose transmission may be inhibited by the peptides of the invention include, but are not  
15       limited to bovine leukosis virus, feline sarcoma and leukemia viruses, simian immunodeficiency, sarcoma and leukemia viruses, and sheep progress pneumonia viruses.

20       /       Non retroviral viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to human respiratory syncytial virus, canine distemper virus, newcastle disease virus, human parainfluenza virus, influenza viruses, measles viruses, Epstein-Barr viruses, hepatitis B  
25       viruses, and simian Mason-Pfizer viruses.

      Non enveloped viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to picornaviruses such as polio viruses, hepatitis A virus, enterovirus, echoviruses  
30       and coxsackie viruses, papovaviruses such as papilloma virus, parvoviruses, adenoviruses and reoviruses.

      As discussed more fully, below, in Section 5.5.1 and in the Example presented, below, in Section 8, DP107, DP178, DP107 analog and DP178 analog peptides  
35       form non-covalent protein-protein interactions which

are required for normal activity of the virus. Thus, the peptides of the invention may also be utilized as components in assays for the identification of compounds that interfere with such protein-protein interactions and may, therefore, act as antiviral agents. These assays are discussed, below, in Section 5.5.1.

As demonstrated in the Example presented below in Section 6, the antiviral activity of the peptides of the invention may show a pronounced type and subtype specificity, *i.e.*, specific peptides may be effective in inhibiting the activity of only specific viruses. This feature of the invention presents many advantages. One such advantage, for example, lies in the field of diagnostics, wherein one can use the antiviral specificity of the peptide of the invention to ascertain the identity of a viral isolate. With respect to HIV, one may easily determine whether a viral isolate consists of an HIV-1 or HIV-2 strain. For example, uninfected CD-4<sup>+</sup> cells may be co-infected with an isolate which has been identified as containing HIV the DP178 (SEQ ID:1) peptide, after which the retroviral activity of cell supernatants may be assayed, using, for example, the techniques described above in Section 5.2. Those isolates whose retroviral activity is completely or nearly completely inhibited contain HIV-1. Those isolates whose viral activity is unchanged or only reduced by a small amount, may be considered to not contain HIV-1. Such an isolate may then be treated with one or more of the other DP178 peptides of the invention, and subsequently be tested for its viral activity in order to determine the identify of the viral isolate. The DP107 and DP178 analogs of the invention may also be utilized in a diagnostic capacity specific to the type and subtype of virus or organism in which the specific

peptide sequence is found. A diagnostic procedure as described, above, for DP178, may be used in conjunction with the DP107/DP178 analog of interest.

#### 5.5.1. SCREENING ASSAYS

5 As demonstrated in the Example presented in Section 8, below, DP107 and DP178 portions of the TM protein gp41 form non-covalent protein-protein interactions. As is also demonstrated, the maintenance of such interactions is necessary for  
10 normal viral infectivity. Thus, compounds which bind DP107, bind DP178, and/or act to disrupt normal DP107/DP178 protein-protein interactions may act as antifusogenic, antiviral or cellular modulatory agents. Described below are assays for the  
15 identification of such compounds. Note that, while, for ease and clarity of discussion, DP107 and DP178 peptides will be used as components of the assays described, but it is to be understood that any of the DP107 analog or DP178 analog peptides described,  
20 above, in Sections 5.1 through 5.3 may also be utilized as part of these screens for compounds.

Compounds which may be tested for an ability to bind DP107, DP178, and/or disrupt DP107/DP178 interactions, and which therefore, potentially  
25 represent antifusogenic, antiviral or intracellular modulatory compounds, include, but are not limited to, peptides made of D- and/or L-configuration amino acids (in, for example, the form of random peptide libraries; see Lam, K.S. et al., 1991, Nature 354:82-  
30 84), phosphopeptides (in, for example, the form of random or partially degenerate, directed phosphopeptide libraries; see, for example, Songyang, Z. et al., 1993, Cell 72:767-778), antibodies, and small organic or inorganic molecules. Synthetic  
35 compounds, natural products, and other sources of

potentially effective materials may be screened in a variety of ways, as described in this Section.

The compounds, antibodies, or other molecules identified may be tested, for example, for an ability to inhibit cell fusion or viral activity, utilizing,  
5 for example, assays such as those described, above, in Section 5.5.

Among the peptides which may be tested are soluble peptides comprising DP107 and/or DP178 domains, and peptides comprising DP107 and/or DP178  
10 domains having one or more mutations within one or both of the domains, such as the M41-P peptide described, below, in the Example presented in Section 8, which contains a isoleucine to proline mutation within the DP178 sequence.

15 In one embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

(a) exposing at least one compound to a peptide comprising a DP107 peptide for a time  
20 sufficient to allow binding of the compound to the DP107 peptide;

(b) removing non-bound compounds; and

(c) determining the presence of the compound bound to the DP107 peptide,  
25 thereby identifying an agent to be tested for antiviral ability.

In a second embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

30 (a) exposing at least one compound to a peptide comprising a DP178 peptide for a time sufficient to allow binding of the compound to the DP178 peptide;

(b) removing non-bound compounds; and  
35

(c) determining the presence of the compound bound to the DP178 peptide, thereby identifying an agent to be tested for antiviral ability.

5 One method utilizing these types of approaches that may be pursued in the isolation of such DP107-binding or DP178-binding compounds is an assay which would include the attachment of either the DP107 or the DP178 peptide to a solid matrix, such as, for example, agarose or plastic beads, microtiter plate  
10 wells, petri dishes, or membranes composed of, for example, nylon or nitrocellulose. In such an assay system, either the DP107 or DP178 protein may be anchored onto a solid surface, and the compound, or test substance, which is not anchored, is labeled,  
15 either directly or indirectly. In practice, microtiter plates are conveniently utilized. The anchored component may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface  
20 with a solution of the protein and drying.

Alternatively, an immobilized antibody, preferably a monoclonal antibody, specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and  
25 stored.

In order to conduct the assay, the labeled compound is added to the coated surface containing the anchored DP107 or DP178 peptide. After the reaction is complete, unreacted components are removed (e.g.,  
30 by washing) under conditions such that any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the compound is pre-labeled, the detection of  
35 label immobilized on the surface indicates that

complexes were formed. Where the labeled component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the compound (the antibody, in turn, may be directly labeled or  
5 indirectly labeled with a labeled anti-Ig antibody).

Alternatively, such an assay can be conducted in a liquid phase, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for DP107 or  
10 DP178, whichever is appropriate for the given assay, or an antibody specific for the compound, i.e., the test substance, in order to anchor any complexes formed in solution, and a labeled antibody specific for the other member of the complex to detect anchored  
15 complexes.

By utilizing procedures such as this, large numbers of types of molecules may be simultaneously screened for DP107 or DP178-binding capability, and thus potential antiviral activity.

20 Further, compounds may be screened for an ability to inhibit the formation of or, alternatively, disrupt DP107/DP178 complexes. Such compounds may then be tested for antifusogenic, antiviral or intercellular modulatory capability. For ease of description, DP107  
25 and DP178 will be referred to as "binding partners." Compounds that disrupt such interactions may exhibit antiviral activity. Such compounds may include, but are not limited to molecules such as antibodies, peptides, and the like described above.

30 The basic principle of the assay systems used to identify compounds that interfere with the interaction between the DP107 and DP178 peptides involves preparing a reaction mixture containing peptides under conditions and for a time sufficient to allow the two  
35 peptides to interact and bind, thus forming a complex.

In order to test a compound for disruptive activity, the reaction is conducted in the presence and absence of the test compound, i.e., the test compound may be initially included in the reaction mixture, or added at a time subsequent to the addition of one of the  
5 binding partners; controls are incubated without the test compound or with a placebo. The formation of any complexes between the binding partners is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing  
10 the test compound indicates that the compound interferes with the interaction of the DP107 and DP178 peptides.

The assay for compounds that interfere with the interaction of the binding partners can be conducted  
15 in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring one of the binding partners onto a solid phase and detecting complexes anchored on the solid phase at the end of the reaction. In homogeneous assays, the entire  
20 reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the  
25 binding partners, e.g., by competition, can be identified by conducting the reaction in the presence of the test substance; i.e., by adding the test substance to the reaction mixture prior to or simultaneously with the binding partners. On the  
30 other hand, test compounds that disrupt preformed complexes, e.g. compounds with higher binding constants that displace one of the binding partners from the complex, can be tested by adding the test compound to the reaction mixture after complexes have  
35

been formed. The various formats are described briefly below.

5 In a heterogeneous assay system, one binding partner, e.g., either the DP107 or DP178 peptide, is anchored onto a solid surface, and its binding partner, which is not anchored, is labeled, either directly or indirectly. In practice, microtiter plates are conveniently utilized. The anchored species may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be  
10 accomplished simply by coating the solid surface with a solution of the protein and drying. Alternatively, an immobilized antibody specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

15 In order to conduct the assay, the binding partner of the immobilized species is added to the coated surface with or without the test compound. After the reaction is complete, unreacted components are removed (e.g., by washing) and any complexes  
20 formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the binding partner was pre-labeled, the detection of label immobilized on the surface  
25 indicates that complexes were formed. Where the binding partner is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the binding partner (the antibody, in turn, may be  
30 directly labeled or indirectly labeled with a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which inhibit complex formation or which disrupt preformed complexes can be detected.

35



Alternatively, the reaction can be conducted in a liquid phase in the presence or absence of the test compound, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for one binding partner to anchor any complexes formed in solution, and a labeled antibody specific for the other binding partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test compounds which inhibit complex or which disrupt preformed complexes can be identified.

In an alternate embodiment of the invention, a homogeneous assay can be used. In this approach, a preformed complex of the DP107 and DP178 peptides is prepared in which one of the binding partners is labeled, but the signal generated by the label is quenched due to complex formation (see, e.g., U.S. Patent No. 4,109,496 by Rubenstein which utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the binding partners from the preformed complex will result in the generation of a signal above background. In this way, test substances which disrupt DP-107/DP-178 protein-protein interaction can be identified.

In an alternative screening assay, test compounds may be assayed for the their ability to disrupt a DP178/DP107 interaction, as measured immunometrically using an antibody specifically reactive to a DP107/DP178 complex (i.e., an antibody that recognizes neither DP107 nor DP178 individually). Such an assay acts as a competition assay, and is based on techniques well known to those of skill in the art.

The above competition assay may be described, by way of example, and not by way of limitation, by using the DP178 and M41Δ178 peptides and by assaying test

compounds for the disruption of the complexes formed by these two peptides by immunometrically visualizing DP178/M41Δ178 complexes via the human recombinant Fab, Fab-d, as described, below, in the Example presented in Section 8. M41Δ178 is a maltose binding fusion  
5 protein containing a gp41 region having its DP178 domain deleted, and is described, below, in the Example presented in Section 8.

Utilizing such an assay, M41Δ178 may be immobilized onto solid supports such as microtiter  
10 wells. A series of dilutions of a test compound may then be added to each M41Δ178-containing well in the presence of a constant concentration of DP-178 peptide. After incubation, at, for example, room temperature for one hour, unbound DP-178 and test  
15 compound are removed from the wells and wells are then incubated with the DP178/M41Δ178-specific Fab-d antibody. After incubation and washing, unbound Fab-d is removed from the plates and bound Fab-d is quantitated. A no-inhibitor control should also be  
20 conducted. Test compounds showing an ability to disrupt DP178/M41Δ178 complex formation are identified by their concentration-dependent decrease in the level of Fab-d binding.

A variation of such an assay may be utilized to  
25 perform a rapid, high-throughput binding assay which is capable of directly measuring DP178 binding to M41Δ178 for the determination of binding constants of the ligand or inhibitory constants for competitors of DP178 binding.

30 Such an assay takes advantage of accepted radioligand and receptor binding principles. (See, for example, Yamamura, H.I. et al., 1985, "Neurotransmitter Receptor Binding", 2nd ed., Raven Press, NY.) As above, M41Δ178 is immobilized onto a  
35 solid support such as a microtiter well. DP178

binding to M41Δ178 is then quantitated by measuring the fraction of DP178 that is bound as <sup>125</sup>I-DP178 and calculating the total amount bound using a value for specific activity (dpm/μg peptide) determined for each labeled DP178 preparation. Specific binding to  
5 M41Δ178 is defined as the difference of the binding of the labeled DP178 preparation in the microtiter wells (totals) and the binding in identical wells containing, in addition, excess unlabeled DP178 (nonspecifics).  
10

#### 5.5 PHARMACEUTICAL FORMULATIONS, DOSAGES AND MODES OF ADMINISTRATION

The peptides of the invention may be administered using techniques well known to those in the art.  
15 Preferably, agents are formulated and administered systemically. Techniques for formulation and administration may be found in "Remington's Pharmaceutical Sciences", 18th ed., 1990, Mack Publishing Co., Easton, PA. Suitable routes may  
20 include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as, intrathecal, direct intraventricular, intravenous, intraperitoneal,  
25 intranasal, or intraocular injections, just to name a few. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiological saline  
30 buffer. For such transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

In instances wherein intracellular administration  
35 of the peptides of the invention or other inhibitory

agents is preferred, techniques well known to those of ordinary skill in the art may be utilized. For example, such agents may be encapsulated into liposomes, then administered as described above. Liposomes are spherical lipid bilayers with aqueous interiors. All molecules present in an aqueous solution at the time of liposome formation are incorporated into the aqueous interior. The liposomal contents are both protected from the external microenvironment and, because liposomes fuse with cell membranes, are effectively delivered into the cell cytoplasm. Additionally, due to their hydrophobicity, when small molecules are to be administered, direct intracellular administration may be achieved.

Nucleotide sequences encoding the peptides of the invention which are to be intracellularly administered may be expressed in cells of interest, using techniques well known to those of skill in the art. For example, expression vectors derived from viruses such as retroviruses, vaccinia viruses, adeno-associated viruses, herpes viruses, or bovine papilloma viruses, may be used for delivery and expression of such nucleotide sequences into the targeted cell population. Methods for the construction of such vectors and expression constructs are well known. See, for example, Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor NY, and Ausubel et al., 1989, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, NY.

With respect to HIV, peptides of the invention, particularly DP107 and DP178, may be used as therapeutics in the treatment of AIDS. In addition, the peptides may be used as prophylactic measures in previously uninfected individuals after acute exposure

to an HIV virus. Examples of such prophylactic use of the peptides may include, but are not limited to, prevention of virus transmission from mother to infant and other settings where the likelihood of HIV transmission exists, such as, for example, accidents  
5 in health care settings wherein workers are exposed to HIV-containing blood products. The successful use of such treatments do not rely upon the generation of a host immune response directed against such peptides.

Effective dosages of the peptides of the  
10 invention to be administered may be determined through procedures well known to those in the art which address such parameters as biological half-life, bioavailability, and toxicity. Given the data presented below in Section 6, DP178, for example, may  
15 prove efficacious in vivo at doses required to achieve circulating levels of about 1 to about 10 ng per ml of peptide.

A therapeutically effective dose refers to that amount of the compound sufficient to result in  
20 amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD<sub>50</sub>  
25 (the dose lethal to 50% of the population) and the ED<sub>50</sub> (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD<sub>50</sub>/ED<sub>50</sub>. Compounds  
30 which exhibit large therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of  
35 circulating concentrations that include the ED<sub>50</sub> with

little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated  
5 initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the  $IC_{50}$  (e.g., the concentration of the test compound which achieves a half-maximal inhibition of the fusogenic  
10 event, such as a half-maximal inhibition of viral infection relative to the amount of the event in the absence of the test compound) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels  
15 in plasma may be measured, for example, by high performance liquid chromatography (HPLC).

The peptides of the invention may, further, serve the role of a prophylactic vaccine, wherein the host raises antibodies against the peptides of the  
20 invention, which then serve to neutralize HIV viruses by, for example, inhibiting further HIV infection.

Administration of the peptides of the invention as a prophylactic vaccine, therefore, would comprise administering to a host a concentration of peptides  
25 effective in raising an immune response which is sufficient to neutralize HIV, by, for example, inhibiting HIV ability to infect cells. The exact concentration will depend upon the specific peptide to be administered, but may be determined by using  
30 standard techniques for assaying the development of an immune response which are well known to those of ordinary skill in the art. The peptides to be used as vaccines are usually administered intramuscularly.

The peptides may be formulated with a suitable  
35 adjuvant in order to enhance the immunological

response. Such adjuvants may include, but are not limited to mineral gels such as aluminum hydroxide; surface active substances such as lysolecithin, pluronic polyols, polyanions; other peptides; oil emulsions; and potentially useful human adjuvants such as BCG and Corynebacterium parvum. Many methods may be used to introduce the vaccine formulations described here. These methods include but are not limited to oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, and intranasal routes.

Alternatively, an effective concentration of polyclonal or monoclonal antibodies raised against the peptides of the invention may be administered to a host so that no uninfected cells become infected by HIV. The exact concentration of such antibodies will vary according to each specific antibody preparation, but may be determined using standard techniques well known to those of ordinary skill in the art. Administration of the antibodies may be accomplished using a variety of techniques, including, but not limited to those described in this section.

For all such treatments described above, the exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. (See e.g. Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p1).

It should be noted that the attending physician would know how to and when to terminate, interrupt, or adjust administration due to toxicity, or to organ dysfunctions. Conversely, the attending physician would also know to adjust treatment to higher levels if the clinical response were not adequate (precluding toxicity). The magnitude of an administered dose in the management of the oncogenic disorder of interest

will vary with the severity of the condition to be treated and the route of administration. The dose and perhaps dose frequency, will also vary according to the age, body weight, and response of the individual patient. A program comparable to that discussed above  
5 may be used in veterinary medicine.

Use of pharmaceutically acceptable carriers to formulate the compounds herein disclosed for the practice of the invention into dosages suitable for systemic administration is within the scope of the  
10 invention. With proper choice of carrier and suitable manufacturing practice, the compositions of the present invention, in particular, those formulated as solutions, may be administered parenterally, such as by intravenous injection. The compounds can be  
15 formulated readily using pharmaceutically acceptable carriers well known in the art into dosages suitable for oral administration. Such carriers enable the compounds of the invention to be formulated as tablets, pills, capsules, liquids, gels, syrups,  
20 slurries, suspensions and the like, for oral ingestion by a patient to be treated.

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective  
25 amount to achieve its intended purpose. Determination of the effective amounts is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein.

In addition to the active ingredients, these  
30 pharmaceutical compositions may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. The preparations formulated  
35



for oral administration may be in the form of tablets, dragees, capsules, or solutions.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

Pharmaceutical preparations for oral use can be obtained by combining the active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be

added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate.

Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be  
5 used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or  
10 dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a  
15 plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In  
20 soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added.

25 6. EXAMPLE: DP178 (SEQ ID:1) IS A POTENT INHIBITOR OF HIV-1 INFECTION

In this example, DP178 (SEQ ID:1) is shown to be a potent inhibitor of HIV-1 mediated CD-4<sup>+</sup> cell-cell fusion and infection by cell free virus. In the  
30 fusion assay, this peptide completely blocks virus induced syncytia formation at concentrations of from 1-10 ng/ml. In the infectivity assay the inhibitory concentration is somewhat higher, blocking infection at 90ng/ml. It is further shown that DP178 (SEQ ID:1)  
35 shows that the antiviral activity of DP178 (SEQ ID:1)

is highly specific for HIV-1. Additionally, a synthetic peptide, DP-185 (SEQ ID:3), representing a HIV-1-derived DP178 homolog is also found to block HIV-1-mediated syncytia formation.

5

## 6.1. MATERIALS AND METHODS

### 6.1.1. PEPTIDE SYNTHESIS

Peptides were synthesized using Fast Moc chemistry on an Applied Biosystems Model 431A peptide synthesizer. Generally, unless otherwise noted, the peptides contained amidated carboxy termini and acetylated amino termini. Amidated peptides were prepared using Rink resin (Advanced Chemtech) while peptides containing free carboxy termini were synthesized on Wang (p-alkoxy-benzyl-alcohol) resin (Bachem). First residues were double coupled to the appropriate resin and subsequent residues were single coupled. Each coupling step was followed by acetic anhydride capping. Peptides were cleaved from the resin by treatment with trifluoroacetic acid (TFA) (10ml), H<sub>2</sub>O (0.5ml), thioanisole (0.5ml), ethanedithiol (0.25ml), and crystalline phenol (0.75g). Purification was carried out by reverse phase HPLC. Approximately 50mg samples of crude peptide were chromatographed on a Waters Delta Pak C18 column (19mm x 30cm, 15μ spherical) with a linear gradient; H<sub>2</sub>O/acetonitrile 0.1% TFA. Lyophilized peptides were stored desiccated and peptide solutions were made in water at about 1mg/ml. Electrospray mass spectrometry yielded the following results: DP178 (SEQ ID:1):4491.87 (calculated 4491.94); DP-180 (SEQ ID:2):4491.45 (calculated 4491.94); DP-185 (SEQ ID:3):not done (calculated 4546.97).

35

#### 6.1.2. VIRUS

The HIV-1<sub>LAI</sub> virus was obtained from R. Gallo (Popovic, M. et al., 1984, Science 224:497-508) and propagated in CEM cells cultured in RPMI 1640  
5 containing 10% fetal calf serum. Supernatant from the infected CEM cells was passed through a 0.2 $\mu$ m filter and the infectious titer estimated in a microinfectivity assay using the AA5 cell line to support virus replication. For this purpose, 25 $\mu$ l of  
10 serial diluted virus was added to 75 $\mu$ l AA5 cells at a concentration of  $2 \times 10^5$ /ml in a 96-well microtitre plate. Each virus dilution was tested in triplicate. Cells were cultured for eight days by addition of  
15 fresh medium every other day. On day 8 post infection, supernatant samples were tested for virus replication as evidenced by reverse transcriptase activity released to the supernatant. The TCID<sub>50</sub> was calculated according to the Reed and Muench formula (Reed, L.J. et al., 1938, Am. J. Hyg. 27:493-497).  
20 The titer of the HIV-1<sub>LAI</sub> and HIV-1<sub>MN</sub> stocks used for these studies, as measured on the AA5 cell line, was approximately  $1.4 \times 10^6$  and  $3.8 \times 10^4$  TCID<sub>50</sub>/ml, respectively.

#### 6.1.3. CELL FUSION ASSAY

25 Approximately  $7 \times 10^4$  Molt cells were incubated with  $1 \times 10^4$  CEM cells chronically infected with the HIV-1<sub>LAI</sub> virus in 96-well plates (one-half area cluster plates; Costar, Cambridge, MA) in a final volume of  
30 100 $\mu$ l culture medium as previously described (Matthews, T.J. et al., 1987, Proc. Natl. Acad. Sci. USA 84: 5424-5428). Peptide inhibitors were added in a volume of 10 $\mu$ l and the cell mixtures were incubated for 24 hr. at 37°C. At that time, multinucleated  
35 giant cells were estimated by microscopic examination

at a 40x magnification which allowed visualization of the entire well in a single field.

#### 6.1.4. CELL FREE VIRUS INFECTION ASSAY

5 Synthetic peptides were incubated at 37°C with either 247 TCID<sub>50</sub> (for experiment depicted in FIG. 2), or 62 TCID<sub>50</sub> (for experiment depicted in FIG.3) units of HIV-1<sub>LAI</sub> virus or 25 TCID<sub>50</sub> units of HIV-2<sub>NIH</sub> and CEM CD4<sup>+</sup> cells at peptide concentrations of 0, 0.04, 0.4, 4.0, and 40µg/ml for 7 days. The resulting reverse  
10 transcriptase (RT) activity in counts per minute was determined using the assay described, below, in Section 6.1.5. See, Reed, L.J. et al., 1938, Am. J. Hyg. 27: 493-497 for an explanation of TCID<sub>50</sub> calculations.

15

#### 6.1.5. REVERSE TRANSCRIPTASE ASSAY

The micro-reverse transcriptase (RT) assay was adapted from Goff et al. (Goff, S. et al., 1981, J. Virol. 38:239-248) and Willey et al. (Willey, R. et al., 1988, J. Virol. 62:139-147). Supernatants from  
20 virus/cell cultures are adjusted to 1% Triton-X100. A 10µl sample of supernatant was added to 50µl of RT cocktail in a 96-well U-bottom microtitre plate and the samples incubated at 37°C for 90 min. The RT  
25 cocktail contained 75mM KCl, 2mM dithiothreitol, 5mM MgCl<sub>2</sub>, 5µg/ml poly A (Pharmacia, cat. No. 27-4110-01), 0.25 units/ml oligo dT (Pharmacia, cat. No. 27-7858-01), 0.05% NP40, 50mM Tris-HCl, pH 7.8, 0.5µM non-radioactive dTTP, and 10µCi/ml <sup>32</sup>P-dTTP (Amersham, cat.  
30 No. PB.10167).

After the incubation period, 40µl of reaction mixture was applied to a Schleicher and Schuell (S+S) NA45 membrane (or DE81 paper) saturated in 2 x SSC buffer (0.3M NaCl and 0.003M sodium citrate) held in a  
35 S+S Minifold over one sheet of GB003 (S+S) filter

paper, with partial vacuum applied. Each well of the minifold was washed four times with 200 $\mu$ l 2xSSC, under full vacuum. The membrane was removed from the minifold and washed 2 more times in a pyrex dish with an excess of 2xSSC. Finally, the membrane was drained  
5 on absorbent paper, placed on Whatman #3 paper, covered with Saran wrap, and exposed to film overnight at -70°C.

## 6.2. RESULTS

### 10 6.2.1. PEPTIDE INHIBITION OF INFECTED CELL-INDUCED SYNCYTIA FORMATION

The initial screen for antiviral activity assayed peptides' ability to block syncytium formation induced by overnight co-cultivation of uninfected Molt4 cells  
15 with chronically HIV-1 infected CEM cells. The results of several such experiments are presented herein. In the first of these experiments, serial DP178 (SEQ ID:1) peptide concentrations between 10 $\mu$ g/ml and 12.5ng/ml were tested for blockade of the  
20 cell fusion process. For these experiments, CEM cells chronically infected with either HIV-1<sub>LAI</sub>, HIV-1<sub>MN</sub>, HIV-1<sub>RF</sub>, or HIV-1<sub>SF2</sub> virus were cocultivated overnight with uninfected Molt 4 cells. The results (FIG. 4) show that DP178 (SEQ ID:1) afforded complete protection  
25 against each of the HIV-1 isolates down to the lowest concentration of DP178 (SEQ ID:1) used. For HIV<sub>LAI</sub> inhibition, the lowest concentration tested was 12.5ng/ml; for all other HIV-1 viruses, the lowest concentration of DP178 (SEQ ID:1) used in this study  
30 was 100ng/ml. A second peptide, DP-180 (SEQ ID:2), containing the same amino acid residues as DP178 (SEQ ID:1) but arranged in a random order exhibited no evidence of anti-fusogenic activity even at the high concentration of 40 $\mu$ g/ml (FIG. 4). These observations  
35 indicate that the inhibitory effect of DP178 (SEQ

ID:1) is primary sequence-specific and not related to non-specific peptide/protein interactions. The actual endpoint (i.e., the lowest effective inhibitory concentration) of DP178 inhibitory action is within the range of 1-10 ng/ml.

5       The next series of experiments involved the preparation and testing of a DP178 (SEQ ID:1) homolog for its ability to inhibit HIV-1-induced syncytia formation. As shown in FIG. 1, the sequence of DP-185 (SEQ ID:3) is slightly different from DP178 (SEQ ID:1) in that its primary sequence is taken from the HIV-1<sub>SF2</sub> isolate and contains several amino acid differences relative to DP178 (SEQ ID:1) near the N terminus. As shown in FIG. 4, DP-185 (SEQ ID:3), exhibits inhibitory activity even at 312.5ng/ml, the lowest concentration tested.

15       The next series of experiments involved a comparison of DP178 (SEQ ID:1) HIV-1 and HIV-2 inhibitory activity. As shown in FIG. 5, DP178 (SEQ ID:1) blocked HIV-1-mediated syncytia formation at peptide concentrations below 1ng/ml. DP178 (SEQ ID:1) failed, however, to block HIV-2 mediated syncytia formation at concentrations as high as 10μg/ml. This striking 4 log selectivity of DP178 (SEQ ID:1) as an inhibitor of HIV-1-mediated cell fusion demonstrates an unexpected HIV-1 specificity in the action of DP178 (SEQ ID:1). DP178 (SEQ ID:1) inhibition of HIV-1-mediated cell fusion, but the peptide's inability to inhibit HIV-2 mediated cell fusion in the same cell type at the concentrations tested provides further evidence for the high degree of selectivity associated with the antiviral action of DP178 (SEQ ID:1).

35

6.2.2. PEPTIDE INHIBITION OF INFECTION BY  
CELL-FREE VIRUS

DP178 (SEQ ID:1) was next tested for its ability to block CD-4<sup>+</sup> CEM cell infection by cell free HIV-1 virus. The results, shown in FIG. 2, are from an experiment in which DP178 (SEQ ID:1) was assayed for its ability to block infection of CEM cells by an HIV-1<sub>LAI</sub> isolate. Included in the experiment were three control peptides, DP-116 (SEQ ID:9), DP-125 (SEQ ID:8), and DP-118 (SEQ ID:10). DP-116 (SEQ ID:9) represents a peptide previously shown to be inactive using this assay, and DP-125 (SEQ ID:8; Wild, C. et al., 1992, Proc. Natl. Acad. Sci. USA 89:10,537) and DP-118 (SEQ ID:10) are peptides which have previously been shown to be active in this assay. Each concentration (0, 0.04, 0.4, 4, and 40 µg/ml) of peptide was incubated with 247 TCID<sub>50</sub> units of HIV-1<sub>LAI</sub> virus and CEM cells. After 7 days of culture, cell-free supernatant was tested for the presence of RT activity as a measure of successful infection. The results, shown in FIG. 2, demonstrate that DP178 (SEQ ID:1) inhibited the de novo infection process mediated by the HIV-1 viral isolate at concentrations as low as 90ng/ml (IC<sub>50</sub>=90ng/ml). In contrast, the two positive control peptides, DP-125 (SEQ ID:8) and DP-118 (SEQ ID:10), had over 60-fold higher IC<sub>50</sub> concentrations of approximately 5 µg/ml.

In a separate experiment, the HIV-1 and HIV-2 inhibitory action of DP178 (SEQ ID:1) was tested with CEM cells and either HIV-1<sub>LAI</sub> or HIV-2<sub>NIHZ</sub>. 62 TCID<sub>50</sub> HIV-1<sub>LAI</sub> or 25 GCID<sub>50</sub> HIV-2<sub>NIHZ</sub> were used in these experiments, and were incubated for 7 days. As may be seen in FIG. 3, DP178 (SEQ ID:1) inhibited HIV-1 infection with an IC<sub>50</sub> of about 31ng/ml. In contrast, DP178 (SEQ ID:1) exhibited a much higher IC<sub>50</sub> for HIV-2<sub>NIHZ</sub>, thus making DP178 (SEQ ID:1) two logs more potent



as a HIV-1 inhibitor than a HIV-2 inhibitor. This finding is consistent with the results of the fusion inhibition assays described, above, in Section 6.2.1, and further supports a significant level of selectivity (i.e., for HIV-1 over HIV-2).

5

7. EXAMPLE: THE HIV-1 INHIBITOR, DP178 (SEQ ID:1) IS NON-CYTOTOXIC

In this Example, the 36 amino acid synthetic peptide inhibitor DP178 (SEQ ID:1) is shown to be non-cytotoxic to cells in culture, even at the highest peptide concentrations (40µg/ml) tested.

10

7.1. MATERIALS AND METHODS

Cell proliferation and toxicity assay:

Approximately  $3.8 \times 10^5$  CEM cells for each peptide concentration were incubated for 3 days at 37°C in T25 flasks. Peptides tested were DP178 (SEQ ID:1) and DP-116 (SEQ ID:9), as described in FIG. 1. Peptides were synthesized as described, above, in Section 6.1. The concentrations of each peptide used were 0, 2.5, 10, and 40µg/ml. Cell counts were taken at incubation times of 0, 24, 48, and 72 hours.

15

20

7.2. RESULTS

Whether the potent HIV-1 inhibitor DP178 (SEQ ID:1) exhibited any cytotoxic effects was assessed by assaying the peptide's effects on the proliferation and viability of cells in culture. CEM cells were incubated in the presence of varying concentrations of DP178 (SEQ ID:1), and DP-116 (SEQ ID:9), a peptide previously shown to be ineffective as a HIV inhibitor (Wild, C. et al., 1992, Proc. Natl. Acad. Sci. USA 89:10,537-10,541). Additionally, cells were incubated in the absence of either peptide.

30

35

The results of the cytotoxicity study demonstrate that DP178 (SEQ ID:1) exhibits no cytotoxic effects on cells in culture. As can be seen, below, in Table XXIV, even the proliferation and viability characteristics of cells cultured for 3 days in the presence of the highest concentration of DP178 (SEQ ID:1) tested (40 $\mu$ g/ml) do not significantly differ from the DP-116 (SEQ ID:9) or the no-peptide controls. The cell proliferation data is also represented in graphic form in FIG. 6. As was demonstrated in the Working Example presented above in Section 6, DP178 (SEQ ID:1) completely inhibits HIV-1 mediated syncytia formation at peptide concentrations between 1 and 10ng/ml, and completely inhibits cell-free viral infection at concentrations of at least 90ng/ml. Thus, this study demonstrates that even at peptide concentrations greater than 3 log higher than the HIV inhibitory dose, DP178 (SEQ ID:1) exhibits no cytotoxic effects.

TABLE XXIV

			% Viability at time (hours)			
5	<u>Peptide</u>	<u>Peptide</u> <u>Concentration <math>\mu</math>g/ml</u>	0	24	48	72
	DP178 (SEQ ID:1)	40	98	97	95	97
10		10	98	97	98	98
		2.5	98	93	96	96
	DP116 (SEQ ID:9)	40	98	95	98	97
15		10	98	95	93	98
		2.5	98	96	98	99
	No Peptide	0	98	97	99	98
20						

8. EXAMPLE: THE INTERACTION OF DP178 AND DP107

Soluble recombinant forms of gp41 used in the example described below provide evidence that the DP178 peptide associates with a distal site on gp41 whose interactive structure is influenced by the DP107 leucine zipper motif. A single mutation disrupting the coiled-coil structure of the leucine zipper domain transformed the soluble recombinant gp41 protein from an inactive to an active inhibitor of HIV-1 fusion. This transformation may result from liberation of the potent DP178 domain from a molecular clasp with the leucine zipper, DP107, determinant. The results also indicate that the anti-HIV activity of various gp41 derivatives (peptides and recombinant proteins) may be

due to their ability to form complexes with viral gp41 and interfere with its fusogenic process.

### 8.1. MATERIALS AND METHODS

#### 5                    8.1.1. CONSTRUCTION OF FUSION PROTEINS AND GP41 MUTANTS

Construction of fusion proteins and mutants shown in FIG. 7 was accomplished as follows: the DNA sequence corresponding to the extracellular domain of gp41 (540-686) was cloned into the Xmn I site of the expression vector pMal-p2 (New England Biolab) to give M41. The gp41 sequence was amplified from pgtat (Malim et al., 1988, Nature 355: 181-183) by using polymerase chain reaction (PCR) with upstream primer 10 5'-ATGACGCTGACGGTACAGGCC-3' (primer A) and downstream primer 5'-TGACTAAGCTTAATACCACAGCCAATTTGTTAT-3' (primer B). M41-P was constructed by using the T7-Gen in vitro mutagenesis kit from United States Biochemicals (USB) following the supplier's 15 instructions. The mutagenic primer (5'-GGAGCTGCTTGGGGCCCCAGAC-3') introduces an Ile to Pro mutation in M41 at position 578. M41Δ107, from which the DP-107 region has been deleted, was made using a deletion mutagenic primer 5'- 20 CCAAATCCCCAGGAGCTGCTCGAGCTGCACTATACCAGAC-3' (primer C) following the USB T7-Gen mutagenesis protocol. M41Δ178, from which the DP-178 region has been deleted, was made by cloning the DNA fragment corresponding to gp41 amino acids 540-642 into the 25 Xmn I site of pMal-p2. Primer A and 5'-ATAGCTTCTAGATTAATTGTTAATTTCTCTGTCCC-3' (primer D) were used in the PCR with the template pgtat to generate the inserted DNA fragments. M41-P was used as the template with primer A and D in PCR to generate M41- 30 PΔ178. All inserted sequences and mutated residues 35

were checked by restriction enzyme analysis and confirmed by DNA sequencing.

#### 8.1.2. PURIFICATION AND CHARACTERIZATION OF FUSION PROTEINS

5        The fusion proteins were purified according to the protocol described in the manufacturer's brochure of protein fusion and purification systems from New England Biolabs (NEB). Fusion proteins (10 ng) were analyzed by electrophoresis on 8% SDS polyacrylamide  
10        gels. Western blotting analysis was performed as described by Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2d Ed, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, Ch. 18, pp. 64-75. An HIV-1 positive serum diluted 1000-fold,  
15        or a human Fab derived from repertoire cloning was used to react with the fusion proteins. The second antibody was HRP-conjugated goat antihuman Fab. An ECL Western blotting detection system (Amersham) was used to detect the bound antibody. A detailed  
20        protocol for this detection system was provided by the manufacturer. Rainbow molecular weight markers (Amersham) were used to estimate the size of fusion proteins.

#### 25        8.1.3. CELL FUSION ASSAYS FOR ANTI-HIV ACTIVITY

Cell fusion assays were performed as previously described (Matthews et al., 1987, Proc. Natl. Acad. Sci. USA 84: 5424-5481). CEM cells ( $7 \times 10^4$ ) were incubated with HIV-1<sub>IIIb</sub> chronically infected CEM cells  
30        ( $10^4$ ) in 96-well flat-bottomed half-area plates (Costar) in 100  $\mu$ l culture medium. Peptide and fusion proteins at various concentrations in 10  $\mu$ l culture medium were incubated with the cell mixtures at 37°C for 24 hours. Multinucleated syncytia were estimated  
35        with microscopic examination. Both M41 and M41-P did

not show cytotoxicity at the concentrations tested and shown in FIG. 8.

Inhibition of HIV-1 induced cell-cell fusion activity was carried out in the presence of 10 nM DP178 and various concentrations of M41Δ178 or M41-PA178 as indicated in FIG. 9. There was no observable syncytia in the presence of 10 nM DP178. No peptide or fusion protein was added in the control samples.

8.1.4. ELISA ANALYSIS OF DP178 BINDING TO THE LEUCINE ZIPPER MOTIF OF GP41

The amino acid sequence of DP178 used is: YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF. For enzyme linked immunoassay (ELISA), M41Δ178 or M41-PA178 (5 μg/ml) in 0.1M NaHCO<sub>3</sub>, pH 8.6, were coated on 96 wells Linbro ELISA plates (Flow Lab, Inc.) overnight. Each well was washed three times with distilled water then blocked with 3% bovine serum albumin (BSA) for 2 hours. After blocking, peptides with 0.5% BSA in TBST (40 mM Tris-HCl pH7.5, 150 mM NaCl, 0.05% Tween 20) were added to the ELISA plates and incubated at room temperature for 1 hour. After washing three times with TBST, Fab-d was added at a concentration of 10 ng/ml with 0.5% BSA in TBST. The plates were washed three times with TBST after incubation at room temperature for 1 hour. Horse radish peroxidase (HRP) conjugated goat antihuman Fab antiserum at a 2000 fold dilution in TBST with 0.5% BSA was added to each well and incubated at room temperature for 45 minutes. The plates were then washed four times with TBST. The peroxidase substrate o-phenylene diamine (2.5 mg/ml) and 0.15% H<sub>2</sub>O<sub>2</sub> were added to develop the color. The reaction was stopped with an equal volume of 4.5 N H<sub>2</sub>SO<sub>4</sub> after incubation at room temperature for 10 minutes. The optical density of the stopped reaction mixture was measured with a micro plate reader

(Molecular Design) at 490 nm. Results are shown in FIG. 10.

## 8.2. RESULTS

### 8.2.1. THE EXPRESSION AND CHARACTERIZATION OF THE ECTODOMAIN OF gp41

5           As a step toward understanding the roles of the two helical regions in gp41 structure and function, the ectodomain of gp41 was expressed as a maltose binding fusion protein (M41) (FIG. 7). The fusogenic  
10 peptide sequence at the N-terminal of gp41 was omitted from this recombinant protein and its derivatives to improve solubility. The maltose binding protein facilitated purification of the fusion proteins under relatively mild, non-denaturing conditions. Because  
15 the M41 soluble recombinant gp41 was not glycosylated, lacked several regions of the transmembrane protein (*i.e.*, the fusion peptide, the membrane spanning, and the cytoplasmic domains), and was expressed in the absence of gp120, it was not expected to precisely  
20 reflect the structure of native gp41 on HIV-1 virions. Nevertheless, purified M41 folded in a manner that preserved certain discontinuous epitopes as evidenced by reactivity with human monoclonal antibodies, 98-6, 126-6, and 50-69, previously shown to bind  
25 conformational epitopes on native gp41 expressed in eukaryotic cells (Xu et al., 1991, J. Virol. 65: 4832-4838; Chen, 1994, J. Virol. 68:2002-2010). Thus, at least certain regions of native gp41 defined by these antibodies appear to be reproduced in the recombinant  
30 fusion protein M41. Furthermore, M41 reacted with a human recombinant Fab (Fab-d) that recognizes a conformational epitope on gp41 and binds HIV-1 virions as well as HIV-1 infected cells but not uninfected cells as analyzed by FACS. Deletion of either helix  
35 motif, *i.e.*, DP107 or DP178, of the M41 fusion protein

eliminated reactivity with Fab-d. These results indicate that both helical regions, separated by 60 amino acids in the primary sequence, are required to maintain the Fab-d epitope.

5

#### 8.2.2. ANTI-HIV ACTIVITY OF THE RECOMBINANT ECTODOMAIN OF GP41

The wild type M41 fusion protein was tested for anti-HIV-1 activity. As explained, *supra*, synthetic  
10 peptides corresponding to the leucine zipper (DP107) and the C-terminal putative helix (DP178) show potent anti-HIV activity. Despite inclusion of both these regions, the recombinant M41 protein did not affect HIV-1 induced membrane fusion at concentrations as  
15 high as 50  $\mu$ M (Table XXV, below).

TABLE XXV

DISRUPTION OF THE LEUCINE ZIPPER OF  
GP41 FREES THE ANTI-HIV MOTIF

20		<u>DP107</u>	<u>DP178</u>	<u>M41</u>	<u>M41-P</u>	<u>M41-PA178</u>
	Cell fusion (IC <sub>50</sub> )	1 $\mu$ M	1 nM	> 50 $\mu$ M	83 nM	> 50 $\mu$ M
25	Fab-D binding (K <sub>D</sub> )	-	-	3.5x10 <sup>-9</sup>	2.5x10 <sup>-8</sup>	-
	HIV infectiv- ity (IC <sub>50</sub> )	1 $\mu$ M	80 nM	> 16 $\mu$ M	66 nM	> 8 $\mu$ M

30 1 The affinity constants of Fab-d binding to the fusion proteins were determined using a protocol described by B. Friguet et al., 1985, J. Immunol. Method. 77:305-319.

- = No detectable binding of Fab-d to the fusion proteins.

35 *Antiviral Infectivity Assays.* 20  $\mu$ l of serially diluted virus stock was incubated for 60 minutes at ambient temperature with 20  $\mu$ l of the indicated



concentration of purified recombinant fusion protein in RPMI 1640 containing 10% fetal bovine serum and antibiotics in a 96-well microtiter plate. 20  $\mu$ l of CEM4 cells at  $6 \times 10^5$  cells/ml were added to each well, and cultures were incubated at 37°C in a humidified CO<sub>2</sub> incubator. Cells were cultured for 9 days by the addition of fresh medium every 2 to 3 days. On days 5, 7, and 9 postinfection, supernatant samples were assayed for reverse transcriptase (RT) activity, as described below, to monitor viral replication. The 50% tissue culture infectious dose (TCID<sub>50</sub>) was calculated for each condition according to the formula of Reed & Muench, 1937, Am. J. Hyg. 27:493-497. RT activity was determined by a modification of the published methods of Goff et al., 1981, J. Virol. 38:239-248 and Willey et al., 1988, J. Virol. 62:139-147 as described in Chen et al., 1993, AIDS Res. Human Retroviruses 9:1079-1086.

Surprisingly, a single amino acid substitution, proline in place of isoleucine in the middle of the leucine zipper motif, yielded a fusion protein (M41-P) which did exhibit antiviral activity (Table XXV and Fig. 8). As seen in Table XXV, M41-P blocked syncytia formation by 90% at approximately 85 nM and neutralized HIV-1<sub>IIIB</sub> infection by 90% at approximately 70 nM concentrations. The anti-HIV-1 activity of M41-P appeared to be mediated by the C-terminal helical sequence since deletion of that region from M41-P yielded an inactive fusion protein, M41-PA178 (Table XXV). This interpretation was reinforced by experiments demonstrating that a truncated fusion protein lacking the DP178 sequence, M41 $\Delta$ 178, abrogated the potent anti-fusion activity of the DP178 peptide in a concentration-dependent manner (FIG. 9). The same truncated fusion protein containing the proline mutation disrupting the leucine zipper, M41-PA178, was not active in similar competition experiments (FIG. 9). The results indicate that the DP178 peptide associates with a second site on gp41 whose interactive structure is dependent on a wild type leucine zipper sequence. A similar interaction may occur within the wild type fusion protein, M41, and act to form an intramolecular clasp which sequesters

the DP178 region, making it unavailable for anti-viral activity.

5 A specific association between these two domains is also indicated by other human monoclonal Fab-d studies. For example, Fab-d failed to bind either the DP178 peptide or the fusion protein M41Δ178, but its epitope was reconstituted by simply mixing these two reagents together (FIG. 10). Again, the proline mutation in the leucine zipper domain of the fusion protein, M41-PA178, failed to reconstitute the epitope  
10 in similar mixing experiments.

9. EXAMPLE: METHOD FOR COMPUTER-ASSISTED  
IDENTIFICATION OF DP107-LIKE  
AND DP178-LIKE SEQUENCES

15 A number of known coiled-coil sequences have been well described in the literature and contain heptad repeat positioning for each amino acid. Coiled-coil nomenclature labels each of seven amino acids of a heptad repeat A through G, with amino acids A and D  
20 tending to be hydrophobic positions. Amino acids E and G tend to be charged. These four positions (A, D, E, and G) form the amphipathic backbone structure of a monomeric alpha-helix. The backbones of two or more amphipathic helices interact with each other to form  
25 di-, tri-, tetrameric, etc., coiled-coil structures. In order to begin to design computer search motifs, a series of well characterized coiled coils were chosen including yeast transcription factor GCN4, Influenza Virus hemagglutinin loop 36, and human proto-oncogenes  
30 c-Myc, c-Fos, and c-Jun. For each peptide sequence, a strict homology for the A and D positions, and a list of the amino acids which could be excluded for the B, C, E, F, and G positions (because they are not observed in these positions) was determined. Motifs  
35 were tailored to the DP107 and DP178 sequences by

deducing the most likely possibilities for heptad positioning of the amino acids of HIV-1 Bru DP-107, which is known to have coiled-coil structure, and HIV-1 Bru DP178, which is still structurally undefined. The analysis of each of the sequences is contained in FIG. 12. For example, the motif for GCN4 was designed as follows:

1. The only amino acids (using standard single letter amino acid codes) found in the A or D positions of GCN4 were [LMNV].
2. All amino acids were found at B, C, E, F, and G positions except {CFGIMPTW}.
3. The PESEARCH motif would, therefore, be written as follows:  
 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-  
 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-  
 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-  
 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)

Translating or reading the motif: "at the first A position either L, M, N, or V must occur; at positions B and C (the next two positions) accept everything except C, F, G, I, M, P, T, or W; at the D position either L, M, N, or V must occur; at positions E, F, and G (the next 3 positions) accept everything except C, F, G, I, M, P, T, or W." This statement is contained four times in a 28-mer motif and five times in a 35-mer motif. The basic motif key then would be: [LMNV]-{CFGIMPTW}. The motif keys for the remaining well described coiled-coil sequences are summarized in FIG. 12.

The motif design for DP107 and DP178 was slightly different than the 28-mer model sequences described above due to the fact that heptad repeat positions are not defined and the peptides are both longer than 28 residues. FIG. 13 illustrates several possible

sequence alignments for both DP107 and DP178 and also includes motif designs based on 28-mer, 35-mer, and full-length peptides. Notice that only slight differences occur in the motifs as the peptides are lengthened. Generally, lengthening the base peptide  
5 results in a less stringent motif. This is very useful in broadening the possibilities for identifying DP107-or DP-178-like primary amino acid sequences referred to in this document as "hits".

10 In addition to making highly specific motifs for each type peptide sequence to be searched, it is also possible to make "hybrid" motifs. These motifs are made by "crossing" two or more very stringent motifs to make a new search algorithm which will find not only both "parent" motif sequences but also any  
15 peptide sequences which have similarities to one, the other, or both "parents". For example, in FIG. 14 the "parent" sequence of GCN4 is crossed with each of the possible "parent" motifs of DP-107. Now the hybrid motif must contain all of the amino acids found in the  
20 A and D positions of both parents, and exclude all of the amino acids not found in either parent at the other positions. The resulting hybrid from crossing GCN4 or [LMNV]{CFGIMPTW} and DP107 (28-mer with the first L in the D position) or [ILQT]{CDFIMPST}, is  
25 [ILMNQTV]{CFIMPT}. Notice that now only two basic hybrid motifs exist which cover both framing possibilities, as well as all peptide lengths of the parent DP-107 molecule. FIG. 15 represents the "hybridizations" of GCN4 with DP-178. FIG. 16  
30 represents the "hybridizations" of DP107 and DP178. It is important to keep in mind that the represented motifs, both parent and hybrid, are motif keys and not the depiction of the full-length motif needed to actually do the computer search.

35

Hybridizations can be performed on any combination of two or more motifs. FIG. 17 summarizes several three-motif hybridizations including GCN4, DP107 (both frames), and DP178 (also both frames). Notice that the resulting motifs are now becoming much more similar to each other. In fact, the first and third hybrid motifs are actually subsets of the second and fourth hybrid motifs respectively. This means that the first and third hybrid motifs are slightly more stringent than the second and fourth. It should also be noted that with only minor changes in these four motifs, or by hybridizing them, a single motif could be obtained which would find all of the sequences. However, it should be remembered that stringency is also reduced. Finally, the most broad-spectrum and least-stringent hybrid motif is described in FIG. 18 which summarizes the hybridization of GCN4, DP107 (both frames), DP178 (both frames), c-Fos, c-Jun, c-Myc, and Flu loop 36.

A special set of motifs was designed based on the fact that DP-178 is located only approximately ten amino acids upstream of the transmembrane spanning region of gp41 and just C-terminal to a proline which separates DP107 and DP178. It has been postulated that DP178 may be an amphipathic helix when membrane associated, and that the proline might aid in the initiation of the helix formation. The same arrangement was observed in Respiratory Syncytial Virus; however, the DP178-like region in this virus also had a leucine zipper just C-terminal to the proline. Therefore, N-terminal proline-leucine zipper motifs were designed to analyze whether any other viruses might contain this same pattern. The motifs are summarized in FIG. 19.

The PC/Gene protein database contains 5879 viral amino acid sequences (library file PVIRUSES; CD-ROM

release 11.0). Of these, 1092 are viral enveloped or glycoprotein sequences (library file PVIRUSE1). Tables V through XIV contain lists of protein sequence names and motif hit locations for all the motifs searched.

5

10. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION  
OF DP107 AND DP178-LIKE SEQUENCES  
IN HUMAN IMMUNODEFICIENCY VIRUS

FIG. 20 represents search results for HIV-1 BRU isolate gp41 (PC/Gene protein sequence PENV\_HV1BR). Notice that the hybrid motif which crosses DP-107 and DP-178 (named 107x178x4; the same motif as found in FIG. 16 found three hits including amino acids 550-599, 636-688, and 796-823. These areas include DP-107 plus eight N-terminal and four C-terminal amino acids; DP178 plus seven N-terminal and ten C-terminal amino acids; and an area inside the transmembrane region (cytoplasmic). FIG. 20 also contains the results obtained from searching with the motif named ALLMOTI5, for which the key is found in FIG. 17 ({CDGHP}{CFP}x5). This motif also found three hits including DP107 (amino acids 510-599), DP178 (615-717), and a cytoplasmic region (772-841). These hits overlap the hits found by the motif 107x178x4 with considerable additional sequences on both the amino and carboxy termini. This is not surprising in that 107x178x4 is a subset of the ALLMOTI5 hybrid motif. Importantly, even though the stringency of ALLMOTI5 is considerably less than 107x178x4, it still selectively identifies the DP107 and DP178 regions of gp41 shown to contain sequences for inhibitory peptides of HIV-1. The results of these two motif searches are summarized in Table V under the PC/Gene protein sequence name PENV HV1BR. The proline-leucine zipper motifs also gave several hits in HIV-1 BRU including 503-525 which is

at the very C-terminus of gp120, just upstream of the cleavage site (P7LZIPC and P12LZIPC); and 735-768 in the cytoplasmic domain of gp41 (P23LZIPC). These results are found in Tables VIII, IX, and X under the same sequence name as mentioned above. Notice that  
5 the only area of HIV-1 BRU which is predicted by the Lupas algorithm to contain a coiled-coil region, is from amino acids 635-670. This begins eight amino acids N-terminal to the start and ends eight amino acids N-terminal to the end of DP178. DP107, despite  
10 the fact that it is a known coiled coil, is not predicted to contain a coiled-coil region using the Lupas method.

11. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION  
15 OF DP107-LIKE AND DP178-LIKE  
SEQUENCES IN HUMAN RESPIRATORY  
SYNCYTIAL VIRUS

FIG. 21 represents search results for Human Respiratory Syncytial Virus (RSV; Strain A2) fusion glycoprotein F1 (PC/Gene protein sequence name PVGLF\_HRSVA). Motif 107x178x4 finds three hits including amino acids 152-202, 213-243, and 488-515. The arrangement of these hits is similar to what is found in HIV-1 except that the motif finds two regions with similarities to DP-178, one just downstream of what  
20 would be called the DP107 region or amino acids 213-243, and one just upstream of the transmembrane region (also similar to DP178) or amino acids 488-515. Motif ALLMOTI5 also finds three areas including amino acids  
25 116-202, 267-302, and 506-549. The proline-leucine zipper motifs also gave several hits including amino acids 205-221 and 265-287 (P1LZIPC 265-280, P12LZIPC), and 484-513 (P7LZIPC and P12LZIPC 484-506, P23LZIPC). Notice that the PLZIP motifs also identify regions  
30 which share location similarities with DP-178 of HIV-1.  
35

12. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP107-LIKE AND DP178-LIKE SEQUENCES  
IN SIMIAN IMMUNODEFICIENCY VIRUS

Motif hits for Simian immunodeficiency Virus gp41  
(AGM3 isolate; PC/Gene protein sequence name  
5 PENV\_SIVAG) are shown in FIG. 22. Motif 107x178x4  
finds three hits including amino acids 566-593, 597-  
624, and 703-730. The first two hits only have three  
amino acids between them and could probably be  
combined into one hit from 566-624 which would  
10 represent a DP107-like hit. Amino acids 703 to 730  
would then represent a DP178-like hit. ALLMOTI5 also  
finds three hits including amino acids 556-628 (DP107-  
like), 651-699 (DP178-like), and 808-852 which  
represents the transmembrane spanning region. SIV  
15 also has one region from 655-692 with a high  
propensity to form a coiled coil as predicted by the  
Lupas algorithm. Both 107x178x4 and ALLMOTI5 motifs  
find the same region. SIV does not have any PLZIP  
motif hits in gp41.  
20 The identification of DP178/DP107 analogs for a  
second SIV isolate (MM251) is demonstrated in the  
Example presented, below, in Section 19.

13. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
25 DP107-LIKE AND DP178 LIKE SEQUENCES  
IN CANINE DISTEMPER VIRUS

Canine Distemper Virus (strain Onderstepoort)  
fusion glycoprotein F1 (PC/Gene Protein sequence name  
PVGLF\_CDVO) has regions similar to Human RSV which are  
30 predicted to be DP107-like and DP178-like (FIG. 23).  
Motif 107x178x4 highlights one area just C-terminal to  
the fusion peptide at amino acids 252-293. Amino  
acids 252-286 are also predicted to be coiled coil  
using the Lupas algorithm. Almost 100 amino acids C-  
35 terminal to the first region is a DP178-like area at  
residues 340-367. ALLMOTI5 highlights three areas of



interest including: amino acids 228-297, which completely overlaps both the Lupas prediction and the DP107-like 107x178x4 hit; residues 340-381, which overlaps the second 107x178x4 hit; and amino acids 568-602, which is DP178-like in that it is located just N-terminal to the transmembrane region. It also overlaps another region (residues 570-602) predicted by the Lupas method to have a high propensity to form a coiled coil. Several PLZIP motifs successfully identified areas of interest including P6 and P12LZIPC which highlight residues 336-357 and 336-361 respectively; P1 and P12LZIPC which find residues 398-414; and P12 and P23LZIPC which find residues 562-589 and 562-592 respectively.

14. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN NEWCASTLE DISEASE VIRUS

FIG. 24 shows the motif hits found in Newcastle Disease Virus (strain Australia-Victoria/32; PC Gene protein sequence name PVGLF\_NDVA). Motif 107x178x4 finds two areas including a DP107-like hit at amino acids 151-178 and a DP178-like hit at residues 426-512. ALLMOTI5 finds three areas including residues 117-182, 231-272, and 426-512. The hits from 426-512 include a region which is predicted by the Lupas method to have a high coiled-coil propensity (460-503). The PLZIP motifs identify only one region of interest at amino acids 273-289 (P1 and 12LZIPC).

15. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN HUMAN PARAINFLUENZA VIRUS

Both motifs 107x178x4 and ALLMOTI5 exhibit DP107-like hits in the same region, 115-182 and 117-182 respectively, of Human Parainfluenza Virus (strain NIH 47885; PC/Gene protein sequence name PVGLF\_p13H4;

(FIG. 25). In addition, the two motifs have a DP178-like hit just slightly C-terminal at amino acids 207-241. Both motifs also have DP178-like hits nearer the transmembrane region including amino acids 457-497 and 462-512 respectively. Several PLZIP motif hits are  
5 also observed including 283-303 (P5LZIPC), 283-310 (P12LZIPC), 453-474 (P6LZIPC), and 453-481 (P23LZIPC). The Lupas algorithm predicts that amino acids 122-176 may have a propensity to form a coiled-coil.

10 16. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP107-LIKE AND DP178-LIKE SEQUENCES OF  
INFLUENZA A VIRUS

FIG. 26 illustrates the Lupas prediction for a coiled coil in Influenza A Virus (strain A/Aichi/2/68)  
15 at residues 379-436, as well as the motif hits for 107x178x4 at amino acids 387-453, and for ALLMOTI5 at residues 380-456. Residues 383-471 (38-125 of HA2) were shown by Carr and Kim to be an extended coiled coil when under acidic pH (Carr and Kim, 1993, Cell  
20 73: 823-832). The Lupas algorithm predicts a coiled-coil at residues 379-436. All three methods successfully predicted the region shown to actually have coiled-coil structure; however, ALLMOTI5 predicted the greatest portion of the 88 residue  
25 stretch.

17. EXAMPLE: POTENTIAL RESPIRATORY SYNCYTIAL VIRUS  
DP178/DP107 ANALOGS: CD AND  
ANTIVIRAL CHARACTERIZATION

30 In the Example presented herein, respiratory syncytial virus (RSV) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 11, above, were tested for anti-RSV activity. Additionally, circular dichroism (CD) structural analyses were conducted on  
35 the peptides, as discussed below. It is demonstrated

that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that several of these peptides exhibit a substantial helical character.

5

#### 17.1 MATERIALS AND METHODS

Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a  
10 Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptides were synthesized according to the methods described, above, in Section 6.1. Peptide concentrations were determined from  $A_{280}$  using Edlehoch's method (1967, Biochemistry 6:1948).

15

Anti-RSV antiviral activity assays: The assay utilized herein tested the ability of the peptides to disrupt the ability of HEp2 cells acutely infected with RSV (i.e., cells which are infected with a multiplicity of infection of greater than 2) to fuse  
20 and cause syncytial formation on a monolayer of uninfected an uninfected line of Hep-2 cells. The lower the observed level of fusion, the greater the antiviral activity of the peptide was determined to be.

25

Uninfected confluent monolayers of Hep-2 cells were grown in microtiter wells in 3% EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum [FBS; which had been heat inactivated for 30 minutes  
30 at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented at 3%, antibiotics (penicillin/streptomycin; Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

35

To prepare Hep2 cells for addition to uninfected cells, cultures of acutely infected Hep2 cells were

washed with DPBS (Dulbecco's Phosphate Buffered Saline w/o calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected Hep-2 cells.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Hep-2 cells, then adding peptides (at the dilutions described below) in 3% EMEM, and 100 acutely RSV-infected Hep2 cells per well. Wells were then incubated at 37°C for 48 hours.

After incubation, cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of either Crystal Violet stain or XTT. With respect to Crystal Violet, approximately 50µl 0.25% Crystal Violet stain in methanol were added to each well. The wells were rinsed immediately, to remove excess stain, and were allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

With respect to XTT (2,3-bis[2-Methoxy-4-nitro-5-sulfophenyl]-2H-tetrazolium-5-carboxyanilide inner salt), 50µl XTT (1mg/ml in RPMI buffered with 100mM HEPES, pH 7.2-7.4, plus 5% DMSO) were added to each well. The OD<sub>450/690</sub> was measured (after blanking against growth medium without cells or reagents, and against reagents) according to standard procedures.

Peptides: The peptides characterized in the study presented herein were:

1) peptides T-142 to T-155 and T-575, as shown in FIG. 27A, and peptides T-22 to T-27, T-68, T-334 and T-371 to T-375 and T-575, as shown in FIG. 27B;

2) peptides T-120 to T-141 and T-576, as shown in FIG. 27B, and peptides T-12, T-13, T-15, T-19, T-28 to T-30, T-66, T-69, T-70 and T-576, as shown in FIG. 27D; and  
3) peptides T-67 and T-104 to T-119 and T-384, as shown in FIG. 28A, and peptides T-71, T-613 to T-617, T-662 to T-676 and T-730, as shown in FIG. 28B.

The peptides of group 1 represent portions of the RSV F2 protein DP178/107-like region. The peptides of group 2 represent portions of the RSV F1 protein DP107-like region. The peptides of groups 3 represent portions of the RSV F1 protein DP178-like region.

Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used. The IC<sub>50</sub> data for each peptide represents the average of several experiments conducted utilizing that peptide.

## 17.2 RESULTS

The data summarized in FIGS. 27A-B and 28A-B represent antiviral and structural information obtained from peptides derived from the RSV F2 DP178/DP107-like F2 region (FIG. 27A-B), the RSV F1 DP-107-like region (FIG. 27C-D) and the RSV DP178-like F2 region (FIG. 28A-B).

As shown in FIGS. 27A-D, a number of the RSV DP178/DP107-like peptides exhibited a detectable level of antiviral activity. Peptides from the RSV DP178/DP107-like F2 region (FIG. 27A-B), for example, T-142 to T-145 and T-334 purified peptides, exhibited detectable levels of antiviral activity, as evidenced by their IC<sub>50</sub> values. Further, a number of RSV F1 DP107-like peptides (FIG. 27C-D) exhibited a sizable level of antiviral activity as purified peptides, including, for example, peptides T-124 to T-127, T-

131, T-135 and T-137 to T-139, as demonstrated by their low IC<sub>50</sub> values. In addition, CD analysis FIG. 27A, 27C) reveals that many of the peptides exhibit some detectable level of helical structure.

5 The results summarized in FIG. 28A-B demonstrate that a number of DP178-like purified peptides exhibit a range of potent anti-viral activity. These peptides include, for example, T-67, T-104, T-105 and T-107 to T-119, as listed in FIG. 28A, and T-665 to T-669 and T-671 to T-673, as listed in FIG. 28B. In addition,  
10 some of the DP178-like peptides exhibited some level of helicity.

Thus, the computer assisted searches described, hereinabove, successfully identified viral peptide domains that represent highly promising anti-RSV  
15 antiviral compounds.

18. EXAMPLE: POTENTIAL HUMAN PARAINFLUENZA VIRUS  
TYPE 3 DP178/DP107 ANALOGS: CD AND  
ANTIVIRAL CHARACTERIZATION

20 In the Example presented herein, human parainfluenza virus type 3 (HPIV3) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 15, above, were tested for anti-HPIV3 activity.  
25 Additionally, circular dichroism (CD) structural analyses were conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that several of  
30 these peptides exhibit a substantial helical character.

18.1 MATERIALS AND METHODS

Structural analyses: Structural analyses  
35 consisted of circular dichroism (CD) studies. The CD

spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were  
5 determined from  $A_{280}$  using Edlehoch's method (1967, Biochemistry 6:1948).

Anti-HPIV3 antiviral activity assays: The assay utilized herein tested the ability of the peptides to  
10 disrupt the ability of Hep2 cells chronically infected with HPIV3 to fuse and cause syncytial formation on a monolayer of an uninfected line of CV-1W cells. The more potent the lower the observed level of fusion, the greater the antiviral activity of the peptide.

Uninfected confluent monolayers of CV-1W cells  
15 were grown in microtiter wells in 3% EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum [FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented  
20 at 3%, antibiotics/antimycotics (Gibco BRL Life Technologies Cat. No. 15040-017) added at 1%, and glutamine added at 1%.

To prepare Hep2 cells for addition to uninfected cells, cultures of chronically infected Hep2 cells  
25 were washed with DPBS (Dulbecco's Phosphate Buffered Saline w/o calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and  
30 resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected CV-1W cells.

The antiviral assay was conducted by, first,  
35 removing all media from the wells containing uninfected CV-1W cells, then adding peptides (at the

dilutions described below) in 3% EMEM, and 500 chronically HPIV3-infected Hep2 cells per well. Wells were then incubated at 37°C for 24 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Alternatively, instead of Crystal Violet analysis, cells were assayed with XTT, as described, above, in Section 17.1.

Peptides: The peptides characterized in the study presented herein were:

- 1) Peptides 157 to 188, as shown in FIG. 29A, and peptides T-38 to T-40, T-42 to T-46 and T-582, as shown in FIG. 29B. These peptides are derived from the DP107 region of the HPIV3 F1 fusion protein (represented by HPF3 107, as shown in FIG. 29A); and
- 2) Peptides 189 to 210, as shown in FIG. 30A, and T-269, T-626, T-383 and T-577 to T-579, as shown in FIG. 30B. These peptides are primarily derived from the DP178 region of the HPIV3 F1 fusion protein (represented by HPF3 178, as shown in FIG. 30A). Peptide T-626 contains two mutated amino acid residues (represented by a shaded background). Additionally, peptide T-577 represents F1 amino acids 65-100, T-578 represents F1 amino acids 207-242 and T-579 represents F1 amino acids 273-309.

Each peptide was tested at 2-fold serial dilutions ranging from 500µg/ml to approximately



500ng/ml. For each of the assays, a well containing no peptide was also used.

## 18.2 RESULTS

5 The data summarized in FIGS. 29A-C and 30A-B represent antiviral and structural information obtained from peptides derived from the HPIV3 fusion protein DP107-like region (FIG. 29A-C) and the HPIV3 fusion protein DP178-like region (FIG. 30A-B).

10 As shown in FIG. 29A-B, a number of the HPIV3 DP107-like peptides exhibited potent levels of antiviral activity. These peptides include, for example, peptides T-40, T-172 to T-175, T-178, T-184 and T-185.

15 CD analysis reveals that a number of the peptides exhibit detectable to substantial level of helical structure. The CD spectra for one of the peptides, 184, which exhibits substantial helicity is summarized in FIG. 29C.

20 The results summarized in FIG. 30A-B demonstrate that a number of the DP178-like peptides tested exhibit a range of anti-viral activity. These peptides include, for example, peptides 194 to 211, as evidenced by their low  $IC_{50}$  values. In fact, peptides 201 to 205 exhibit  $IC_{50}$  values in the nanogram/ml  
25 range. In addition, many of the DP178-like peptides exhibited some level of helicity.

Thus, the computer assisted searches described, hereinabove, have successfully identified viral  
30 peptide domains that represent highly promising anti-HPIV3 antiviral compounds.

## 19. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN IMMUNODEFICIENCY VIRUS

35 FIG. 31 represents search results for SIV isolate MM251 (PC/Gene® protein sequence PENV\_SIVM2). Both

107x178x4 and ALLMOTI5 search motifs identified two regions with similarities to DP107 and/or DP178.

The peptide regions found by 107x178x4 were located at amino acid residues 156-215 and 277-289. The peptide regions found by ALLMOTI5 were located at amino acid residues 156-219 and 245-286. Both motifs, therefore, identify similar regions.

Interestingly, the first SIV peptide region (i.e., from amino acid residue 156 to approximately amino acid residue 219) correlates with a DP107 region, while the second region identified (i.e., from approximately amino acid residue 245 to approximately amino acid residue 289) correlates with the DP178 region of HIV. In fact, an alignment of SIV isolate MM251 and HIV isolate BRU, followed by a selection of the best peptide matches for HIV DP107 and DP178, reveals that the best matches are found within the peptide regions identified by the 107x178x4 and ALLMOTI5 search motifs.

It should be noted that a potential coiled-coil region at amino acid residues 242-282 is predicted by the Lupas program. This is similar to the observation in HIV in which the coiled-coil is predicted by the Lupas program to be in the DP178 rather than in the DP107 region. It is possible, therefore, that SIV may be similar to HIV in that it may contain a coiled-coil structure in the DP107 region, despite such a structure being missed by the Lupas algorithm. Likewise, it may be that the region corresponding to a DP178 analog in SIV may exhibit an undefined structure, despite the Lupas program's prediction of a coiled-coil structure.

35

20. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP178/DP107 ANALOGS IN EPSTEIN-BARR  
VIRUS

The results presented herein describe the identification of DP178/DP107 analogs within two different Epstein-Barr Virus proteins. Epstein-Barr is a human herpes virus which is the causative agent of, for example, infectious mononucleosis (IM), and is also associated with nasopharyngeal carcinomas (NPC), Burkitt's lymphoma and other diseases. The virus predominantly exists in the latent form and is activated by a variety of stimuli.

FIG. 32 depicts the search motif results for the Epstein-Barr Virus (Strain B95-8; PC/Gene® protein sequence PVGLB\_EBV) glycoprotein gp110 precursor (gp115). The 107x178x4 motif identified two regions of interest, namely the regions covered by amino acid residues 95-122 and 631-658. One PZIP region was identified at amino acid residue 732-752 which is most likely a cytoplasmic region of the protein. The Lupas algorithm predicts a coiled-coil structure for amino acids 657-684. No ALLMOTI5 regions were identified.

FIG. 33 depicts the search motif results for the Zebra (or EB1) trans-activator protein (BZLF1) of the above-identified Epstein-Barr virus. This protein is a transcription factor which represents the primary mediator of viral reactivation. It is a member of the b-ZIP family of transcription factors and shares significant homology with the basic DNA-binding and dimerization domains of the cellular oncogenes c-fos and C/EBP. The Zebra protein functions as a homodimer.

Search results demonstrate that the Zebra protein exhibits a single region which is predicted to be either of DP107 or DP178 similarity, and is found between the known DNA binding and dimerization regions of the protein. Specifically, this region is located

at amino acid residues 193-220, as shown in FIG. 33.  
The Lupas program predicted no coiled-coil regions.

21. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP178/DP107 ANALOGS IN MEASLES VIRUS

5 FIG. 34 illustrates the motif search results for  
the fusion protein F1 of measles virus, strain  
Edmonston (PC Gene® protein sequence PVGLF\_MEASE),  
successfully identifying DP178/DP107 analogs.

The 107x178x4 motif identifies a single region at  
10 amino acid residues 228-262. The ALLMOTI5 search  
motif identifies three regions, including amino acid  
residues 116-184, 228-269 and 452-500. Three regions  
containing proline residues followed by a leucine  
zipper-like sequence were found beginning at proline  
15 residues 214, 286 and 451.

The Lupas program identified two regions it  
predicted had potential for coiled-coil structure,  
which include amino acid residues 141-172 and 444-483.

20 22. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP178/DP107 ANALOGS IN HEPATITIS B  
VIRUS

FIG. 35 depicts the results of a PZIP motif  
search conducted on the Hepatitis B virus subtype AYW.  
Two regions of interest within the major surface  
25 antigen precursor S protein were identified. The  
first lies just C-terminal to the proposed fusion  
peptide of the major surface antigen (Hbs) which is  
found at amino acid residues 174-191. The second  
region is located at amino acid residues 233-267. The  
30 Lupas program predicts no coiled-coil repeat regions.

In order to test the potential anti-HBV antiviral  
activity of these D178/DP107 analog regions, peptides  
derived from area around the analog regions are  
synthesized, as shown in FIG. 52A-B. These peptides  
35 represent one amino acid peptide "walks" through the

putative DP178/DP107 analog regions. The peptides are synthesized according to standard Fmoc chemistry on Rinkamide MBHA resins to provide for carboxy terminal blockade (Chang, C.D. and Meinhofer, J., 1978, Int. J. Pept. Protein Res. 11:246-249; Fields, G.B. and Noble, R.L., 1990, Int. J. Pept. Protein Res. 35:161-214). Following complete synthesis, the peptide amino-terminus is blocked through automated acetylation and the peptide is cleaved with trifluoroacetic acid (TFA) and the appropriate scavengers (King, D.S. et al., 1990, Int. J. Pept. Res. 36:255-266). After cleavage, the peptide is precipitated with ether and dried under vacuum for 24 hours.

The anti-HBV activity of the peptides is tested by utilizing standard assays to determine the test peptide concentration required to cause an acceptable (e.g., 90%) decrease in the amount of viral progeny formed by cells exposed to an HBV viral inoculum. Candidate antiviral peptides are further characterized in model systems such as wood chuck tissue culture and animal systems, prior to testing on humans.

23. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP178/DP107 ANALOGS IN SIMIAN MASON-  
PFIZER MONKEY VIRUS

The results depicted herein illustrate the results of search motifs conducted on the Simian Mason-Pfizer monkey virus. The motifs reveal DP178/DP107 analogs within the enveloped (TM) protein GP20, as shown in FIG. 36.

The 107x178x4 motifs identifies a region at amino acid residues 422-470. The ALLMOTI5 finds a region at amino acid residues 408-474. The Lupas program predicted a coiled-coil structure a amino acids 424-459.

35

24. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP178/DP107 ANALOGS IN BACTERIAL  
PROTEINS

The results presented herein demonstrate the identification of DP178/DP107 analogs corresponding to sequences present in proteins of a variety of bacterial species.

FIG. 37 depicts the search motif results for the *Pseudomonas aeruginosa* fimbrial protein (Pilin). Two regions were identified by motifs 107x178x4 and ALLMOTI5. The regions located at amino acid residues 30-67 and 80-144 were identified by the 107x178x4 motif. The regions at amino acid residues 30-68 and 80-125 were identified by the ALLMOTI5.

FIG. 38 depicts the search motif results for the *Pseudomonas gonorrhoeae* fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 66-97 was identified by the 107x178x4 motif. The region located at amino acid residues 66-125 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

FIG. 39 depicts the search motif results for the *Hemophilus Influenza* fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The region located at amino acid residues 102-148 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

FIG. 40 depicts the search motif results for the *Staphylococcus aureus* toxic shock syndrome *Hemophilus Influenza* fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The

region located at amino acid residues 102-148 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

5       FIG. 41 summarizes the motif search results conducted on the *Staphylococcus aureus* enterotoxin Type E protein. These results demonstrate the successful identification of DP178/DP107 analogs corresponding to peptide sequences within this protein, as described below.

10       The ALLMOTI5 motif identified a region at amino acid residues 22-27. The 107x178x4 motif identified two regions, with the first at amino acid residues 26-69 and the second at 88-115. A P12LZIPC motif search identified two regions, at amino acid residues 163-181 and 230-250.

15       The Lupas program predicted a region with a high propensity for coiling at amino acid residues 25-54. This sequence is completely contained within the first region identified by both ALLMOTI5 and 107x178x4 motifs.

20       FIG. 42 depicts the search motif results conducted on a second *Staphylococcus aureus* toxin, enterotoxin A. Two regions were identified by the ALLMOTI5 motif, at amino acid residues 22-70 and amino acid residues 164-205. The 107x178x4 motif found two  
25       regions, the first at amino acid residues 26-69 and the second at amino acid residues 165-192. A P23LZIPC motif search revealed a region at amino acid residues 216-250. No coiled-coil regions were predicted by the Lupas program.

30       FIG. 43 shows the motif search results conducted on the *E. coli* heat labile enterotoxin A protein, demonstrating that identification of DP178/DP107 analogs corresponding to peptides located within this protein. Two regions were identified by the ALLMOTI5  
35       motif, with the first residing at amino acid residues

55-115, and the second residing at amino acid residues 216-254. The 107x178x4 motif identified a single region at amino acid residues 78-105. No coiled-coil regions were predicted by the Lupas program.

5 25. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP178/DP107 ANALOGS WITHIN VARIOUS  
HUMAN PROTEINS

10 The results presented herein demonstrate the identification of DP178/DP107 analogs corresponding to peptide sequences present within several different human proteins.

15 FIG. 44 illustrates the search motif results conducted on the human c-fos oncoprotein. The ALLMOTI5 motif identified a single region at amino acid residues 155-193. The 107x178x4 motif identified one region at amino acid residues 162-193. The Lupas program predicted a region at amino acid residues 148-201 to have coiled-coil structure.

20 FIG. 45 illustrates the search motif results conducted on the human lupus KU autoantigen protein P70. The ALLMOTI5 motif identified a single region at amino acid residues 229-280. The 107x178x4 motif identified one region at amino acid residues 235-292. The Lupas program predicted a region at amino acid residues 232-267 to have coiled-coil structure.

25 FIG. 46 illustrates the search motif results conducted on the human zinc finger protein 10. The ALLMOTI5 motif identified a single region at amino acid residues 29-81. The 107x178x4 motif identified one region at amino acid residues 29-56. A P23LZIPC motif search found a single region at amino acid residues 420-457. The Lupas program predicted no coiled-coil regions.

35



26. EXAMPLE: POTENTIAL MEASLES VIRUS DP178/DP107  
ANALOGS: CD AND ANTIVIRAL  
CHARACTERIZATION

---

5 In the Example presented herein, measles (MeV)  
virus DP178-like peptides identified by utilizing the  
computer-assisted search motifs described in the  
Examples presented in Sections 9 and 21, above, are  
tested for anti-MeV activity. Additionally, circular  
dichroism (CD) structural analyses are conducted on  
the peptides, as discussed below. It is demonstrated  
10 that several of the identified peptides exhibit potent  
antiviral capability. Additionally, it is shown that  
none of the these peptides exhibit a substantial  
helical character.

15 26.1 MATERIALS AND METHODS

Structural analyses: The CD spectra were  
measured in a 10mM sodium phosphate, 150mM sodium  
chloride, pH 7.0, buffer at approximately 10mM  
concentrations, using a 1 cm pathlength cell on a  
20 Jobin/Yvon Autodichrograph Mark V CD  
spectrophotometer. Peptide concentrations were  
determined from  $A_{280}$  using Edlehoch's method (1967,  
Biochemistry 6:1948).

Anti-MeV antiviral activity syncytial reduction  
25 assay: The assay utilized herein tested the ability  
of the peptides to disrupt the ability of Vero cells  
acutely infected with MeV (*i.e.*, cells which are  
infected with a multiplicity of infection of 2-3) to  
fuse and cause syncytial formation on a monolayer of  
30 an uninfected line of Vero cells. The more potent the  
peptide, the lower the observed level of fusion, the  
greater the antiviral activity of the peptide.

Uninfected confluent monolayers of Vero cells  
were grown in microtiter wells in 10% FBS EMEM (Eagle  
35 Minimum Essential Medium w/o L-glutamine [Bio  
Whittaker Cat. No. 12-125F], with fetal bovine serum

[FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented at 10%, antibiotics/antimycotics (Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

5 To prepare acutely infected Vero cells for addition to the uninfected cells, cultures of acutely infected Vero cells were washed twice with HBSS (Bio Whittaker Cat. No. 10-543F) and cell monolayers were removed with trypsin (Bio Whittaker Cat. No. 17-161E).  
10 Once cells detached, media was added, any remaining clumps of cells were dispersed, and hemacytometer cell counts were performed.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Vero cells, then adding peptides (at the  
15 dilutions described below) in 10% FBS EMEM, and 50-100 acutely MeV-infected Vero cells per well. Wells were then incubated at 37°C for a maximum of 18 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the  
20 wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were  
25 then counted, using a dissecting microscope.

Anti-MeV antiviral activity plaque reduction assay: The assay utilized herein tested the ability of the peptides to disrupt the ability of MeV to infect permissive, uninfected Vero cells, leading to  
30 the infected cells' fusing with uninfected cells to produce syncytia. The lower the observed level of syncytial formation, the greater the antiviral activity of the peptide.

35 Monolayers of uninfected Vero cells are grown as described above.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Vero cells, then adding peptides (at the dilutions described below) in 10% FBS EMEM, and MeV stock virus at a final concentration of 30 plaque forming units (PFU) per well. Wells were then incubated at 37°C for a minimum of 36 hours and a maximum of 48 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Peptides: The peptides characterized in the study presented herein were peptides T-252A0 to T-256A0, T-257B1/C1, and T-258B1 to T-265B0, and T-266A0 to T-268A0, as shown in FIG. 47. These peptides represent a walk through the DP178-like region of the MeV fusion protein.

Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

## 26.2 RESULTS

The data summarized in FIG. 47 represents antiviral and structural information obtained via "peptide walks" through the DP178-like region of the MeV fusion protein.

As shown in FIG. 47, the MeV DP178-like peptides exhibited a range of antiviral activity as crude peptides. Several of these peptides were chosen for purification and further antiviral characterization.

The IC<sub>50</sub> values for such peptides were determined, as shown in FIG. 47, and ranged from 1.35µg/ml (T-257B1/C1) to 0.072µg/ml (T-265B1). None of the DP178-like peptides showed, by CD analysis, a detectable level of helicity.

Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified viral peptide domains that represent highly promising anti-MeV antiviral compounds.

#### 27. EXAMPLE: POTENTIAL SIV DP178/DP107 ANALOGS: ANTIVIRAL CHARACTERIZATION

In the Example presented herein, simian immunodeficiency virus (SIV) DP178-like peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9, 12 and 19, above, were tested for anti-SIV activity. It is demonstrated that several of the identified peptides exhibit potent antiviral capability.

##### 27.1 MATERIALS AND METHODS

Anti-SIV antiviral assays: The assay utilized herein were as reported in Langolis et al. (Langolis, A.J. et al., 1991, AIDS Research and Human Retroviruses 7:713-720).

Peptides: The peptides characterized in the study presented herein were peptides T-391 to T-400, as shown in FIG. 48. These peptides represent a walk through the DP178-like region of the SIV TM protein.

Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

## 27.2 RESULTS

The data summarized in FIG. 48 represents antiviral information obtained via "peptide walks" through the DP178-like region of the SIV TM protein.

5 As shown in FIG. 48, peptides T-391 to T-400 were tested and exhibited a potent antiviral activity as crude peptides.

10 Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified viral peptide domains that represent highly promising anti-SIV antiviral compounds.

### 28. EXAMPLE: ANTI-VIRAL ACTIVITY OF DP107 AND DP-178 PEPTIDE TRUNCATIONS AND MUTATIONS

15 The Example presented in this Section represents a study of the antiviral activity of DP107 and DP178 truncations and mutations. It is demonstrated that several of these DP107 and DP178 modified peptides exhibit substantial antiviral activity.

20

#### 28.1 MATERIALS AND METHODS

Anti-HIV assays: The antiviral assays performed were as those described, above, in Section 6.1. Assays utilized HIV-1/IIIB and/or HIV-2 NIH2 isolates. 25 Purified peptides were used, unless otherwise noted in FIGS. 49A-C.

Peptides: The peptides characterized in the study presented herein were:

- 30 1) FIGS. 49A-C present peptides derived from the region around and containing the DP178 region of the HIV-1 BRU isolate. Specifically, this region spanned from gp41 amino acid residue 615 to amino acid residue 717. The peptides listed contain 35 truncations of this region and/or mutations

which vary from the DP178 sequence amino acid sequence. Further, certain of the peptides have had amino- and/or carboxy-terminal groups either added or removed, as indicated in the figures; and

- 5           2) FIG. 50. presents peptides which represent truncations of DP107 and/or the gp41 region surrounding the DP107 amino acid sequence of HIV-1 BRU isolate. Certain of the peptides are unblocked or biotinylated, as indicated  
10           in the figure.

Blocked peptides contained an acyl N-terminus and an amido C-terminus.

## 28.2 RESULTS

15           Anti-HIV antiviral data was obtained with the group 1 DP178-derived peptides listed in FIG. 49A-C. The full-length, non-mutant DP178 peptide (referred to in FIG. 49A-C as T20) results shown are for 4ng/ml.

20           In FIG. 49A, a number of the DP178 truncations exhibited a high level of antiviral activity, as evidenced by their low  $IC_{50}$  values. These include, for example, test peptides T-50, T-624, T-636 to T-641, T-645 to T-650, T-652 to T-654 and T-656. T-50  
25           represents a test peptide which contains a point mutation, as indicated by the residue's shaded background. The HIV-1-derived test peptides exhibited a distinct strain-specific antiviral activity, in that none of the peptides tested on the HIV-2 NIHZ isolate demonstrated appreciable anti-HIV-2 antiviral  
30           activity.

          Among the peptides listed in FIG. 49B, are test peptides representing the amino (T-4) and carboxy (T-3) terminal halves of DP178 were tested. The amino terminal peptide was not active ( $IC_{50} > 400 \mu g/ml$ ) whereas  
35           the carboxy terminal peptide showed potent antiviral

activity ( $IC_{50}$  =  $3\mu g/ml$ ). A number of additional test peptides also exhibited a high level of antiviral activity. These included, for example, T-61/T-102, T-217 to T-221, T-235, T-381, T-677, T-377, T-590, T-378, T-591, T-271 to T-272, T-611, T-222 to T-223 and  
5 T-60/T-224. Certain of the antiviral peptides contain point mutations and/or amino acid residue additions which vary from the DP178 amino acid sequence.

10 In FIG. 49C, point mutations and/or amino and/or carboxy-terminal modifications are introduced into the DP178 amino acid sequence itself. As shown in the figure, the majority of the test peptides listed exhibit potent antiviral activity.

15 Truncations of the DP107 peptide (referred to in FIG. 50 as T21) were also produced and tested, as shown in FIG. 50. FIG. 50 also presents data concerning blocked and unblocked peptides which contain additional amino acid residues from the gp41 region in which the DP107 sequence resides. Most of these peptides showed antiviral activity, as evidenced by  
20 their low  $IC_{50}$  values.

Thus, the results presented in this Section demonstrate that not only do the full length DP107 and DP178 peptides exhibit potent antiviral activity, but truncations and/or mutant versions of these peptides  
25 can also possess substantial antiviral character.

29: EXAMPLE: POTENTIAL EPSTEIN-BARR DP178/DP107  
ANALOGS: ANTIVIRAL CHARACTERIZATION

30 In the Example presented herein, peptides derived from the Epstein-Barr (EBV) DP-178/DP107 analog region of the Zebra protein identified, above, in the Example presented in Section 20 are described and tested for anti-EBV activity. It is demonstrated that among these peptides are ones which exhibit potential anti-  
35 viral activity.

## 29.1 MATERIALS AND METHODS

### Electrophoretic Mobility Shift Assays (EMSA):

Briefly, an EBV Zebra protein was synthesized utilizing SP6 RNA polymerase in vitro transcription and wheat germ in vitro translation systems (Promega Corporation recommendations; Butler, E.T. and Chamberlain, M.J., 1984, J. Biol. Chem. 257:5772; Pelham, H.R.B. and Jackson, R.J., 1976, Eur. J. Biochem. 67:247). The in vitro translated Zebra protein was then preincubated with increasing amounts of peptide up to 250 ng/ml prior to the addition of 10,000 to 20,000 c.p.m. of a <sup>32</sup>P-labeled Zebra response element DNA fragment. After a 20 minute incubation in the presence of the response element, the reaction was analyzed on a 4% non-denaturing polyacrylamide gel, followed by autoradiography, utilizing standard gel-shift procedures. The ability of a test peptide to prevent Zebra homodimer DNA binding was assayed by the peptide's ability to abolish the response element gel migration retardation characteristic of a protein-bound nucleic acid molecule.

Peptides: The peptides characterized in this study represent peptide walks through the region containing, and flanked on both sides by, the DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. Specifically, the peptide walks covered the region from amino acid residue 173 to amino acid residue 246 of the EBV Zebra protein.

Each of the tested peptides were analyzed at a range of concentrations, with 150ng/ml being the lowest concentration at which any of the peptides exerted an inhibitory effect.



## 29.2 RESULTS

The EBV Zebra protein transcription factor contains a DP178/DP107 analog region, as demonstrated in the Example presented, above, in Section 20. This protein appears to be the primary factor responsible for the reactivation capability of the virus. A method by which the DNA-binding function of the Zebra virus may be abolished may, therefore, represent an effective antiviral technique. In order to identify potential anti-EBV DP178/DP107 peptides, therefore, peptides derived from the region identified in Section 20, above, were tested for their ability to inhibit Zebra protein DNA binding.

The test peptides' ability to inhibit Zebra protein DNA binding was assayed via the EMSA assays described, above, in Section 28.1. The data summarized in FIG. 51A-B presents the results of EMSA assays of the listed EBV test peptides. These peptides represent one amino acid "walks" through the region containing, and flanked on both sides by, the DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. As shown in FIG. 51A-B, the region from which these peptides are derived lies from EBV Zebra protein amino acid residue 173 to 246. A number of the test peptides which were assayed exhibited an ability to inhibit Zebra protein homodimer DNA binding, including 439, 441, 444 and 445.

Those peptides which exhibit an ability to inhibit Zebra protein DNA binding represent potential anti-EBV antiviral compounds whose ability to inhibit EBV infection can be further characterized.

The present invention is not to be limited in scope by the specific embodiments described which are intended as single illustrations of individual aspects

of the invention, and functionally equivalent methods  
and components are within the scope of the invention.  
Indeed, various modifications of the invention, in  
addition to those shown and described herein will  
become apparent to those skilled in the art from the  
5 foregoing description and accompanying drawings. Such  
modifications are intended to fall within the scope of  
the appended claims.

10

15

20

25

30

35